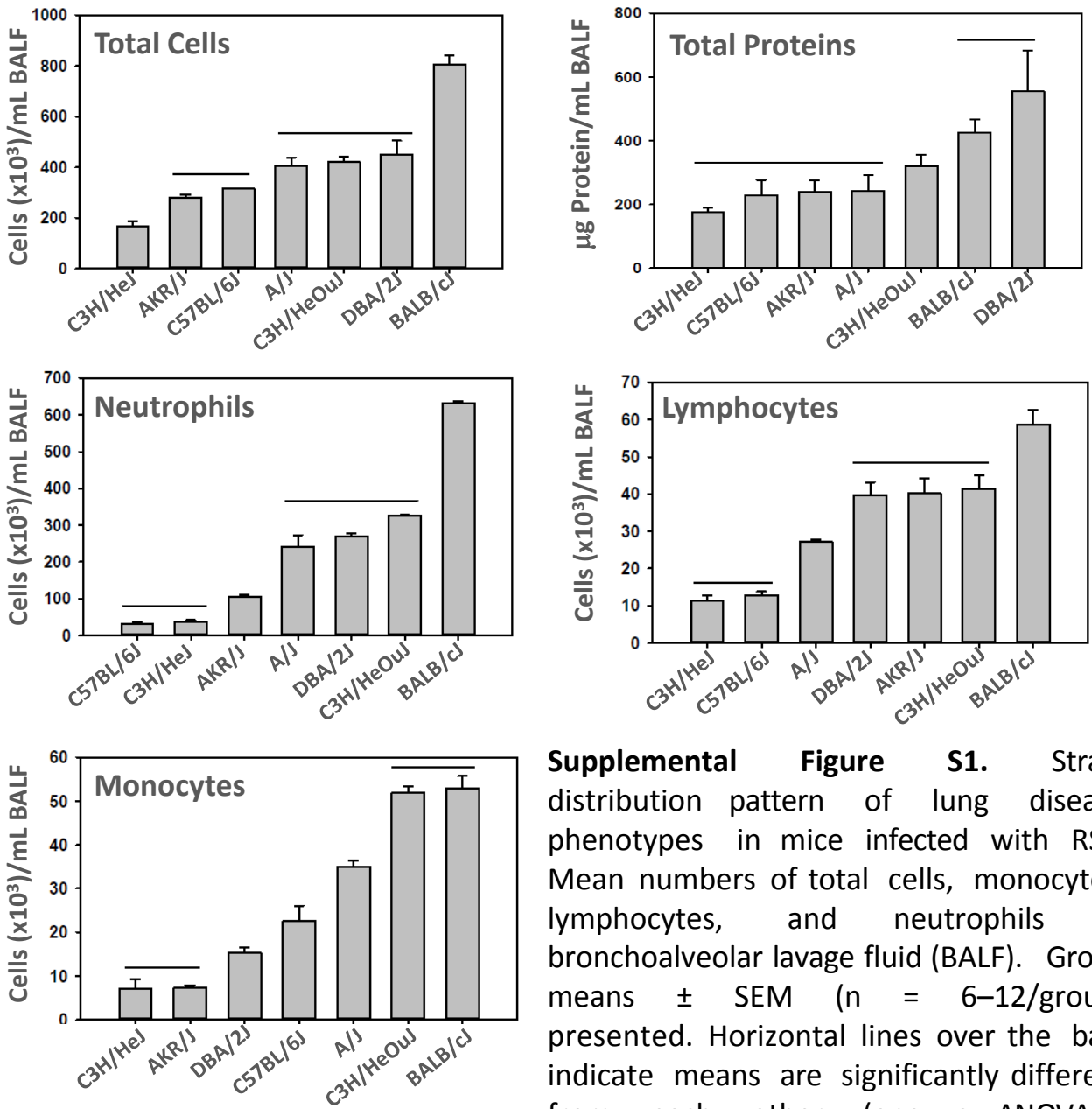


Supplemental Figure S1.



Supplemental Figure S1. Strain distribution pattern of lung disease phenotypes in mice infected with RSV. Mean numbers of total cells, monocytes, lymphocytes, and neutrophils in bronchoalveolar lavage fluid (BALF). Group means \pm SEM ($n = 6-12$ /group) presented. Horizontal lines over the bars indicate means are significantly different from each other (one-way ANOVA, $p < 0.05$).

Table S1. Lung genes significantly altered by respiratory syncytial virus (RSV) in C3H/HeOul (Oul) mice (One-Way ANOVA at p<0.01).

Blue(-): fold decrease by RSV vs vehicle. Red : fold increase by RSV vs vehicle.

Gene ID	p	FC-RSV 1 d	FC-RSV 5 d	RefSeq Transcript ID	Gene Symbol	Gene Title	Gene Ontology Biological Process
1438148_a	0.000207	47.49	1.85	NM_203320	<i>Cxcl3</i>	chemokine (C-X-C motif) ligand 3	0006935 // chemotaxis // inferred from electronic annotation//0006954 // inflammatory response // not
1450826_a	0.000532	30.08	2.38	NM_011315	<i>Saa3</i>	serum amyloid A 3	0006953 // acute-phase response // inferred from electronic annotation//0035634 // response to stilbenoid // inferred from
1427126_a	0.000011	20.30	1.88	NM_010478	<i>Hspa1b</i>	heat shock protein 1B	0000723 // telomere maintenance // inferred from mutant phenotype//0000902 // cell morphogenesis // inferred from
1452388_a	0.000002	17.83	1.49	NM_010479	<i>Hspa1a</i>	heat shock protein 1A	0000723 // telomere maintenance // inferred from mutant phenotype//0000902 // cell morphogenesis // inferred from
1449984_a	0.000086	12.91	1.25	NM_009140	<i>Cxcl2</i>	chemokine (C-X-C motif) ligand 2	0001975 // response to amphetamine // inferred from electronic annotation//0002237 // response to molecule of bacterial
1451054_a	0.000144	10.14	1.42	NM_008768	<i>Orm1</i>	orosomucoid 1	0002682 // regulation of immune system process // inferred from electronic annotation//0006810 // transport // inferred
1419075_s	0.000015	8.43	1.12	NM_009117//XM_00654	<i>Saa1</i>	serum amyloid A 1	0006953 // acute-phase response // inferred from electronic annotation//0008203 // cholesterol metabolic process //
1450297_a	0.000023	8.01	-1.09	NM_031168	<i>Il6</i>	interleukin 6	0001781 // neutrophil apoptotic process // inferred from direct assay//0001781 // neutrophil apoptotic process // inferred
1419561_a	0.000044	7.54	1.31	NM_011337	<i>Ccl3</i>	chemokine (C-C motif) ligand 3	0000165 // MAPK cascade // inferred from sequence or structural similarity//0001649 // osteoblast differentiation // inferred
1418930_a	0.000816	7.38	1.84	NM_021274	<i>Cxcl10</i>	chemokine (C-X-C motif) ligand 10	0002690 // positive regulation of leukocyte chemotaxis // not recorded//0006935 // chemotaxis // not recorded//0006954
1419728_a	0.000073	7.09	-1.00	NM_009141	<i>Cxcl5</i>	chemokine (C-X-C motif) ligand 5	0001776 // leukocyte homeostasis // inferred from mutant phenotype//0001816 // cytokine production // not
1460227_a	0.000017	6.49	1.13	NM_001044384//NM_01	<i>Timp1</i>	tissue inhibitor of metalloproteinase 1	0001775 // cell activation // not recorded//0007568 // aging // inferred from electronic annotation//0008284 // positive
1420438_a	0.000001	6.37	1.00	NM_011016	<i>Orm2</i>	orosomucoid 2	0002682 // regulation of immune system process // inferred from electronic annotation//0006810 // transport // inferred
1449015_a	0.001511	5.80	1.28	NM_020509	<i>Retnla</i>	resistin like alpha	
1421228_a	0.000166	5.13	1.46	NM_013654	<i>Ccl7</i>	chemokine (C-C motif) ligand 7	0006935 // chemotaxis // inferred from electronic annotation//0006954 // inflammatory response // inferred from electronic
1436530_a	0.000002	5.08	1.13	NM_001081957	<i>Wfdc17</i>	WAP four-disulfide core domain 17	0010466 // negative regulation of peptidase activity // inferred from electronic annotation
1427747_a	0.000031	4.67	1.12	NM_008491	<i>Lcn2</i>	lipocalin 2	0002376 // immune system process // inferred from electronic annotation//0006810 // transport // inferred from electronic
1420380_a	0.000006	4.38	1.08	NM_011333	<i>Ccl2</i>	chemokine (C-C motif) ligand 2	0000165 // MAPK cascade // inferred from electronic annotation//0001525 // angiogenesis // traceable author
1423944_a	0.000019	4.30	-1.05	NM_017371	<i>Hpx</i>	hemopexin	0002639 // positive regulation of immunoglobulin production // inferred from mutant phenotype//0002925 // positive
1427381_a	0.000079	4.21	-1.02	NM_008392//XM_00651	<i>Irg1</i>	immunoresponsive gene 1	0002376 // immune system process // inferred from electronic annotation//0002760 // positive regulation of antimicrobial
1423566_a	0.000006	4.17	1.47	NM_013559//XM_0065C	<i>Hsph1</i>	heat shock 105kDa/110kDa protein 1	0000902 // cell morphogenesis // inferred from electronic annotation//0006950 // response to stress // inferred from
1421578_a	0.000007	4.14	1.12	NM_013652	<i>Ccl4</i>	chemokine (C-C motif) ligand 4	0006935 // chemotaxis // inferred from electronic annotation//0006954 // inflammatory response // not
1417314_a	0.000086	3.97	1.26	NM_001142706//NM_01	<i>Cfb</i>	complement factor B	0002376 // immune system process // inferred from electronic annotation//0006508 // proteolysis // inferred from electronic
1419209_a	0.000018	3.73	-1.00	NM_008176	<i>Cxcl1</i>	chemokine (C-X-C motif) ligand 1	0002237 // response to molecule of bacterial origin // not recorded//0002526 // acute inflammatory response // not
1419100_a	0.000029	3.18	-1.01	NM_009252	<i>Serpina3n</i>	serine (or cysteine) peptidase inhibitor, clade A, member 3N	0006953 // acute-phase response // inferred from electronic annotation//0006954 // inflammatory response // inferred from
1418645_a	0.000319	3.08	1.26	NM_010401	<i>Hal</i>	histidine ammonia lyase	0006547 // histidine metabolic process // inferred from electronic annotation//0006548 // histidine catabolic process //
1416755_a	0.000000	3.01	1.15	NM_018808//XM_00653	<i>Dnajb1</i>	DnaJ (Hsp40) homolog, subfamily B, member 1	0006457 // protein folding // inferred from electronic annotation//0006950 // response to stress // inferred from electronic
1420330_a	0.000007	2.95	-1.06	NM_019948	<i>Clec4e</i>	C-type lectin domain family 4, member e	0002376 // immune system process // inferred from electronic annotation//0006955 // immune response // inferred from
1449227_a	0.000006	2.86	1.09	NM_009890	<i>Ch25h</i>	cholesterol 25-hydroxylase	0006629 // lipid metabolic process // inferred from electronic annotation//0006633 // fatty acid biosynthetic process //
1417851_a	0.000065	2.86	1.51	NM_018866	<i>Cxcl13</i>	chemokine (C-X-C motif) ligand 13	0002518 // lymphocyte chemotaxis across high endothelial venule // inferred from mutant phenotype//0006935 //
1450783_a	0.000626	2.79	1.62	NM_008331	<i>Ifit1</i>	interferon-induced protein with tetratricopeptide repeats 1	0002376 // immune system process // inferred from electronic annotation//0009615 // response to virus // inferred from
1434484_a	0.000023	2.71	-1.01	NM_183249	<i>Wfdc21</i>	WAP four-disulfide core domain 21	0010466 // negative regulation of peptidase activity // inferred from electronic annotation//0032496 // response to
1423017_a	0.000010	2.67	1.06	NM_001039701//NM_01	<i>Il1rn</i>	interleukin 1 receptor antagonist	0001660 // fever generation // not recorded//0001960 // negative regulation of cytokine-mediated signaling pathway // not
1417936_a	0.000013	2.59	-1.01	NM_011338	<i>Ccl9</i>	chemokine (C-C motif) ligand 9	0006935 // chemotaxis // inferred from electronic annotation//0006955 // immune response // inferred from electronic
1437595_a	0.000087	2.50	1.23	NM_183160	<i>Tmem252</i>	transmembrane protein 252	
1422029_a	0.000885	2.48	1.12	NM_001159738//NM_01	<i>Ccl20</i>	chemokine (C-C motif) ligand 20	0006935 // chemotaxis // not recorded//0006954 // inflammatory response // inferred from electronic
1416576_a	0.000026	2.45	1.07	NM_007707//XM_00653	<i>Socs3</i>	suppressor of cytokine signaling 3	0001932 // regulation of protein phosphorylation // inferred from direct assay//0007165 // signal transduction // not
1425890_a	0.000440	2.45	1.05	NM_020498//XM_00652	<i>Ly6i</i>	lymphocyte antigen 6 complex, locus I	
1421551_s	0.001410	2.44	1.30	NM_008327//NM_0119+ Ifi202b//LOC1000+		interferon activated gene 202B//interferon-activable protein 202-like	0002376 // immune system process // inferred from electronic annotation//0006954 // inflammatory response // inferred
1457666_s	0.002476	2.43	1.34	NM_008327//NM_0119+ Ifi202b//LOC1000+		interferon activated gene 202B//interferon-activable protein 202-like	0002376 // immune system process // inferred from electronic annotation//0006954 // inflammatory response // inferred
1421074_a	0.000002	2.39	1.15	NM_007825//XM_00653	<i>Cyp7b1</i>	cytochrome P450, family 7, subfamily b, polypeptide 1	0006629 // lipid metabolic process // inferred from electronic annotation//0006699 // bile acid biosynthetic process //
1431808_a	0.000034	2.36	1.07	NM_001159299//NM_01	<i>Itih4</i>	inter alpha-trypsin inhibitor, heavy chain 4	0006953 // acute-phase response // inferred from electronic annotation//0010466 // negative regulation of peptidase
1449498_a	0.000072	2.33	1.03	NM_010766	<i>Marco</i>	macrophage receptor with collagenous structure	0002376 // immune system process // inferred from electronic annotation//0006897 // endocytosis // inferred from mutant
1419725_a	0.000125	2.25	-1.07	NM_011867//XM_00651	<i>Slc26a4</i>	solute carrier family 26, member 4	0006810 // transport // inferred from electronic annotation//0006820 // anion transport // inferred from sequence or
1418945_a	0.000588	2.24	-1.01	NM_010809	<i>Mmp3</i>	matrix metalloproteinase 3	0006508 // proteolysis // inferred from electronic annotation//0030163 // protein catabolic process // inferred from mutant
1420591_a	0.001704	2.22	1.14	NM_030720//XM_00652	<i>Gpr84</i>	G protein-coupled receptor 84	0007165 // signal transduction // inferred from electronic annotation//0007186 // G-protein coupled receptor signaling
1424509_a	0.001525	2.18	1.05	NM_026862//XM_00654	<i>Cd177</i>	CD177 antigen	
1419282_a	0.000964	2.17	1.40	NM_011331	<i>Ccl12</i>	chemokine (C-C motif) ligand 12	0000165 // MAPK cascade // not recorded//0001525 // angiogenesis // inferred from direct assay//0002548 // monocyte
1425829_a	0.000197	2.16	-1.01	NM_054098	<i>Steap4</i>	STEAP family member 4	0006810 // transport // inferred from electronic annotation//0006811 // ion transport // inferred from electronic
1417268_a	0.000032	2.13	1.04	NM_009841	<i>Cd14</i>	CD14 antigen	0002237 // response to molecule of bacterial origin // inferred from direct assay//0002376 // immune system process //
1449326_x	0.001231	2.13	1.05	NM_011314//XM_00654	<i>Saa2</i>	serum amyloid A 2	0006953 // acute-phase response // inferred from electronic annotation//0035634 // response to stilbenoid // inferred from
1450586_a	0.000861	2.12	1.17	NM_007539	<i>Bdkrb1</i>	bradykinin receptor, beta 1	0001933 // negative regulation of protein phosphorylation // not recorded//0002687 // positive regulation of leukocyte
1416288_a	0.000001	2.09	1.15	NM_001164671//NM_01	<i>Dnaj1</i>	DnaJ (Hsp40) homolog, subfamily A, member 1	0006457 // protein folding // inferred from electronic annotation//0007283 // spermatogenesis // inferred from mutant
1435160_a	0.000009	2.08	1.05	NM_001290654//NM_01	<i>Ahsa2</i>	AHA1, activator of heat shock protein ATPase 2	0006950 // response to stress // inferred from electronic annotation//0032781 // positive regulation of ATPase activity //
1425151_a	0.000002	2.06	1.01	NM_027988//XM_00652	<i>Nox1</i>	NADPH oxidase organizer 1	0006801 // superoxide metabolic process // inferred from direct assay//0007154 // cell communication // inferred from
1451537_a	0.000011	2.04	1.01	NM_007695//XM_00652	<i>Chil1</i>	chitinase-like 1	0005975 // carbohydrate metabolic process // inferred from electronic annotation//0006032 // chitin catabolic process //
1440344_a	0.000142	2.01	1.04	NR_028555	<i>Snord89</i>	small nucleolar RNA, C/D box 89	
1418486_a	0.000072	1.99	1.19	NM_011704//XM_00651	<i>Vnn1</i>	vanin 1	0002526 // acute inflammatory response // inferred from direct assay//0002544 // chronic inflammatory response // inferred
1415810_a	0.001434	1.99	-1.01	NM_001111078//NM_01	<i>Uhrf1</i>	ubiquitin-like, containing PHD and RING finger domains, 1	0000122 // negative regulation of transcription from RNA polymerase II promoter // inferred from direct assay//0000122 //
1422535_a	0.000818	1.98	1.11	NM_001037134//NM_01	<i>Ccne2</i>	cyclin E2	0000079 // regulation of cyclin-dependent protein serine/threonine kinase activity // inferred from electronic
1421976_a	0.000051	1.97	1.37	NM_001164197//NM_01	<i>Mmp19</i>	matrix metalloproteinase 19	0001525 // angiogenesis // inferred from electronic annotation//0001541 // ovarian follicle development // inferred from
1423954_a	0.000255	1.95	1.02	NM_009778	<i>C3</i>	complement component 3	0001798 // positive regulation of type IIa hypersensitivity // inferred from mutant phenotype//0001934 // positive regulation
1452047_a	0.000001	1.95	1.13	NM_009786	<i>Cacybp</i>	calyculin binding protein	0007507 // heart development // inferred from electronic annotation//0007568 // aging // inferred from electronic
1419598_a	0.000000	1.93	1.21	NM_026835	<i>Ms4a6d</i>	membrane-spanning 4-domains, subfamily A, member 6D	

Table S1

Gene_ID	p	FC-RSV 1 d	FC-RSV 5 d	RefSeq Transcript ID	Gene Symbol	Gene Title	Gene Ontology Biological Process
1436387_a	0.000440	1.93	1.20	NM_001284189//NM_0: C330006P03Rik//	RIKEN cDNA C330006P03 gene//	homer homolog 1 (Drosophila)	0003009 // skeletal muscle contraction // inferred from mutant phenotype//0007216 // G-protein coupled glutamate
1422924_a	0.000070	1.93	-1.06	NM_009404//XM_00652 Tnfrsf9	tumor necrosis factor (ligand) superfamily, member 9		0006955 // immune response // inferred from electronic annotation//00032729 // positive regulation of interferon-gamma
1418281_a	0.002761	1.91	-1.22	NM_011234	Rad51 homolog		0000724 // double-strand break repair via homologous recombination // inferred from direct assay//0000724 // double-
1416558_a	0.000071	1.91	1.03	NM_010790//XM_00653 Melk	maternal embryonic leucine zipper kinase		0006468 // protein phosphorylation // inferred from sequence or structural similarity//0006915 // apoptotic process // not
1428034_a	0.000043	1.90	-1.03	NM_001077508//NM_0: Tnfrsf9	tumor necrosis factor receptor superfamily, member 9		0042127 // regulation of cell proliferation // inferred from direct assay//0070207 // protein homotrimerization // inferred
1418424_a	0.000364	1.89	1.09	NM_009398	Tnfrsf6	tumor necrosis factor alpha induced protein 6	0007155 // cell adhesion // inferred from electronic annotation//0030335 // positive regulation of cell migration // not
1419607_a	0.000187	1.88	1.07	NM_001278601//NM_0: Tnf	tumor necrosis factor		0000060 // protein import into nucleus, translocation // not recorded//0000122 // negative regulation of transcription from
1417494_a	0.002239	1.87	-1.01	NM_001042611//NM_0: Cp	ceruloplasmin		0006810 // transport // inferred from electronic annotation//0006811 // ion transport // inferred from electronic
1421811_a	0.000070	1.87	-1.07	NM_011580//NM_0137: Pald1//Thbs1	phosphatase domain containing, paladin 1//thrombospondin 1		0000187 // activation of MAPK activity // not recorded//0001937 // negative regulation of endothelial cell proliferation // not
1448627_s	0.001419	1.87	-1.17	NM_023209//XM_00651 Pbk	PDZ binding kinase		0001933 // negative regulation of protein phosphorylation // inferred from mutant phenotype//0006468 // protein
1417290_a	0.000729	1.86	-1.05	NM_029796	Lrg1	leucine-rich alpha-2-glycoprotein 1	0001938 // positive regulation of endothelial cell proliferation // inferred from mutant phenotype//0030511 // positive
1453196_a	0.002039	1.86	1.33	NM_011854//XM_00653 Oasl2	2'-5' oligoadenylate synthetase-like 2		0002376 // immune system process // inferred from electronic annotation//0006164 // purine nucleotide biosynthetic
1417795_a	0.001239	1.85	1.08	NM_007697//XM_0065C Chl1	cell adhesion molecule with homology to L1CAM		0001764 // neuron migration // inferred from mutant phenotype//0007155 // cell adhesion // inferred from electronic
1421473_a	0.000273	1.85	1.09	NM_010554//XM_00645 Il1a	interleukin 1 alpha		0001660 // fever generation // inferred from electronic annotation//0006954 // inflammatory response // inferred from
1452218_a	0.000072	1.84	1.11	NM_134033	Ccdc117	coiled-coil domain containing 117	
1451983_a	0.000841	1.84	1.27	NM_010573	Irx1	Iroquois related homeobox 1 (Drosophila)	0001656 // metanephros development // inferred from expression pattern//0006355 // regulation of transcription, DNA-
1423233_a	0.000023	1.82	1.25	NM_007679	Cebpd	CCAAT/enhancer binding protein (C/EBP), delta	0002244 // hematopoietic progenitor cell differentiation // inferred from genetic interaction//0006351 // transcription, DNA-
1420723_a	0.000376	1.82	1.10	NM_011979	Vnn3	vanin 3	0006807 // nitrogen compound metabolic process // inferred from electronic annotation//00015939 // pantothenate
1423125_a	0.000132	1.82	1.14	NM_001111051//NM_0: Cdk1	doublecortin-like kinase 1		0001764 // neuron migration // inferred from genetic interaction//0006468 // protein phosphorylation // inferred from
1433902_a	0.000684	1.81	1.29	NM_001008785//NM_0: Kbtbd8	kelch repeat and BTB (POZ) domain containing 8		
1421366_a	0.002031	1.78	-1.04	NM_001038604//NM_0: Clec5a	C-type lectin domain family 5, member a		0002076 // osteoblast development // inferred from direct assay//0002376 // immune system process // inferred from
1460645_a	0.000083	1.78	1.04	NM_025844//XM_00651 Chordc1	cysteine and histidine-rich domain (CHORD)-containing, zinc-binding		0006950 // response to stress // inferred from electronic annotation//0010824 // regulation of centrosome duplication //
1427429_a	0.000080	1.77	-1.04	NM_009969//XM_00653 Csf2	colony stimulating factor 2 (granulocyte-macrophage)		0001892 // embryonic placenta development // inferred from mutant phenotype//0006955 // immune response // inferred
1422053_a	0.000552	1.76	1.04	NM_008380//XM_00651 Inhba	inhibin beta-A		0000082 // G1/S transition of mitotic cell cycle // not recorded//0001541 // ovarian follicle development // not
1422430_a	0.001103	1.76	-1.09	NM_001163359//NM_0: Fignl1	fidgetin-like 1		0001649 // osteoblast differentiation // inferred from mutant phenotype//0006281 // DNA repair // inferred from electronic
1422943_a	0.000657	1.76	1.49	NM_013560	Hspb1	heat shock protein 1	0006469 // negative regulation of protein kinase activity // inferred from direct assay//0006950 // response to stress //
1420804_s	0.000023	1.76	-1.13	NM_001163161//NM_0: Clec4d	C-type lectin domain family 4, member d		0002376 // immune system process // inferred from electronic annotation//0045087 // innate immune response // inferred
1456391_a	0.000630	1.74	2.28	NM_001134741//NM_0: Tdrd5	tudor domain containing 5		0007275 // multicellular organismal development // inferred from electronic annotation//0007283 // spermatogenesis //
1450424_a	0.001055	1.74	1.15	NM_010531//XM_0065C Il18bp	interleukin 18 binding protein		0032496 // response to lipopolysaccharide // inferred from electronic annotation//0042088 // T-helper 1 type immune
1419530_a	0.000339	1.74	1.15	NM_008352//XM_00653 Il12b	interleukin 12b		0001916 // positive regulation of T cell mediated cytotoxicity // inferred from direct assay//0002230 // positive regulation of
1418264_a	0.000452	1.73	1.08	NM_021790//NM_1810t Cenpk	centromere protein K		0045944 // positive regulation of transcription from RNA polymerase II promoter // inferred from direct assay
1420031_a	0.000142	1.72	-1.08	NM_007691	Chek1	checkpoint kinase 1	0000077 // DNA damage checkpoint // inferred from direct assay//0000077 // DNA damage checkpoint // inferred from
1416258_a	0.000379	1.71	-1.10	NM_001271729//NM_0: Tk1	thymidine kinase 1		0001889 // liver development // inferred from electronic annotation//0006260 // DNA replication // inferred from electronic
1418847_a	0.000095	1.70	-1.01	NM_009705	Arg2	arginase type II	0000050 // urea cycle // inferred from electronic annotation//0001657 // uretic bud development // inferred from
1421079_a	0.000670	1.70	1.02	NM_015743//XM_00653 Nr4a3	nuclear receptor subfamily 4, group A, member 3		0001707 // mesoderm formation // inferred from mutant phenotype//0006351 // transcription, DNA-templated // inferred
1428713_s	0.000088	1.70	1.04	NM_178856	Gins2	GINS complex subunit 2 (Psf2 homolog)	0006260 // DNA replication // inferred from electronic annotation
1449184_a	0.000559	1.70	1.04	NM_009402	Pglyrp1	peptidoglycan recognition protein 1	0002221 // pattern recognition receptor signaling pathway // not recorded//0002376 // immune system process // inferred
1446951_a	0.001132	1.69	1.19	NM_177161//XM_0065C P4ha3	procollagen-proline, 2-oxoglutarate 4-dioxygenase (proline 4-		0019511 // peptidyl-proline hydroxylation // not recorded//0055114 // oxidation-reduction process // not recorded
1424278_a	0.000136	1.68	-1.07	NM_001012272//NM_0: Birc5	baculoviral IAP repeat-containing 5		0000086 // G2/M transition of mitotic cell cycle // not recorded//0000226 // microtubule cytoskeleton organization //
1452070_a	0.000131	1.68	1.00	NM_026117//NM_2076: Dedd2	death effector domain-containing DNA binding protein 2		0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 // regulation of transcription, DNA-
1419253_a	0.000127	1.67	1.01	NM_008638//XM_0065C Mthfd2	methylenetetrahydrofolate dehydrogenase (NAD+ dependent),		0006730 // one-carbon metabolic process // not recorded//0008152 // metabolic process // inferred from electronic
1417262_a	0.000341	1.67	1.21	NM_011198	Ptgs2	prostaglandin-endoperoxide synthase 2	0001516 // prostaglandin biosynthetic process // inferred from direct assay//0001516 // prostaglandin biosynthetic process
1450652_a	0.001362	1.67	1.18	NM_007802//XM_0065C Ctsk	cathepsin K		0001957 // intramembranous ossification // inferred from electronic annotation//0006508 // proteolysis // inferred from
1449025_a	0.002251	1.66	1.46	NM_010501	Ifit3	interferon-induced protein with tetratricopeptide repeats 3	0002376 // immune system process // inferred from electronic annotation//0008285 // negative regulation of cell
1422062_a	0.000063	1.66	1.06	NM_001113326//NM_0: Msr1	macrophage scavenger receptor 1		0006897 // endocytosis // inferred from electronic annotation//0006898 // receptor-mediated endocytosis // inferred from
1417821_a	0.001234	1.65	-1.13	NM_033075	D17H6556E-5	DNA segment, Chr 17, human D6556E 5	0019058 // viral life cycle // inferred from electronic annotation
1415909_a	0.000141	1.65	1.13	NM_016737	Stip1	stress-induced phosphoprotein 1	
1415945_a	0.000068	1.65	-1.01	NM_008566//XM_00653 Mcm5	minichromosome maintenance deficient 5, cell division cycle 46 (S.		0006260 // DNA replication // inferred from electronic annotation//0006270 // DNA replication initiation // inferred from
1417394_a	0.000016	1.64	1.14	NM_010637	Klf4	Kruppel-like factor 4 (gut)	0000122 // negative regulation of transcription from RNA polymerase II promoter // not recorded//0006351 // transcription,
1418932_a	0.000768	1.63	1.01	NM_017373//XM_00651 Nfii3	nuclear factor, interleukin 3, regulated		0000122 // negative regulation of transcription from RNA polymerase II promoter // not recorded//0006351 // transcription,
1415922_s	0.000015	1.62	-1.02	NM_010807	Marcks1	MARCKS-like 1	0008284 // positive regulation of cell proliferation // inferred from direct assay
1421852_a	0.000215	1.62	1.11	NM_021542//XM_00651 Kcnk5	potassium channel, subfamily K, member 5		0006810 // transport // inferred from electronic annotation//0006811 // ion transport // inferred from electronic
1428572_a	0.000049	1.62	-1.06	NM_027395	Basp1	brain abundant, membrane attached signal protein 1	0045892 // negative regulation of transcription, DNA-templated // not recorded//0045892 // negative regulation of
1416802_a	0.002132	1.61	-1.08	NM_026410	Cdca5	cell division cycle associated 5	0000082 // G1/S transition of mitotic cell cycle // not recorded//0006302 // double-strand break repair // not
1421979_a	0.000349	1.61	1.37	NM_011077	Phex	phosphate regulating endonucleotidase homolog, X-linked	0006508 // proteolysis // not recorded//0019637 // organophosphate metabolic process // inferred from mutant
1427102_a	0.000483	1.61	-1.43	NM_011410//XM_00653 Sifn4//Sifn3	schlafen 4//schlafen 3		0008285 // negative regulation of cell proliferation // inferred from direct assay
1448239_a	0.002698	1.61	-1.14	NM_010442	Hmxo1	heme oxygenase (decycling) 1	0001525 // angiogenesis // not recorded//0001666 // response to hypoxia // inferred from electronic annotation//0002246
1418206_a	0.000097	1.60	1.20	NM_022324	Sdf2l1	stromal cell-derived factor 2-like 1	0034976 // response to endoplasmic reticulum stress // not recorded//0042981 // regulation of apoptotic process // not
1429171_a	0.001971	1.60	1.02	NM_019438//XR_37681: Ncapg	non-SMC condensin I complex, subunit G		0007076 // mitotic chromosome condensation // not recorded
1419721_a	0.000138	1.60	1.02	NM_030701	Hcar2	hydroxycarboxylic acid receptor 2	0001781 // neutrophil apoptotic process // not recorded//0006915 // apoptotic process // inferred from electronic
1417602_a	0.000111	1.60	1.67	NM_011066//XM_00652 Per2	period circadian clock 2		0000122 // negative regulation of transcription from RNA polymerase II promoter // inferred from direct assay//0000122 //
1442116_a	0.001214	1.59	1.06	NM_201367	Gpr176	G protein-coupled receptor 176	0007165 // signal transduction // inferred from electronic annotation//0007186 // G-protein coupled receptor signaling
1418825_a	0.001124	1.59	1.30	NM_008326//XM_00653 Irgm1	immunity-related GTPase family M member 1		0002376 // immune system process // inferred from electronic annotation//0006914 // autophagy // inferred from electronic
1450716_a	0.000372	1.59	1.06	NM_009621	Adamts1	a disintegrin-like and metalloproteinase (reprolysin type) with	0001542 // ovulation from ovarian follicle // inferred from mutant phenotype//0001822 // kidney development // inferred
1418835_a	0.000029	1.59	-1.02	NM_009344	Phlda1	pleckstrin homology-like domain, family A, member 1	0006915 // apoptotic process // inferred from electronic annotation//0007010 // cytoskeleton organization // inferred from
1436583_a	0.000449	1.58	-1.17	NM_183089//XM_00652 Dsccl	defective in sister chromatid cohesion 1 homolog (S. cerevisiae)		0006260 // DNA replication // inferred from electronic annotation//0006275 // regulation of DNA replication // not

Table S1

Gene_ID	p	FC-RSV 1 d	FC-RSV 5 d	RefSeq Transcript ID	Gene Symbol	Gene Title	Gene Ontology Biological Process
1435184_a	0.000131	1.58	1.44	NM_001039181//NM_01 Npr3		natriuretic peptide receptor 3	0001501 // skeletal system development // inferred from direct assay//0001501 // skeletal system development // inferred
1419057_a	0.000566	1.57	1.31	NM_019810	<i>Slc5a1</i>	solute carrier family 5 (sodium/glucose cotransporter), member 1	0001656 // metanephros development // inferred from mutant phenotype//0006810 // transport // inferred from electronic
1431087_a	0.000743	1.57	1.04	NM_026282//XR_37913	<i>Spc24</i>	SPC24, NDC80 kinetochore complex component, homolog (S.	0007049 // cell cycle // inferred from electronic annotation//0007067 // mitotic nuclear division // inferred from electronic
1421307_a	0.000102	1.57	1.13	NM_024495	<i>Car13</i>	carbonic anhydrase 13	0006730 // one-carbon metabolic process // inferred from electronic annotation
1426858_a	0.000181	1.57	1.03	NM_008381	<i>Inhbb</i>	inhibin beta-B	0001654 // eye development // traceable author statement//0009267 // cellular response to starvation // inferred from
1419532_a	0.000684	1.57	-1.12	NM_010555//XM_00645	<i>Il1r2</i>	interleukin 1 receptor, type II	0019221 // cytokine-mediated signaling pathway // inferred from electronic annotation
1419413_a	0.000456	1.57	-1.07	NM_011332//XM_00653	<i>Ccl17</i>	chemokine (C-C motif) ligand 17	0006935 // chemotaxis // traceable author statement//0006955 // immune response // inferred from electronic
1439827_a	0.000664	1.57	1.08	NM_017501//XM_00652	<i>Adamts12</i>	a disintegrin-like and metallopeptidase (reprolysin type) with	0006508 // proteolysis // inferred from electronic annotation//0007160 // cell-matrix adhesion // not recorded//0016477 //
1429056_a	0.000220	1.56	1.00	NM_025832//XM_00651	<i>Naa16</i>	N(alpha)-acetyltransferase 16, NatA auxiliary subunit	0006474 // N-terminal protein amino acid acetylation // not recorded//0043066 // negative regulation of apoptotic process
1418992_a	0.000510	1.56	1.08	NM_001242368//NM_01 F10		coagulation factor X	0006508 // proteolysis // not recorded//0007596 // blood coagulation // not recorded//0007599 // hemostasis // inferred
1417009_a	0.000280	1.56	1.01	NM_023143//NM_0011: C1ra//C1rb		complement component 1, r subcomponent A//complement	0002376 // immune system process // inferred from electronic annotation//0006508 // proteolysis // not
1421921_a	0.000834	1.56	-1.22	NM_009253//XM_00651	<i>Serpina3m</i>	serine (or cysteine) peptidase inhibitor, clade A, member 3M	0010466 // negative regulation of peptidase activity // inferred from electronic annotation//0010951 // negative regulation
1419152_a	0.000391	1.56	-1.03	NM_026515//XR_37945	<i>2810417H13Rik</i>	RIKEN cDNA 2810417H13 gene	0006260 // DNA replication // not recorded//0006281 // DNA repair // inferred from electronic annotation//0006974 //
1437250_a	0.000185	1.55	1.00	NM_001005423//XM_01 Mreg		melanoregulin	0030318 // melanocyte differentiation // inferred from mutant phenotype//0032402 // melanosome transport // inferred
1429165_a	0.000029	1.55	1.07	NM_025653	<i>3110001I22Rik</i>	RIKEN cDNA 3110001I22 gene	0006915 // apoptotic process // inferred from electronic annotation//0043066 // negative regulation of apoptotic process //
1420622_a	0.000131	1.55	1.19	NM_031165	<i>Hspa8b</i>	heat shock protein 8	0009002 // cell morphogenesis // inferred from electronic annotation//0006200 // ATP catabolic process // inferred from
1424556_a	0.001029	1.55	-1.08	NM_144795//XM_00653	<i>Pycr1</i>	pyrroline-5-carboxylate reductase 1	0006561 // proline biosynthetic process // not recorded//0006950 // response to stress // inferred from electronic
1419482_a	0.000734	1.55	1.16	NM_009779	<i>C3ar1</i>	complement component 3a receptor 1	0002430 // complement receptor mediated signaling pathway // not recorded//0002462 // tolerance induction to nonself
1428480_a	0.001594	1.54	1.01	NM_026560	<i>Cdca8</i>	cell division cycle associated 8	0000089 // mitotic metaphase // not recorded//0007049 // cell cycle // inferred from electronic annotation//0007067 //
1417925_a	0.001641	1.54	-1.05	NM_009137	<i>Ccl22</i>	chemokine (C-C motif) ligand 22	0006935 // chemotaxis // inferred from electronic annotation//0006954 // inflammatory response // inferred from electronic
1423809_a	0.000073	1.54	-1.09	NM_001163763//NM_01 Tcf19		transcription factor 19	
1416077_a	0.000386	1.54	-1.07	NM_009627	<i>Adm</i>	adrenomedullin	0001570 // vasculogenesis // not recorded//0001666 // response to hypoxia // inferred from electronic
1422473_a	0.000233	1.53	1.05	NM_001177980//NM_01 Pde4b		phosphodiesterase 4B, cAMP specific	0001780 // neutrophil homeostasis // inferred from mutant phenotype//0006198 // cAMP catabolic process // inferred from
1424041_s	0.000059	1.53	-1.01	NM_001097617//NM_11 C1s1		complement component 1, r subcomponent 1	0002376 // immune system process // inferred from electronic annotation//0006508 // proteolysis // not
1449851_a	0.000006	1.53	1.34	NM_001159367//NM_01 Per1		period circadian clock 1	0000122 // negative regulation of transcription from RNA polymerase II promoter // inferred from direct assay//0002028 //
1454742_a	0.000142	1.53	1.12	NM_145839//NM_1813: Rasgef1b		RasGEF domain family, member 1B	0007264 // small GTPase mediated signal transduction // inferred from electronic annotation//0032318 // regulation of Ras
1435476_a	0.000167	1.53	1.03	NM_001077189//NM_01 Fcgr2b		Fc receptor, IgG, low affinity IIB	0001811 // negative regulation of type I hypersensitivity // inferred from mutant phenotype//0002638 // negative regulation
1416698_a	0.000151	1.53	1.03	NM_016904	<i>Cks1b</i>	CDC28 protein kinase 1b	0007049 // cell cycle // inferred from electronic annotation//0045859 // regulation of protein kinase activity // inferred from
1418580_a	0.001746	1.52	1.12	NM_023386//XM_00652	<i>Rtp4</i>	receptor transporter protein 4	0001580 // detection of chemical stimulus involved in sensory perception of bitter taste // not recorded//0006612 // protein
1431734_a	0.000000	1.52	1.05	NM_025926//NM_02721	<i>Dnajb4</i>	DnaJ (Hsp40) homolog, subfamily B, member 4	0006457 // protein folding // inferred from electronic annotation
1434079_s	0.000386	1.51	-1.07	NM_008564	<i>Mcm2</i>	minichromosome maintenance deficient 2 mitotin (S. cerevisiae)	0006260 // DNA replication // inferred from electronic annotation//0006268 // DNA unwinding involved in DNA replication //
1429270_a	0.000111	1.51	-1.02	NM_001168244//NM_01 Syce2		synaptonemal complex central element protein 2	0007049 // cell cycle // inferred from electronic annotation//0007126 // meiotic nuclear division // inferred from electronic
1426645_a	0.000034	1.51	1.23	NM_010480//XM_00651	<i>Hsp90aa1</i>	heat shock protein 90, alpha (cytosolic), class A member 1	0001764 // neuron migration // not recorded//0003009 // skeletal muscle contraction // inferred from electronic
1417001_a	0.000476	1.51	1.03	NM_023665	<i>Rsrp1</i>	arginine/serine rich protein 1	
1425753_a	0.001294	1.51	-1.13	NM_001040691//NM_01 Ung		uracil DNA glycosylase	0006281 // DNA repair // traceable author statement//0006284 // base-excision repair // not recorded//0006974 // cellular
1452595_a	0.001147	1.51	1.06	NM_172845	<i>Adamts4</i>	a disintegrin-like and metallopeptidase (reprolysin type) with	0006508 // proteolysis // inferred from direct assay//0006508 // proteolysis // not recorded//0042742 // defense response
1426519_a	0.000128	1.50	1.21	NM_011030//XM_00651	<i>P4ha1</i>	procollagen-proline, 2-oxoglutarate 4-dioxygenase (proline 4-	0018401 // peptidyl-proline hydroxylation to 4-hydroxy-L-proline // inferred from direct assay//0030199 // collagen fibril
1428069_a	0.000398	1.50	1.05	NM_025866//XM_0065C	<i>Cdca7</i>	cell division cycle associated 7	0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 // regulation of transcription, DNA-
1416431_a	0.000003	1.49	-1.04	NM_026473	<i>Tubb6</i>	tubulin, beta 6 class V	0006184 // GTP catabolic process // inferred from electronic annotation//0007017 // microtubule-based process // inferred
1448650_a	0.002754	1.49	-1.10	NM_011132//XM_00653	<i>Pole</i>	polymerase (DNA directed), epsilon	0000082 // G1/S transition of mitotic cell cycle // not recorded//0000731 // DNA synthesis involved in DNA repair // not
1416761_a	0.000583	1.49	-1.03	NM_008289	<i>Hmd11b2</i>	hydroxysteroid 11-beta dehydrogenase 2	0001666 // response to hypoxia // inferred from electronic annotation//0002017 // regulation of blood volume by renal
1438498_a	0.000301	1.48	-1.10	NM_001029929//XM_01 Zmynd15		zinc finger, MYND-type containing 15	0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 // regulation of transcription, DNA-
1416342_a	0.001666	1.48	1.01	NM_011607//XM_00653	<i>Tnc</i>	tenascin C	0001649 // osteoblast differentiation // not recorded//0007155 // cell adhesion // inferred from electronic
1419204_a	0.000076	1.48	1.06	NM_007865//XM_00652	<i>Dll1</i>	delta-like 1 (Drosophila)	0001701 // in utero embryonic development // non-traceable author statement//0001756 // somitogenesis // inferred from
1448380_a	0.000314	1.48	1.08	NM_011150//XM_00653	<i>Lgals3bp</i>	lectin, galactoside-binding, soluble, 3 binding protein	0006898 // receptor-mediated endocytosis // inferred from sequence or structural similarity//0007155 // cell adhesion //
1417541_a	0.001891	1.48	-1.05	NM_008234//XM_00652	<i>Hells</i>	helicase, lymphoid specific	0001655 // urogenital system development // inferred from mutant phenotype//0006306 // DNA methylation // inferred
1417985_a	0.000635	1.48	-1.03	NM_025980	<i>Nrarp</i>	Notch-regulated ankyrin repeat protein	0000122 // negative regulation of transcription from RNA polymerase II promoter // inferred from genetic
1428487_s	0.000107	1.48	1.11	NM_001039710//NM_01 Coq10b		coenzyme Q10 homolog B (S. cerevisiae)	
1416364_a	0.000023	1.47	1.16	NM_008302	<i>Hsp90ab1</i>	heat shock protein 90 alpha (cytosolic), class B member 1	0001890 // placenta development // inferred from mutant phenotype//0006457 // protein folding // inferred from electronic
1420056_s	0.000062	1.47	-1.01	NM_033398//XM_00653	<i>Jmjd6</i>	jumonji domain containing 6	0001568 // blood vessel development // inferred from mutant phenotype//0001822 // kidney development // inferred from
1440216_a	0.000906	1.47	-1.04	NM_053088	<i>Ifitm5</i>	interferon induced transmembrane protein 5	0007275 // multicellular organismal development // traceable author statement//0009607 // response to biotic stimulus //
1424671_a	0.000036	1.47	1.20	NM_024413	<i>Plekfh1</i>	pleckstrin homology domain containing, family F (with FYVE domain)	0006915 // apoptotic process // inferred from electronic annotation//0007032 // endosome organization // not
1418421_a	0.000070	1.46	-1.17	NM_007528	<i>Bcl6b</i>	B cell CLL/lymphoma 6, member B	0000122 // negative regulation of transcription from RNA polymerase II promoter // inferred from direct assay
1421811_a	0.000319	1.46	-1.04	NM_011580//NM_0137: Pald1//Thbs1		phosphatase domain containing, paladin 1//thrombospondin 1	0000187 // activation of MAPK activity // not recorded//0001937 // negative regulation of endothelial cell proliferation // not
1420772_a	0.000020	1.46	1.42	NM_001077364//NM_01 Tsc2d3		TSC22 domain family, member 3	0000122 // negative regulation of transcription from RNA polymerase II promoter // inferred from direct assay//0006355 //
1418949_a	0.001658	1.46	1.06	NM_011819//XM_0065C	<i>Gdf15</i>	growth differentiation factor 15	
1458040_a	0.000568	1.46	1.98		<i>D7Wsu130e</i>	DNA segment, Chr 7, Wayne State University 130, expressed	
1419573_a	0.000001	1.45	1.02	NM_008495	<i>Lgals1</i>	lectin, galactose binding, soluble 1	0002317 // plasma cell differentiation // inferred from direct assay//0006915 // apoptotic process // inferred from electronic
1418936_a	0.001031	1.45	1.10	NM_010755//XM_00652	<i>Maff</i>	v-maf musculoaponeurotic fibrosarcoma oncogene family, protein F	0001701 // in utero embryonic development // inferred from genetic interaction//0006351 // transcription, DNA-templated
1418901_a	0.000033	1.45	1.09	NM_001287738//NM_01 Cebpb		CCAAT/enhancer binding protein (C/EBP), beta	0001892 // embryonic placenta development // inferred from genetic interaction//0006351 // transcription, DNA-templated
1418204_s	0.000932	1.45	-1.06	NM_019467//XM_00652	<i>Aif1</i>	allograft inflammatory factor 1	0001774 // microglial cell activation // not-traceable author statement//0001934 // positive regulation of protein
1420499_a	0.000001	1.45	1.06	NM_008102	<i>Gch1</i>	GTP cyclohydrolase 1	0006184 // GTP catabolic process // not recorded//0006461 // protein complex assembly // not recorded//0006729 //
1420394_s	0.000244	1.44	-1.11	NM_001291892//NM_01 Gp49a//Lilrb4		glycoprotein 49 A//leukocyte immunoglobulin-like receptor, subfamily	0002376 // immune system process // inferred from electronic annotation
1420394_s	0.000244	1.44	-1.11	NM_001291892//NM_01 Gp49a//Lilrb4		glycoprotein 49 A//leukocyte immunoglobulin-like receptor, subfamily	0002376 // immune system process // inferred from electronic annotation
1451064_a	0.001000	1.44	1.06	NM_001205339//NM_1: Psat1		phosphoserine aminotransferase 1	0006564 // L-serine biosynthetic process // inferred from electronic annotation//0008152 // metabolic process // inferred
1450299_a	0.000124	1.44	-1.05	NM_007390	<i>Chna7</i>	cholinergic receptor, nicotinic, alpha polypeptide 7	0000187 // activation of MAPK activity // not recorded//0001666 // response to hypoxia // not recorded//0001988 //

Table S1

Gene ID	p	FC-RSV 1 d	FC-RSV 5 d	RefSeq Transcript ID	Gene Symbol	Gene Title	Gene Ontology Biological Process
1422286_a	0.000219	1.43	1.12	NM_001164074//NM_01 Tgfr1	TGFB-induced factor homeobox 1	0000122 // negative regulation of transcription from RNA polymerase II promoter // inferred from genetic	
1428593_a	0.000289	1.43	1.05	NM_029368//XM_00645 Tex30	testis expressed 30		
1450829_a	0.000143	1.43	1.00	NM_001166402//NM_01 Tnfrsf3	tumor necrosis factor, alpha-induced protein 3	0001922 // B-1 B cell homeostasis // inferred from mutant phenotype//0002237 // response to molecule of bacterial origin //	
1419676_a	0.000195	1.43	1.06	NM_013606//NR_00350 Mx2	myxovirus (influenza virus) resistance 2	0002376 // immune system process // inferred from electronic annotation//0006184 // GTP catabolic process // traceable	
1422170_a	0.000074	1.43	1.04	NM_017391 Slc5a3	solute carrier family 5 (inositol transporters), member 3	0006020 // inositol metabolic process // inferred from mutant phenotype//0006412 // translation // inferred from electronic	
1449164_a	0.000073	1.42	-1.08	NM_001291058//NM_01 Cd68	CD68 antigen	0071310 // cellular response to organic substance // inferred from direct assay	
1422931_a	0.000126	1.42	1.13	NM_008037 Fosl2	fos-like antigen 2	0001666 // response to hypoxia // not recorded//0006351 // transcription, DNA-templated // inferred from electronic	
1424118_a	0.002009	1.42	-1.04	NM_001199123//NM_01 Spc25	SPC25, NDC80 kinetochore complex component, homolog (S.	0007049 // cell cycle // inferred from electronic annotation//0007052 // mitotic spindle organization // not	
1422452_a	0.000005	1.42	-1.03	NM_013863 Bag3	BCL2-associated athanogene 3	0006915 // apoptotic process // inferred from electronic annotation//0007420 // brain development // inferred from	
1448170_a	0.000023	1.42	-1.03	NM_009174 Siah2	seven in absentia 2	0006511 // ubiquitin-dependent protein catabolic process // inferred from electronic annotation//0006915 // apoptotic	
1449027_a	0.000837	1.42	1.11	NM_133955 Rhou	ras homolog gene family, member U	0000082 // G1/S transition of mitotic cell cycle // inferred from direct assay//0006184 // GTP catabolic process // inferred	
1426351_a	0.000231	1.42	1.08	NM_010477//XM_00645 Hspd1	heat shock protein 1 (chaperonin)	0002236 // detection of misfolded protein // not recorded//0002368 // B cell cytokine production // not recorded//0002755	
1418322_a	0.000375	1.42	1.03	NM_001110850//NM_01 Crem	cAMP responsive element modulator	0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 // regulation of transcription, DNA-	
1442123_a	0.002693	1.41	1.14	XR_388783 Tnfrsf130s	tumor necrosis factor (ligand) superfamily, member 13, opposite strand		
1435158_a	0.000000	1.41	1.31	NM_028226//XM_00653 Rbm12b1	RNA binding motif protein 12 B1		
1434442_a	0.000959	1.41	1.10	NM_175096 Stbd1	starch binding domain 1		
1424147_a	0.000046	1.41	1.09	NM_146036//XM_00651 Ahsa1	AHA1, activator of heat shock protein ATPase 1	0006457 // protein folding // inferred from sequence or structural similarity//0006950 // response to stress // inferred from	
1424754_a	0.000296	1.41	1.22	NM_001025610//NM_01 Ms4a7	membrane-spanning 4-domains, subfamily A, member 7		
1450843_a	0.002655	1.41	1.11	NM_001111043//NM_01 Serpinh1	serine (or cysteine) peptidase inhibitor, clade H, member 1	0003433 // chondrocyte development involved in endochondral bone morphogenesis // inferred from mutant	
1428776_a	0.000034	1.41	1.11	NM_029415//XM_00653 Slc10a6	solute carrier family 10 (sodium/bile acid cotransporter family),	0006810 // transport // inferred from electronic annotation//0006811 // ion transport // inferred from electronic	
1416514_a	0.000535	1.40	-1.12	NM_007984 Fcsm1	fascin homolog 1, actin bundling protein (Strongylocentrotus	0016477 // cell migration // inferred from mutant phenotype//0016477 // cell migration // not recorded//0030036 // actin	
1416129_a	0.001216	1.40	1.11	NM_133753//XM_00653 Errf1	ERBB receptor feedback inhibitor 1	0007175 // negative regulation of epidermal growth factor-activated receptor activity // inferred from mutant	
1421365_a	0.001202	1.40	1.21	NM_008046//XM_00651 Fst	foliastatin	0000122 // negative regulation of transcription from RNA polymerase II promoter // not recorded//0001501 // skeletal	
1419066_a	0.001108	1.40	1.08	NM_030244 Ier5l	immediate early response 5-like		
1452598_a	0.001499	1.40	-1.08	NM_001163476//NM_01 Gins1	GIN5 complex subunit 1 (Psf1 homolog)	0001833 // inner cell mass cell proliferation // inferred from mutant phenotype//0006260 // DNA replication // inferred from	
1415834_a	0.000421	1.40	1.04	NM_002628 Dusp6	dual specificity phosphatase 6	0000188 // inactivation of MAPK activity // not recorded//0001933 // negative regulation of protein phosphorylation //	
1422462_a	0.002231	1.39	1.02	NM_001278115//NM_01 Ube2t	ubiquitin-conjugating enzyme E2T (putative)	0006281 // DNA repair // not recorded//0006513 // protein monoubiquitination // not recorded//0006974 // cellular	
1417785_a	0.000248	1.39	-1.03	NM_134102//XM_00652 Pla1a	phospholipase A1 member A	0006629 // lipid metabolic process // inferred from electronic annotation//0016042 // lipid catabolic process // inferred from	
1418025_a	0.000098	1.39	1.11	NM_011498 Bhlhe40	basic helix-loop-helix family, member e40	0000122 // negative regulation of transcription from RNA polymerase II promoter // inferred from direct assay//0000122 //	
1429441_a	0.000443	1.38	1.24	NM_001168297//NM_01 Fbxo30	F-box protein 30	0016567 // protein ubiquitination // inferred from electronic annotation	
1418133_a	0.000058	1.38	-1.01	NM_033601//XM_00653 Bcl3	B cell leukemia/lymphoma 3	0000060 // protein import into nucleus, translocation // not recorded//0002268 // follicular dendritic cell differentiation //	
1426381_a	0.000694	1.38	1.01	NM_001081214//NM_1 Pprc1	peroxisome proliferative activated receptor, gamma, coactivator-	0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 // regulation of transcription, DNA-	
1423909_a	0.000013	1.38	-1.01	NM_001098271//NM_01 Tmem176a	transmembrane protein 176A	2001199 // negative regulation of dendritic cell differentiation // inferred from mutant phenotype	
1416773_a	0.000174	1.38	1.44	NM_009516//XM_0065C Wee1	WEE 1 homolog 1 (S. pombe)	0000226 // microtubule cytoskeleton organization // inferred from mutant phenotype//0006468 // protein phosphorylation	
1417266_a	0.000398	1.38	1.10	NM_009139 Ccl6	chemokine (C-C motif) ligand 6	0006935 // chemotaxis // inferred from electronic annotation//0006955 // immune response // inferred from electronic	
1419534_a	0.000665	1.37	1.16	NM_138648//XM_0065C Olr1	oxidized low density lipoprotein (lectin-like) receptor 1	0002376 // immune system process // inferred from electronic annotation//0006898 // receptor-mediated endocytosis //	
1421326_a	0.000206	1.37	1.00	NM_007780//XM_00652 Csf2rb2//Csf2rb2	colony stimulating factor 2 receptor, beta, low-affinity (granulocyte-	019221 // cytokine-mediated signaling pathway // inferred from electronic annotation	
1419172_a	0.001039	1.37	1.02	NM_010049 Dhfr	dihydrofolate reductase	0006545 // glycine biosynthetic process // inferred from electronic annotation//0006730 // one-carbon metabolic process //	
1449399_a	0.000007	1.37	-1.53	NM_008361//XM_00645 Il1b	interleukin 1 beta	0000122 // negative regulation of transcription from RNA polymerase II promoter // not recorded//0000165 // MAPK cascade	
1425243_a	0.000296	1.37	1.09	NM_144943//XM_0065C Cd207	CD207 antigen	0051607 // defense response to virus // not recorded	
1419519_a	0.000143	1.37	-1.01	NM_001111274//NM_01 Igf1	insulin-like growth factor 1	0001649 // osteoblast differentiation // inferred from expression pattern//0001775 // cell activation // not	
1421322_a	0.000805	1.37	1.11	NM_001159417//NM_01 Irf9	interferon regulatory factor 9	0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 // regulation of transcription, DNA-	
1419004_s	0.000667	1.37	1.01	NM_007534//NM_0075: Bcl2a1a//Bcl2a1b	B cell leukemia/lymphoma 2 related protein A1a//B cell	0001782 // B cell homeostasis // inferred from direct assay//0002903 // negative regulation of B cell apoptotic process //	
1419318_a	0.001337	1.36	-1.06	NM_011316 Saa4	serum amyloid A 4	0006953 // acute-phase response // inferred from electronic annotation	
1418969_a	0.001527	1.36	1.01	NM_001285980//NM_01 Skp2	S-phase kinase-associated protein 2 (p45)	0000082 // G1/S transition of mitotic cell cycle // inferred from direct assay//0000086 // G2/M transition of mitotic cell cycle	
1418714_a	0.000459	1.36	1.02	NM_008748//XM_0065C Dusp8	dual specificity phosphatase 8	0000188 // inactivation of MAPK activity // --//0000188 // inactivation of MAPK activity // inferred from electronic	
1426625_a	0.000279	1.36	1.07	NM_030199//XM_00652 Zfp623	zinc finger protein 623	0006355 // regulation of transcription, DNA-templated // not recorded	
1417486_a	0.002125	1.36	1.12	NM_001159523//NM_01 Shd	src homology 2 domain-containing transforming protein D		
1452462_a	0.000333	1.36	1.07	NM_001110100//NM_01 Bapn	BTG3 associated nuclear protein	0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 // regulation of transcription, DNA-	
1439716_a	0.001178	1.36	1.35	NM_177905//XM_00651 Pwll4	piwi-like RNA-mediated gene silencing 4	0006417 // regulation of translation // inferred from electronic annotation//0007126 // meiotic nuclear division // inferred	
1417574_a	0.000343	1.35	-1.02	NM_001012477//NM_01 Cxcl12	chemokine (C-X-C motif) ligand 12	0001569 // patterning of blood vessels // inferred from mutant phenotype//0001666 // response to hypoxia // inferred from	
1451340_a	0.000422	1.35	1.02	NM_001172205//NM_01 Arid5a	AT rich interactive domain 5A (MRF1-like)	0002062 // chondrocyte differentiation // inferred from direct assay//0006351 // transcription, DNA-templated // inferred	
1418440_a	0.000510	1.35	-1.04	NM_007739 Col8a1	collagen, type VIII, alpha 1	0001525 // angiogenesis // inferred from electronic annotation//0007155 // cell adhesion // inferred from electronic	
1435626_a	0.002184	1.35	1.18	NM_022331//XM_00653 Herpud1	homocysteine-inducible, endoplasmic reticulum stress-inducible,	0006511 // ubiquitin-dependent protein catabolic process // inferred from direct assay//0006511 // ubiquitin-dependent	
1416563_a	0.000422	1.35	1.04	NM_016748//XM_0065C Ctps	cytidine 5'-triphosphate synthase	0006221 // pyrimidine nucleotide biosynthetic process // inferred from electronic annotation//0006241 // CTP biosynthetic	
1452521_a	0.001683	1.35	1.07	NM_011113//XM_00653 Plaur	plasminogen activator, urokinase receptor	0001222 // positive regulation of gene expression // not recorded//0016310 // phosphorylation // inferred from electronic	
1460410_a	0.000928	1.35	1.33	NM_030208//XM_0065C Trmt44	tRNA methyltransferase 44	0008033 // tRNA processing // inferred from electronic annotation//0032259 // methylation // inferred from electronic	
1430530_s	0.001546	1.35	1.06	NM_001290761//NM_01 Nmr1	NmrA-like family domain containing 1	0006694 // steroid biosynthetic process // inferred from electronic annotation//0006813 // potassium ion transport //	
1419149_a	0.002306	1.35	1.20	NM_008871 Serpine1	serine (or cysteine) peptidase inhibitor, clade E, member 1	0001300 // chronological cell aging // inferred from electronic annotation//0001525 // angiogenesis // inferred from	
1434129_s	0.001107	1.35	1.05	NM_172589 Lhfp12	lipoma HMGIC fusion partner-like 2		
1449453_a	0.001848	1.35	1.06	NM_009763//XM_0065C Bst1	bone marrow stromal cell antigen 1	0008152 // metabolic process // inferred from electronic annotation	
1417947_a	0.001441	1.35	-1.03	NM_011045 Pcnr	proliferating cell nuclear antigen	0000077 // DNA damage checkpoint // inferred from electronic annotation//0000122 // negative regulation of transcription	
1436186_a	0.000508	1.35	-1.13	NM_001013368//XM_01 E2f8	E2F transcription factor 8	0000122 // negative regulation of transcription from RNA polymerase II promoter // inferred from mutant	
1416200_a	0.000221	1.35	1.16	NM_001164724//NM_1: Il33	interleukin 33	0002686 // negative regulation of leukocyte migration // inferred from genetic interaction//0002826 // negative regulation of	
1448550_a	0.002327	1.35	1.04	NM_008489 Lbp	lipopolysaccharide binding protein	0002232 // leukocyte chemotaxis involved in inflammatory response // inferred from mutant phenotype//0002281 //	
1427298_a	0.000311	1.35	-1.21	NR_002870//NR_029796 Dnm3os//Mir214	dynam3, 3, opposite strand//microRNA 214	0001501 // skeletal system development // inferred from mutant phenotype//0003323 // type B pancreatic cell development	

Table S1

Gene_ID	p	FC-RSV 1 d	FC-RSV 5 d	RefSeq Transcript ID	Gene Symbol	Gene Title	Gene Ontology Biological Process
1460283_a	0.000207	1.34	-1.26	NM_001161790///NM_01	<i>Mefv</i>	Mediterranean fever	0002376 // immune system process // inferred from electronic annotation///0006954 // inflammatory response // not
1420028_s	0.001682	1.34	-1.01	NM_008563	<i>Mcm3</i> ///AK205147	minichromosome maintenance deficient 3 (S. cerevisiae)///Mus	0006260 // DNA replication // inferred from electronic annotation///0006270 // DNA replication initiation // inferred from
1418248_a	0.001622	1.34	1.04	NM_013463	<i>Gla</i>	galactosidase, alpha	0005975 // carbohydrate metabolic process // inferred from electronic annotation///0008152 // metabolic process // inferred
1449363_a	0.002354	1.34	-1.07	NM_007498	<i>Atf3</i>	activating transcription factor 3	0000122 // negative regulation of transcription from RNA polymerase II promoter // inferred from direct assay///0006094 //
1415871_a	0.001063	1.34	-1.11	NM_009369	<i>Tgfb1</i>	transforming growth factor, beta induced	0001525 // angiogenesis // inferred from electronic annotation///0002062 // chondrocyte differentiation // inferred from
1449360_a	0.001186	1.34	-1.03	NM_001287389///NM_01	<i>Csf2rb2</i> ///Csf2rb	colony stimulating factor 2 receptor, beta 2, low-affinity (granulocyte-	0019221 // cytokine-mediated signaling pathway // inferred from electronic annotation
1419627_s	0.002516	1.34	1.06	NM_001190320///NM_01	<i>Clec4n</i>	C-type lectin domain family 4, member n	0002376 // immune system process // inferred from electronic annotation///0043123 // positive regulation of I-kappaB
1417300_a	0.000036	1.33	1.07	NM_133888	<i>Smpd13b</i>	sphingomyelin phosphodiesterase, acid-like 3B	0006685 // sphingomyelin catabolic process // inferred from electronic annotation///0008152 // metabolic process // inferred
1422130_a	0.001691	1.33	1.33	NM_008730	<i>Nptx1</i>	neuronal pentraxin 1	0006839 // mitochondrial transport // not recorded///0035865 // cellular response to potassium ion // not
1419564_a	0.000338	1.33	1.20	NM_001085415///NM_01	<i>Zfp467</i>	zinc finger protein 467	0006351 // transcription, DNA-templated // inferred from electronic annotation///0006355 // regulation of transcription, DNA-
1428053_a	0.000641	1.33	1.52	NM_153071///XM_00651	<i>Gprc6a</i>	G protein-coupled receptor, family C, group 6, member A	0002232 // leukocyte chemotaxis involved in inflammatory response // inferred from mutant phenotype///0002385 //
1417160_s	0.001766	1.33	1.09	NM_007969	<i>Wfdc18</i>	WAP four-disulfide core domain 18	0010466 // negative regulation of peptidase activity // inferred from electronic annotation
1418547_a	0.000533	1.33	-1.03	NM_009364///XM_0065C	<i>Tfpi2</i>	tissue factor pathway inhibitor 2	0007596 // blood coagulation // inferred from electronic annotation///0007599 // hemostasis // inferred from electronic
1419410_a	0.000153	1.33	-1.05	NM_016767	<i>Batf</i>	basic leucine zipper transcription factor, ATF-like	0001816 // cytokine production // inferred from mutant phenotype///0002320 // lymphoid progenitor cell differentiation //
1416600_a	0.000715	1.33	-1.05	NM_001081549///NM_01	<i>Rcan1</i>	regulator of calcineurin 1	0002931 // response to ischemia // inferred from mutant phenotype///0006950 // response to stress // inferred from genetic
1420361_a	0.000007	1.33	-1.22	NM_013612///XM_00645	<i>Slc11a1</i>	solute carrier family 11 (proton-coupled divalent metal ion	0000060 // protein import into nucleus, translocation // inferred from mutant phenotype///0000165 // MAPK cascade // not
1440890_a	0.000196	1.32	1.24	NM_001164624///NM_11	<i>Zfp809</i>	zinc finger protein 809	0006355 // regulation of transcription, DNA-templated // not recorded
1454617_a	0.000540	1.32	1.24	NM_001042591///XM_0C	<i>Arrdc3</i>	arrestin domain containing 3	0001659 // temperature homeostasis // inferred from mutant phenotype///0031651 // negative regulation of heat generation
1425215_a	0.000069	1.32	-1.01	NM_001168509///NM_01	<i>Ffar2</i>	free fatty acid receptor 2	0002232 // leukocyte chemotaxis involved in inflammatory response // inferred from mutant phenotype///0002385 //
1449088_a	0.000705	1.32	-1.12	NM_007994	<i>Fbp2</i>	fructose biphosphatase 2	0005975 // carbohydrate metabolic process // inferred from electronic annotation///0006094 // gluconeogenesis // not
1428052_a	0.000007	1.32	1.16	NM_026670///XM_0065C	<i>Zmym1</i>	zinc finger, MYM domain containing 1	0006200 // ATP catabolic process // not recorded///0006351 // transcription, DNA-templated // inferred from electronic
1436174_a	0.001134	1.32	1.10	NM_027435///NM_15311	<i>Atad2</i>	ATPase family, AAA domain containing 2	0001913 // T cell mediated cytotoxicity // inferred from genetic interaction///0006508 // proteolysis // inferred from mutant
1419376_a	0.000662	1.32	1.15	NM_026271	<i>Fibin</i>	fin bud initiation factor homolog (zebrafish)	0009191 // ribonucleoside diphosphate catabolic process // not recorded///0009203 // ribonucleoside triphosphate catabolic
1416382_a	0.002023	1.32	1.02	NM_009982///XM_0065C	<i>Ctsc</i>	cathepsin C	0008152 // metabolic process // inferred from electronic annotation
1432068_a	0.001168	1.32	1.09	NM_053103	<i>Entpd7</i>	ectonucleoside triphosphate diphosphohydrolase 7	0006351 // transcription, DNA-templated // inferred from electronic annotation///0006355 // regulation of transcription, DNA-
1427506_a	0.001769	1.32	-1.01	NM_001081406///NM_01	<i>Lrr1</i>	leucine rich repeat protein 1	0001656 // metanephros development // inferred from expression pattern///0006355 // regulation of transcription, DNA-
1435188_a	0.000432	1.32	1.45	NM_001033302///XM_0C	<i>Clart</i>	circadian associated repressor of transcription	0001666 // response to hypoxia // inferred from mutant phenotype///0006801 // superoxide metabolic process // inferred
1424970_a	0.000078	1.31	1.08	NM_001098233///NM_11	<i>Purg</i>	purine-rich element binding protein G	0000209 // protein polyubiquitination // not recorded///0006260 // DNA replication // inferred from electronic
1426298_a	0.000056	1.31	1.11	NM_010574///XM_00651	<i>Irx2</i>	Iroquois related homeobox 2 (Drosophila)	0006508 // proteolysis // not recorded///0006511 // ubiquitin-dependent protein catabolic process // inferred from electronic
1417633_a	0.000130	1.31	-1.04	NM_011435	<i>Sod3</i>	superoxide dismutase 3, extracellular	0043123 // positive regulation of I-kappaB kinase/NF-kappaB signaling // not recorded
1434695_a	0.000529	1.31	-1.08	NM_029766///XM_00645	<i>Dtl</i>	denticlesless homolog (Drosophila)	0055085 // transmembrane transport // inferred from electronic annotation
1433927_a	0.001545	1.31	-1.03	NM_001013378///NM_01	<i>Usp1</i>	ubiquitin specific peptidase like 1	0007165 // signal transduction // inferred from electronic annotation///0007601 // visual perception // inferred from mutant
1424542_a	0.000073	1.31	-1.26	NM_011311///XM_0065C	<i>S100a4</i>	S100 calcium binding protein A4	0007165 // MAPK cascade // not recorded///0000186 // activation of MAPKK activity // not recorded///0002376 // immune
1435912_a	0.000751	1.31	1.07	NM_177633///XM_00652	<i>Ubxn7</i>	UBX domain protein 7	0006351 // transcription, DNA-templated // inferred from electronic annotation///0006355 // regulation of transcription, DNA-
1455508_a	0.000357	1.30	1.10	NM_177186///XM_00653	<i>Slc35e2</i>	solute carrier family 35, member E2	0000122 // negative regulation of transcription from RNA polymerase II promoter // inferred from direct assay///0001658 //
1421061_a	0.001475	1.30	-1.03	NM_008189	<i>Guca1a</i>	guanylate cyclase activator 1a (retina)	0007157 // heterophilic cell-cell adhesion // not recorded
1419208_a	0.000787	1.30	1.15	NM_007746///XM_00652	<i>Map3k8</i>	mitogen-activated protein kinase kinase 8	0008285 // negative regulation of cell proliferation // inferred from direct assay
1434532_a	0.001280	1.30	1.13	NM_153407///XM_00652	<i>Csrp2</i>	cysteine-serine-rich nuclear protein 2	0006351 // transcription, DNA-templated // inferred from electronic annotation///0006355 // regulation of transcription, DNA-
1417586_a	0.000137	1.30	1.03	NM_001136082///NM_01	<i>Timeless</i>	timeless circadian clock 1	0000122 // negative regulation of transcription from RNA polymerase II promoter // inferred from direct assay///0001658 //
1421217_a	0.001087	1.30	-1.07	NM_001159301///NM_01	<i>Lgals9</i>	lectin, galactose binding, soluble 9	0007157 // heterophilic cell-cell adhesion // not recorded
1453038_a	0.002116	1.30	-1.01	NM_197997///XM_0065C	<i>Zgrf1</i>	zinc finger, GRF-type containing 1	0008285 // negative regulation of cell proliferation // inferred from direct assay
1431116_a	0.000676	1.30	1.08	NM_029881///XM_00651	<i>Tmem200a</i>	transmembrane protein 200A	0006351 // transcription, DNA-templated // inferred from electronic annotation///0006355 // regulation of transcription, DNA-
1450165_a	0.001025	1.30	-1.06	NM_011408	<i>Sifn2</i>	schlafen 2	0001501 // skeletal system development // inferred from mutant phenotype///0030199 // collagen fibril organization //
1448181_a	0.000817	1.29	1.26	NM_023184///XM_0065C	<i>Klf15</i>	Kruppel-like factor 15	0006886 // intracellular protein transport // inferred from electronic annotation///0007186 // G-protein coupled receptor
1422437_a	0.000095	1.29	-1.04	NM_007737	<i>Col5a2</i>	collagen, type V, alpha 2	0030031 // cell projection assembly // inferred from direct assay///0051693 // actin filament capping // inferred from
1437884_a	0.000169	1.29	1.02	NM_029466	<i>Arl5b</i>	ADP-ribosylation factor-like 5B	0016488 // farnesol catabolic process // not recorded///0044597 // daunorubicin metabolic process // not
1450355_a	0.000007	1.29	-1.01	NM_001042534///NM_01	<i>Capg</i>	capping protein (actin filament), gelsolin-like	0000910 // cytokinesis // not recorded///0001525 // angiogenesis // inferred from electronic annotation///0006184 // GTP
1448894_a	0.001776	1.29	-1.05	NM_008012	<i>Akr1b8</i>	aldo-keto reductase family 1, member B8	0029492 // D-serine transport // not recorded///0045892 // negative regulation of transcription, DNA-templated // inferred
1449110_a	0.000728	1.29	1.08	NM_007483	<i>Rhob</i>	ras homolog gene family, member B	0016311 // dephosphorylation // inferred from direct assay///0016311 // dephosphorylation // not recorded///0046854 //
1431843_a	0.000548	1.29	-1.06	NM_008690///XM_00652	<i>Nfkbie</i>	NF-kappaB enhancer 1 polypeptide gene enhancer in B cells	0006184 // GTP catabolic process // inferred from electronic annotation///0006810 // transport // inferred from electronic
1418764_a	0.000175	1.28	1.10	NM_011794///XM_00645	<i>Bpnt1</i>	bisphosphate 3'-nucleotidase 1	0000244 // spliceosomal tri-snRNP complex assembly // not recorded///0006397 // mRNA processing // inferred from
1438097_a	0.001284	1.28	-1.00	NM_011227	<i>Rab20</i>	RAB20, member RAS oncogene family	0001764 // neuron migration // inferred from electronic annotation///0006184 // GTP catabolic process // inferred from
1451884_a	0.000692	1.28	1.08	NM_001110101///NM_01	<i>Lsm2</i>	LSM2 homolog, U6 small nuclear RNA associated (S. cerevisiae)	0006810 // transport // inferred from electronic annotation///0008643 // carbohydrate transport // inferred from electronic
1427347_s	0.000106	1.28	-1.15	NM_009450	<i>Tubb2a</i>	tubulin, beta 2A class IIA	0001503 // ossification // inferred from electronic annotation///0006461 // protein complex assembly // not
1452139_a	0.000578	1.28	1.06	NM_145832///NM_21131	<i>Slc35c1</i>	solute carrier family 35, member C1	0007610 // behavior // inferred from electronic annotation///0008033 // tRNA processing // inferred from electronic
1424020_a	0.001757	1.28	1.12	NM_022989	<i>Arl6ip6</i>	ADP-ribosylation factor-like 6 interacting protein 6	0006629 // lipid metabolic process // inferred from electronic annotation///0006694 // steroid biosynthetic process // inferred
1448416_a	0.000019	1.28	1.11	NM_008597	<i>Mgp</i>	matrix Gla protein	0006810 // transport // inferred from electronic annotation///0006811 // ion transport // inferred from electronic
1426879_a	0.002250	1.28	1.04	NM_026876///XM_00652	<i>Trmt1</i>	TRNA methyltransferase 1 like	0006810 // transport // inferred from electronic annotation///0006811 // ion transport // inferred from electronic
1423418_a	0.001866	1.28	-1.13	NM_001253751///NM_11	<i>Fdps</i>	farnesyl diphosphate synthetase	0007165 // signal transduction // inferred from electronic annotation///0007186 // G-protein coupled receptor signaling
1416560_a	0.000893	1.28	1.02	NM_054055///XM_00645	<i>Slc13a3</i>	solute carrier family 13 (sodium-dependent dicarboxylate transporter),	0006468 // protein phosphorylation // inferred from electronic annotation///0007165 // signal transduction // traceable
1425649_a	0.000413	1.28	-1.01	NM_001135151///NM_01	<i>Slc39a14</i>	solute carrier family 39 (zinc transporter), member 14	0000188 // inactivation of MAPK activity // not recorded///0000188 // inactivation of MAPK activity // inferred from direct
1449310_a	0.000539	1.28	1.20	NM_008964///XM_00651	<i>Ptger2</i>	prostaglandin E receptor 2 (subtype EP2)	0000737 // DNA catabolic process, endonucleolytic // ---//0000737 // DNA catabolic process, endonucleolytic // inferred from
1451014_a	0.001140	1.28	1.04	NM_013845///XM_0065C	<i>Ror1</i>	receptor tyrosine kinase-like orphan receptor 1	0006915 // apoptotic process // inferred from electronic annotation///0007275 // multicellular organismal development //
1418401_a	0.000340	1.27	1.12	NM_001048054///NM_11	<i>Dusp16</i>	dual specificity phosphatase 16	
1424322_a	0.000633	1.27	-1.04	NM_029943///XM_00652	<i>Apex2</i>	apurinic/aprymidinic endonuclease 2	
1416880_a	0.000353	1.27	1.03	NM_008562///XM_0065C	<i>Mcl1</i>	myeloid cell leukemia sequence 1	

Table S1

Gene_ID	p	FC-RSV 1 d	FC-RSV 5 d	RefSeq Transcript ID	Gene Symbol	Gene Title	Gene Ontology Biological Process
1421679_a	0.000082	1.27	-1.11	NM_001111099//NM_01	<i>Cdkn1a</i>	cyclin-dependent kinase inhibitor 1A (P21)	0000079 // regulation of cyclin-dependent protein serine/threonine kinase activity // inferred from mutant
1416572_a	0.000113	1.27	-1.05	NM_008608	<i>Mmp14</i>	matrix metalloproteinase 14 (membrane-inserted)	0001503 // ossification // inferred from genetic interaction//0001525 // angiogenesis // inferred from electronic
1451139_a	0.000554	1.27	1.03	NM_028064//XM_00652	<i>Slc39a4</i>	solute carrier family 39 (zinc transporter), member 4	0006810 // transport // inferred from electronic annotation//0006811 // ion transport // inferred from electronic
1460255_a	0.001522	1.26	1.05	NM_033622//XM_0065C	<i>Tnfrsf13b</i>	tumor necrosis factor (ligand) superfamily, member 13b	0001782 // B cell homeostasis // inferred from mutant phenotype//0002636 // positive regulation of germinal center
1419993_a	0.001427	1.26	1.08	NM_144538//XM_00652	<i>Rab31l1</i>	RAB3A interacting protein (rabin3)-like 1	0006810 // transport // inferred from electronic annotation//0015031 // protein transport // inferred from electronic
1419522_a	0.000270	1.26	1.03	NM_026021//XM_00645	<i>Zmynd19</i>	zinc finger, MYND domain containing 19	
1417719_a	0.000305	1.26	1.14	NM_021788	<i>Sap30</i>	sin3 associated polypeptide	0000122 // negative regulation of transcription from RNA polymerase II promoter // inferred from direct assay//0006351 //
1420964_a	0.000879	1.26	1.06	NM_007930	<i>Enc1</i>	ectodermal-neural cortex 1	0007275 // multicellular organismal development // inferred from electronic annotation//0010499 // proteasomal ubiquitin-
1418334_a	0.000245	1.26	1.08	NM_001190717//NM_01	<i>Dbf4</i>	DBF4 homolog (S. cerevisiae)	0006260 // DNA replication // inferred from electronic annotation//0006468 // protein phosphorylation // not
1418340_a	0.002560	1.26	-1.09	NM_010185//XM_00645	<i>Fcer1g</i>	Fc receptor, IgE, high affinity I, gamma polypeptide	0001798 // positive regulation of type IIa hypersensitivity // inferred from mutant phenotype//0001805 // positive regulation
1416953_a	0.000464	1.26	1.33	NM_010217	<i>Ctgf</i>	connective tissue growth factor	0001502 // cartilage condensation // inferred from direct assay//0001503 // ossification // inferred from mutant
1452754_a	0.002408	1.26	1.14	NM_029720//XM_00652	<i>Crel2</i>	cysteine-rich with EGF-like domains 2	
1448276_a	0.000245	1.26	1.43	NM_001252588//NM_01	<i>Tspan4</i>	tetraspanin 4	
1416527_a	0.001641	1.26	1.02	NM_026405	<i>Rab32</i>	RAB32, member RAS oncogene family	0006184 // GTP catabolic process // inferred from electronic annotation//0006886 // intracellular protein transport //
1424356_a	0.002173	1.25	1.08	NM_144797	<i>Metnl</i>	meteorin, glial cell differentiation regulator-like	0009409 // response to cold // inferred from direct assay//0014850 // response to muscle activity // inferred from direct
1433481_a	0.000645	1.25	1.18	NM_153573//XR_37743	<i>Fkbp14</i>	FK506 binding protein 14	0000413 // protein peptidyl-prolyl isomerization // not recorded//0006457 // protein folding // inferred from electronic
1419132_a	0.000750	1.25	1.04	NM_011905//XM_0065C	<i>Tlr2</i>	toll-like receptor 2	0001666 // response to hypoxia // inferred from electronic annotation//0001774 // microglial cell activation // not
1424276_a	0.000268	1.25	1.08	NM_001127191//NM_01	<i>Snx16</i>	sorting nexin 16	0006622 // protein targeting to lysosome // not recorded//0006810 // transport // inferred from electronic
1460684_a	0.001438	1.25	1.01	NM_028454	<i>Tm7sf2</i>	transmembrane 7 superfamily member 2	0006629 // lipid metabolic process // inferred from electronic annotation//0006694 // steroid biosynthetic process // inferred
1418132_a	0.000035	1.25	1.00	NM_138589//XM_0065C	<i>Ubfd1</i>	ubiquitin family domain containing 1	
1428635_a	0.000254	1.25	1.13	NM_026965	<i>Comt1</i>	catechol-O-methyltransferase domain containing 1	0032259 // methylation // inferred from electronic annotation
1422005_a	0.002655	1.25	1.05	NM_011163//XM_00652	<i>Eif2ak2</i>	eukaryotic translation initiation factor 2-alpha kinase 2	0000186 // activation of MAPKK activity // not recorded//0001819 // positive regulation of cytokine production // inferred
1423648_a	0.001060	1.25	1.05	NM_027959	<i>Pdia6</i>	protein disulfide isomerase associated 6	0006457 // protein folding // not recorded//0006662 // glycerol ether metabolic process // inferred from electronic
1415720_s	0.002037	1.25	1.15	NM_025649	<i>Mad2l1bp</i>	MAD2L1 binding protein	0007093 // mitotic cell cycle checkpoint // not recorded//0007094 // mitotic spindle assembly checkpoint // not
1417625_s	0.000858	1.25	-1.07	NM_001271607//NM_01	<i>Ackr3</i>	atypical chemokine receptor 3	0001525 // angiogenesis // inferred from electronic annotation//0001570 // vasculogenesis // inferred from electronic
1436673_a	0.000515	1.25	1.00	NM_001163703//NM_01	<i>Dcn1d3</i>	DCN1, defective in culin neddylation 1, domain containing 3 (S.	0010225 // response to UV-C // not recorded//0010332 // response to gamma radiation // not recorded//0030308 //
1416064_a	0.001295	1.25	1.11	NM_001163434//NM_01	<i>Hspa5</i>	heat shock protein 5	0000902 // cell morphogenesis // inferred from electronic annotation//0006983 // ER overload response // inferred from
1425412_a	0.000045	1.25	-1.04	NM_145827//XM_00653	<i>Nlrp3</i>	NLR family, pyrin domain containing 3	0002674 // negative regulation of acute inflammatory response // not recorded//0006915 // apoptotic process // inferred
1425154_a	0.000322	1.25	-1.12	NM_001113529//NM_01	<i>Csf1</i>	colony stimulating factor 1 (macrophage)	0001503 // ossification // not recorded//0001954 // positive regulation of cell-matrix adhesion // inferred from genetic
1434735_a	0.000959	1.25	1.52	NM_172563//XM_00653	<i>Hlf</i>	hepatic leukemia factor	0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 // regulation of transcription, DNA-
1415989_a	0.000536	1.24	1.00	NM_011693	<i>Vcam1</i>	vascular cell adhesion molecule 1	0001666 // response to hypoxia // inferred from electronic annotation//0002526 // acute inflammatory response // inferred
1434195_a	0.002153	1.24	1.03	NM_178738//XM_00651	<i>Prss35</i>	protease, serine 35	0006508 // proteolysis // inferred from electronic annotation//0008152 // metabolic process // inferred from electronic
1452732_a	0.000032	1.24	-1.34	NM_026414	<i>Asprv1</i>	aspartic peptidase, retroviral-like 1	0006508 // proteolysis // inferred from direct assay//0016485 // protein processing // inferred from direct assay//0016485
1429106_a	0.001680	1.24	1.33	NM_011020//XM_0065C	<i>4921509J17Rik</i>	RIKEN cDNA 4921509J17 gene//heat shock protein 4 like	0000902 // cell morphogenesis // inferred from electronic annotation//0006457 // protein folding // not recorded//0006950
1427105_a	0.001157	1.24	-1.10	NM_028131//XM_00653	<i>Cenpn</i>	centromere protein N	0007059 // chromosome segregation // inferred from electronic annotation//0007067 // mitotic nuclear division // inferred
1418162_a	0.001151	1.24	1.10	NM_021297	<i>Tlr4</i>	toll-like receptor 4	0000187 // activation of MAPK activity // inferred from mutant phenotype//0001774 // microglial cell activation // not
1429322_a	0.001438	1.24	1.09	NM_028274//NM_1462	<i>Exosc6</i>	exosome component 6//alanyl-tRNA synthetase	0001942 // hair follicle development // inferred from mutant phenotype//0006364 // rRNA processing // inferred from
1439349_a	0.000458	1.24	-1.11	NM_183426//XM_00651	<i>Sbno2</i>	strawberry notch homolog 2 (Drosophila)	0002281 // macrophage activation involved in immune response // inferred from mutant phenotype//0002281 //
1435938_a	0.000281	1.24	-1.04	NM_181589//XM_0065C	<i>Ckap2l</i>	cytoskeleton associated protein 2-like	
1421395_a	0.000717	1.24	1.17	NM_009577	<i>Zik1</i>	zinc finger protein interacting with K protein 1	0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 // regulation of transcription, DNA-
1427916_a	0.001475	1.24	1.03	NM_001253702//NM_01	<i>St7l</i>	suppression of tumorigenicity 7-like	0030198 // extracellular matrix organization // non-traceable author statement//0030308 // negative regulation of cell
1416221_a	0.001807	1.24	1.03	NM_008047	<i>Fstl1</i>	folliculin-like 1	0042594 // response to starvation // inferred from direct assay
1422506_a	0.001011	1.24	-1.07	NM_007793	<i>Cstb</i>	cystatin B	0008344 // adult locomotory behavior // inferred from mutant phenotype//0010466 // negative regulation of peptidase
1418003_a	0.000022	1.23	1.51	NM_025427//XM_00651	<i>Rgcc</i>	regulator of cell cycle	0000082 // G1/S transition of mitotic cell cycle // not recorded//0001100 // negative regulation of exit from mitosis // not
1422767_a	0.000457	1.23	-1.04	NM_016859	<i>Bysl</i>	bystin-like	0000079 // regulation of cyclin-dependent protein serine/threonine kinase activity // inferred from electronic
1426734_a	0.001320	1.23	-1.07	NM_177632	<i>Fam43a</i>	family with sequence similarity 43, member A	
1418681_a	0.000153	1.23	-1.05	NM_026247//NR_03714	<i>Alg13</i>	asparagine-linked glycosylation 13	0005975 // carbohydrate metabolic process // inferred from electronic annotation//0006508 // proteolysis // inferred from
1417490_a	0.000006	1.23	1.03	NM_007798	<i>Ctsb</i>	cathepsin B	0006508 // proteolysis // not recorded//0030574 // collagen catabolic process // not recorded//0046697 // decidualization
1417968_a	0.000077	1.23	1.06	NM_013594//XM_00652	<i>Mbd1</i>	methyl-CpG binding domain protein 1	0006306 // DNA methylation // traceable author statement//0006351 // transcription, DNA-templated // inferred from
1435932_a	0.000026	1.23	1.06	NM_176785	<i>Hps6</i>	Hermansky-Pudlak syndrome 6	0006996 // organelle organization // inferred from mutant phenotype//0007596 // blood coagulation // inferred from
1449930_a	0.001025	1.23	-1.03	NM_025448//XM_0065C	<i>Ssr2</i>	signal sequence receptor, beta	
1417868_a	0.000270	1.23	1.01	NM_022325	<i>Ctsz</i>	cathepsin Z	0006508 // proteolysis // inferred from electronic annotation//0006441 // epithelial tube branching involved in lung
1456756_a	0.000735	1.23	-1.31	NM_172467	<i>Zc3hav1l</i>	zinc finger CCHC-type, antiviral 1-like	
1416177_a	0.000062	1.23	1.02	NM_001252089//NM_01	<i>Rbmxl1</i>	RNA binding motif protein, X linked-like-1	0000381 // regulation of alternative mRNA splicing, via spliceosome // not recorded//0006366 // transcription from RNA
1433733_a	0.001169	1.22	1.80	NM_007771//XM_00651	<i>Cry1</i>	cryptochrome 1 (photolyase-like)	0000122 // negative regulation of transcription from RNA polymerase II promoter // not recorded//0006094 //
1428527_a	0.000169	1.22	-1.09	NM_001190156//NM_01	<i>Snx7</i>	sorting nexin 7	0006810 // transport // inferred from electronic annotation//0006886 // intracellular protein transport // not
1437209_a	0.000335	1.22	1.10	NM_001081073//XM_0C	<i>Cep76</i>	centrosomal protein 76	0046599 // regulation of centriole replication // not recorded
1423006_a	0.000003	1.22	-1.08	NM_008842	<i>Pim1</i>	proliferin integration site 1	0006468 // protein phosphorylation // not recorded//0008283 // cell proliferation // not recorded//0009103 //
1456208_a	0.001282	1.22	-1.18	NM_001081089//XM_0C	<i>Gpat2</i>	glycerol-3-phosphate acyltransferase 2, mitochondrial	0006072 // glycerol-3-phosphate metabolic process // inferred from direct assay//0006629 // lipid metabolic process //
1426348_a	0.001280	1.22	-1.07	NM_009931//XM_0065C	<i>Col4a1</i>	collagen, type IV, alpha 1	0001525 // angiogenesis // inferred from electronic annotation//0001569 // patterning of blood vessels // not
1430535_a	0.000139	1.22	1.09	NM_001081229//NM_01	<i>Tsc22d2</i>	TSC22 domain family, member 2	0006355 // regulation of transcription, DNA-templated // inferred from electronic annotation//0006970 // response to
1427911_a	0.000116	1.22	1.02	NM_001289591//NM_01	<i>Tmem173</i>	transmembrane protein 173	0002218 // activation of innate immune response // inferred from mutant phenotype//0002218 // activation of innate
1417836_a	0.000528	1.22	1.00	NM_024198	<i>Gpx7</i>	glutathione peroxidase 7	0006979 // response to oxidative stress // inferred from electronic annotation//0055114 // oxidation-reduction process //
1428654_a	0.000983	1.22	1.10	NM_025819	<i>Swf1</i>	SWT1 RNA endoribonuclease homolog (S. cerevisiae)	
1416029_a	0.000291	1.22	1.01	NM_001289471//NM_01	<i>Klf10</i>	Kruppel-like factor 10	0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 // regulation of transcription, DNA-
1455945_a	0.000277	1.22	1.14	NM_001007575	<i>Zfp58</i>	zinc finger protein 58	0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 // regulation of transcription, DNA-

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Gene_ID	p	FC-RSV 1 d	FC-RSV 5 d	RefSeq Transcript ID	Gene Symbol	Gene Title	Gene Ontology Biological Process
1425261_a	0.001931	1.22	1.13	NM_009884//XM_00653	<i>Cebpγ</i>	CCAAT/enhancer binding protein (C/EBP), gamma	0001889 // liver development // inferred from sequence or structural similarity//0001889 // liver development // inferred
1416030_a	0.000728	1.22	-1.06	NM_008568//XM_0065C	<i>Mcm7</i>	minichromosome maintenance deficient 7 (S. cerevisiae)	0006260 // DNA replication // inferred from electronic annotation//0006268 // DNA unwinding involved in DNA replication //
1434689_a	0.00123	1.22	1.18	NM_177684//XM_0065C	<i>Zfp637</i>	zinc finger protein 637	
1430666_a	0.001394	1.22	1.03	NM_001081407//NM_0:	<i>Plb1</i>	phospholipase B1	0006629 // lipid metabolic process // inferred from electronic annotation//0006644 // phospholipid metabolic process // not
1438003_a	0.002139	1.22	1.08	NM_001169131//NM_1:	<i>Papd7</i>	PAP-associated domain containing 7	0006260 // DNA replication // inferred from electronic annotation//0006261 // DNA-dependent DNA replication // inferred
1417094_a	0.000888	1.22	-1.04	NM_001146057//NM_0:	<i>Acot7</i>	acyl-CoA thioesterase 7	0009062 // fatty acid catabolic process // inferred from direct assay//0015937 // coenzyme A biosynthetic process // not
1424314_a	0.000827	1.22	-1.00	NM_027541//XM_0065C	<i>Prp3</i>	PRP3 pre-mRNA processing factor 3 homolog (yeast)	0000398 // mRNA splicing, via spliceosome // inferred from electronic annotation//0006397 // mRNA processing // inferred
1419543_a	0.001361	1.21	1.02	NM_009186//XM_00652	<i>Tra2b</i>	transformer 2 beta homolog (Drosophila)	0000302 // response to reactive oxygen species // inferred from electronic annotation//0000381 // regulation of alternative
1415860_a	0.002497	1.21	1.00	NM_010655	<i>Kpna2</i>	karyopherin (importin) alpha 2	0006606 // protein import into nucleus // inferred from direct assay//0006607 // NLS-bearing protein import into nucleus //
1427178_a	0.001420	1.21	1.09	NM_181820	<i>Tmc4</i>	transmembrane channel-like gene family 4	0006810 // transport // inferred from electronic annotation//0006811 // ion transport // inferred from electronic annotation
1416530_a	0.000913	1.21	1.07	NM_013632//NM_0011:	<i>Pnp2//Pnp2</i>	purine-nucleoside phosphorylase//purine-nucleoside phosphorylase 2	0001916 // positive regulation of T cell mediated cytotoxicity // inferred from mutant phenotype//0006139 // nucleobase-
1416256_a	0.001723	1.21	-1.07	NM_011655	<i>Tubb5</i>	tubulin, beta 5 class I	0006184 // GTP catabolic process // inferred from electronic annotation//0006457 // protein folding // traceable author
142648_a	0.002614	1.21	1.24	NM_001044740//NM_0:	<i>Slc7a2</i>	solute carrier family 7 (cationic amino acid transporter, y+ system),	0002537 // nitric oxide production involved in inflammatory response // inferred from mutant phenotype//0003333 // amino
1428752_a	0.000151	1.21	-1.01	NM_146198//XM_0065C	<i>Slc5a11</i>	solute carrier family 5 (sodium/glucose cotransporter), member 11	0006810 // transport // inferred from electronic annotation//0006811 // ion transport // inferred from electronic
1416021_a	0.002140	1.21	-1.05	NM_001272097//NM_0:	<i>Fabp5</i>	fatty acid binding protein 5, epidermal	0006006 // glucose metabolic process // inferred from mutant phenotype//0006629 // lipid metabolic process // inferred
1417158_a	0.001014	1.20	1.08	NM_030260//NM_1730:	<i>Zxdc</i>	ZXD family zinc finger C	0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 // regulation of transcription, DNA-
1423903_a	0.000949	1.20	-1.07	NM_027514	<i>Pvr</i>	poliovirus receptor	0002860 // positive regulation of natural killer cell mediated cytotoxicity directed against tumor cell target // inferred from
1418115_s	0.000245	1.20	1.07	NM_001160180//NM_0:	<i>Tor1a1p2</i>	torsin A interacting protein 2	0007029 // endoplasmic reticulum organization // not recorded//0032781 // positive regulation of ATPase activity // not
1425568_a	0.000022	1.20	1.09	NM_001285452//NM_0:	<i>Tmem33</i>	transmembrane protein 33	
1426754_x	0.000691	1.20	-1.08	NM_175451	<i>Ckap4</i>	cytoskeleton-associated protein 4	
1430569_a	0.002152	1.20	1.04	NM_027412//XR_38650:	<i>Ttc9c</i>	tetratricopeptide repeat domain 9C	0000413 // protein peptidyl-prolyl isomerization // ---//0018208 // peptidyl-proline modification // not recorded//0061077
1415800_a	0.000709	1.20	-1.10	NM_010288//XM_00651	<i>Gja1</i>	gap junction protein, alpha 1	0001649 // osteoblast differentiation // inferred from mutant phenotype//0001701 // in utero embryonic development //
1419192_a	0.002209	1.20	-1.15	NM_001171024//NM_0:	<i>Il4i1//Nup62-il4i1</i>	interleukin 4 induced 1//Nup62-II4i1 protein	0006351 // transcription, DNA-templated // inferred from sequence or structural similarity//0006810 // transport // inferred
1439536_a	0.000251	1.20	1.09	NM_026197//XM_00653	<i>Mettl16</i>	methyltransferase like 16	0032259 // methylation // inferred from electronic annotation//0006479 // protein methylation // inferred from electronic
1448250_a	0.001776	1.20	-1.27	NM_133733//XM_00651	<i>Clmp</i>	CXADR-like membrane protein	0048565 // digestive tract development // not recorded
1416915_a	0.002042	1.20	1.07	NM_010830	<i>Msh6</i>	mutS homolog 6 (E. coli)	0000710 // meiotic mismatch repair // not recorded//0006200 // ATP catalytic process // not recorded//0006281 // DNA
1421720_a	0.000266	1.20	1.07	NM_001256096//NM_0:	<i>Dtx2</i>	deltex 2 homolog (Drosophila)	0007219 // Notch signaling pathway // inferred from direct assay//0007219 // Notch signaling pathway // traceable author
1416998_a	0.001373	1.20	1.01	NM_021511	<i>Rrs1</i>	RRS1 ribosome biogenesis regulator homolog (S. cerevisiae)	0002244 // hematopoietic progenitor cell differentiation // inferred from mutant phenotype//0007080 // mitotic metaphase
1417516_a	0.001240	1.19	1.06	NM_001290183//NM_0:	<i>Ddit3</i>	DNA-damage inducible transcript 3	0001955 // blood vessel maturation // inferred from mutant phenotype//0006351 // transcription, DNA-templated //
1416313_a	0.000394	1.19	1.02	NM_019914//XM_0065C	<i>Mllt11</i>	myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog,	0043065 // positive regulation of apoptotic process // not recorded//0045893 // positive regulation of transcription, DNA-
1418859_a	0.001909	1.19	1.04	NM_133231	<i>Rfxap</i>	regulatory factor X-associated protein	0045893 // positive regulation of transcription, DNA-templated // inferred from direct assay
1421177_a	0.002084	1.19	1.05	NM_025780	<i>Thop2</i>	THAP domain containing, apoptosis associated protein 2	
1415940_a	0.000393	1.19	1.05	NM_001159908//NM_1:	<i>Zfand2a</i>	zinc finger, AN1-type domain 2A	0032466 // positive regulation of proteasomal ubiquitin-dependent protein catabolic process // inferred from mutant
1450791_a	0.000485	1.19	2.39	NM_001287348//NM_0:	<i>Nppb</i>	natriuretic peptide type B	0001666 // response to hypoxia // inferred from electronic annotation//0003085 // negative regulation of systemic arterial
1434859_a	0.000925	1.19	1.05	NM_009471//XM_00652	<i>Umps</i>	uridine monophosphate synthetase	0006207 // 'de novo' pyrimidine nucleobase biosynthetic process // inferred from electronic annotation//0006221 //
1417032_a	0.001350	1.19	-1.02	NM_019803	<i>Ube2g2</i>	ubiquitin-conjugating enzyme E2G 2	0016567 // protein ubiquitination // inferred from electronic annotation//0018279 // protein N-linked glycosylation via
1448059_a	0.002069	1.19	1.11	NM_001164370	<i>Mipol1</i>	mirror-image polydactyl gene 1 homolog (human)	0006144 // purine nucleobase metabolic process // inferred from electronic annotation//0006164 // purine nucleotide
1436979_x	0.002376	1.19	1.03	NM_019869//XM_00653	<i>Rbm14//Rbm14-rf</i>	RNA binding motif protein 14//Rbm14-Rbm4 readthrough//RNA	0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 // regulation of transcription, DNA-
1424972_a	0.000884	1.19	1.11	NM_001205052//NM_0:	<i>Jdp2</i>	Jun dimerization protein 2	0000122 // negative regulation of transcription from RNA polymerase II promoter // inferred from direct assay//0000122 //
1448316_a	0.000386	1.19	-1.10	NM_024217//XM_00653	<i>Cmtm3</i>	CKLF-like MARVEL transmembrane domain containing 3	0006935 // chemotaxis // inferred from electronic annotation//0050861 // positive regulation of B cell receptor signaling
1425806_a	0.002754	1.18	1.02	NM_025315	<i>Med21</i>	mediator complex subunit 21	0001824 // blastocyst development // inferred from mutant phenotype//0006351 // transcription, DNA-templated // inferred
1418382_a	0.001942	1.18	1.19	NM_133237	<i>Apcdd1</i>	adenomatosis polyposis coli down-regulated 1	0001942 // hair follicle development // not recorded//0016055 // Wnt signaling pathway // inferred from electronic
1451503_a	0.002035	1.18	-1.03	NM_030152//XM_00653	<i>No13</i>	nucleolar protein 3 (apoptosis repressor with CARD domain)	0001666 // response to hypoxia // inferred from mutant phenotype//0006397 // mRNA processing // inferred from electronic
1437026_a	0.000354	1.18	1.03	NM_173033//XM_00653	<i>Tstd2</i>	thiosulfate sulfurtransferase (rhodanese)-like domain containing 2	
1425356_a	0.001395	1.18	-1.02	NM_029888//XM_00645	<i>Zfp142</i>	zinc finger protein 142	0006629 // lipid metabolic process // inferred from electronic annotation//0007165 // signal transduction // inferred from
1421828_a	0.000050	1.18	1.06	NM_008466	<i>Kpna3</i>	karyopherin (importin) alpha 3	0006606 // protein import into nucleus // inferred from electronic annotation//0006810 // transport // inferred from
1418673_a	0.000477	1.18	-1.07	NM_011415	<i>Snai2</i>	snail family zinc finger 2	0000122 // negative regulation of transcription from RNA polymerase II promoter // inferred from direct assay//0000122 //
1429502_a	0.000595	1.18	1.01	NM_030201//NR_02749	<i>Hspa13</i>	heat shock protein 70 family, member 13	0000902 // cell morphogenesis // inferred from electronic annotation
1435644_a	0.002485	1.18	-1.04	NM_177364//XM_00651	<i>Sh3pxd2b</i>	SH3 and PX domains 2B	0001501 // skeletal system development // inferred from mutant phenotype//0001501 // skeletal system development // not
1436443_a	0.000415	1.18	1.03	NM_023645//XM_00645	<i>Kdelc1</i>	KDEL (Lys-Asp-Glu-Leu) containing 1	
1418442_a	0.000338	1.18	1.02	NM_001035226//NM_1:	<i>Xpo1</i>	exportin 1, CRM1 homolog (yeast)	0000122 // negative regulation of transcription from RNA polymerase II promoter // not recorded//0006611 // protein export
1423338_a	0.000592	1.18	1.01	NM_025884	<i>Zfp830</i>	zinc finger protein 830	0001832 // blastocyst growth // inferred from mutant phenotype//0007049 // cell cycle // inferred from electronic
1416872_a	0.002706	1.18	-1.02	NM_019656	<i>Tspan6</i>	tetraspanin 6	0007165 // signal transduction // not recorded//0043123 // positive regulation of I-kappaB kinase/NF-kappaB signaling // not
1436521_a	0.002113	1.17	-1.06	NM_153170//XM_00653	<i>Slc36a2</i>	solute carrier family 36 (proton/amino acid symporter), member 2	0006950 // response to stress // inferred from electronic annotation//0010155 // regulation of proton transport // not
1449859_a	0.001187	1.17	1.06	NM_025872//XM_0065C	<i>Golt1b</i>	golgi transport 1 homolog B (S. cerevisiae)	0006810 // transport // inferred from electronic annotation//0007165 // signal transduction // not recorded//0015031 //
1418465_a	0.001539	1.17	-1.13	NM_008677//XM_00652	<i>Ncf4</i>	neutrophil cytosolic factor 4	0007154 // cell communication // inferred from electronic annotation//0043085 // positive regulation of catalytic activity //
1419609_a	0.000074	1.17	-1.15	NM_009912	<i>Ccr1</i>	chemokine (C-C motif) receptor 1	0006816 // calcium ion transport // not recorded//0006874 // cellular calcium ion homeostasis // not recorded//0006887 //
1426722_a	0.002228	1.17	1.01	NM_175121//XM_00652	<i>Slc38a2</i>	solute carrier family 38, member 2	0003333 // amino acid transmembrane transport // inferred from direct assay//0006810 // transport // inferred from
1418150_a	0.001151	1.17	1.02	NM_133215//XM_00653	<i>Mtm4</i>	myotubularin related protein 4	0014894 // response to denervation involved in regulation of muscle adaptation // inferred from electronic
1416166_a	0.001869	1.17	1.03	NM_016764//XM_00652	<i>Prdx4</i>	peroxiredoxin 4	0007283 // spermatogenesis // inferred from mutant phenotype//0008584 // male gonad development // inferred from
1438480_a	0.001818	1.17	1.02	NM_144543//XM_00651	<i>Thyn1</i>	thymocyte nuclear protein 1	
1416748_a	0.001293	1.17	1.02	NM_018736//XM_00651	<i>Mre11a</i>	meiotic recombination 11 homolog A (S. cerevisiae)	0000723 // telomere maintenance // not recorded//0006259 // DNA metabolic process // inferred from electronic
1416303_a	0.002428	1.17	-1.08	NM_019980//XM_00652	<i>Litaf//Gm9861</i>	LPS-induced TN factor//predicted gene 9861	0001817 // regulation of cytokine production // inferred from mutant phenotype//0006351 // transcription, DNA-templated
1416740_a	0.001983	1.17	-1.11	NM_015734//XM_00645	<i>Col5a1</i>	collagen, type V, alpha 1	0001568 // blood vessel development // inferred from mutant phenotype//0003007 // heart morphogenesis // inferred from
1429568_x	0.000238	1.17	1.03	NM_026454//XM_00652	<i>Ube2f</i>	ubiquitin-conjugating enzyme E2F (putative)	0045116 // protein neddylation // inferred from mutant phenotype//0045116 // protein neddylation // not recorded
1422046_a	0.000679	1.17	-1.21	NM_001082960//NM_0:	<i>Itgam</i>	integrin alpha M	0002523 // leukocyte migration involved in inflammatory response // inferred from mutant phenotype//0006412 //

Table S1

Gene_ID	p	FC-RSV 1 d	FC-RSV 5 d	RefSeq Transcript ID	Gene Symbol	Gene Title	Gene Ontology Biological Process
1436716_a	0.000205	1.17	-1.01	NM_008889	<i>Ppp1r14b</i>	protein phosphatase 1, regulatory (inhibitor) subunit 14B	0042325 // regulation of phosphorylation // inferred from electronic annotation//0043086 // negative regulation of catalytic
1425913_a	0.002413	1.16	1.01	NM_001164566//NM_1_0	<i>Spots2l</i>	spermatogenesis associated, serine-rich 2-like	
1452013_a	0.002281	1.16	1.22	NM_009728//XM_00654	<i>Atp10a</i>	ATPase, class V, type 10A	0006810 // transport // inferred from electronic annotation//0006812 // cation transport // inferred from electronic
1415892_a	0.000259	1.16	1.01	NM_009163//XM_00651	<i>Sgpl1</i>	serpingosine phosphate lyase 1	0001553 // luteinization // inferred from mutant phenotype//0001570 // vasculogenesis // inferred from mutant
1427682_a	0.000085	1.16	-1.04	NM_010118//XM_00651	<i>Egr2</i>	early growth response 2	0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 // regulation of transcription, DNA-
1426808_a	0.001125	1.16	-1.03	NM_001145953//NM_0_	<i>Lgals3</i>	lectin, galactose binding, soluble 3	0001501 // skeletal system development // inferred from genetic interaction//0002376 // immune system process // inferred
1416273_a	0.000226	1.16	-1.04	NM_009396//XM_00651	<i>Tnfrsf2</i>	tumor necrosis factor, alpha-induced protein 2//Mus musculus 7 days	0001525 // angiogenesis // inferred from electronic annotation//0006887 // exocytosis // inferred from electronic
1417998_a	0.002526	1.16	1.03	NM_019766//XM_00394	<i>Gm9769</i>	predicted pseudogene 9769//prostaglandin E synthase 3 (cytosolic)	0001516 // prostaglandin biosynthetic process // inferred from mutant phenotype//0001516 // prostaglandin biosynthetic
1417998_a	0.002526	1.16	1.03	NM_019766//XM_00394	<i>Gm9769</i>	predicted pseudogene 9769//prostaglandin E synthase 3 (cytosolic)	0001516 // prostaglandin biosynthetic process // inferred from mutant phenotype//0001516 // prostaglandin biosynthetic
1420631_a	0.002627	1.16	1.02	NM_016916//XM_00645	<i>Btcap</i>	bladder cancer associated protein homolog (human)	0006915 // apoptotic process // inferred from electronic annotation//0007049 // cell cycle // inferred from electronic
1419420_a	0.001442	1.16	1.15	NM_012028	<i>St6galnac5</i>	ST6 (alpha-N-acetyl-neuraminyl-2,3-beta-galactosyl-1,3)-N-	0006486 // protein glycosylation // inferred from electronic annotation//0006688 // glycosphingolipid biosynthetic process //
1434843_a	0.001441	1.16	1.12	NM_177805//XM_00651	<i>Fam179b</i>	family with sequence similarity 179, member B	
1424211_a	0.000366	1.16	1.37	NM_027460//XM_00653	<i>Slc25a33</i>	solute carrier family 25, member 33	0006810 // transport // inferred from electronic annotation
1420404_a	0.002083	1.16	1.00	NM_019388//XM_00652	<i>Cd86</i>	CD86 antigen	0001878 // response to yeast // inferred from electronic annotation//0002224 // toll-like receptor signaling pathway //
1426386_a	0.000351	1.16	1.01	NM_025433	<i>Rpl7l1</i>	ribosomal protein L7-like 1	
1423265_a	0.000679	1.16	1.15	NM_010799	<i>Minpp1</i>	multiple inositol polyphosphate histidine phosphatase 1	0008152 // metabolic process // inferred from electronic annotation//0016311 // dephosphorylation // not recorded
1424648_a	0.000505	1.16	1.09	NM_025931	<i>Ifi27</i>	intraflagellar transport 27	0006184 // GTP catabolic process // inferred from electronic annotation//0007165 // signal transduction // inferred from
1435114_a	0.002488	1.16	-1.03	NM_172598//XM_00651	<i>Wdhd1</i>	WD repeat and HMGB-box DNA binding protein 1	0006396 // RNA processing // inferred from mutant phenotype//0033044 // regulation of chromosome organization //
1422334_a	0.000416	1.15	-1.02	NM_023134	<i>Sftpa1</i>	surfactant associated protein A1	0001666 // response to hypoxia // inferred from electronic annotation//0007623 // circadian rhythm // inferred from
1416683_a	0.000868	1.15	1.05	NM_001159521//NM_0_	<i>Plexb2</i>	plexin B2	0001843 // neural tube closure // inferred from mutant phenotype//0001932 // regulation of protein phosphorylation //
1423602_a	0.002027	1.15	1.07	NM_009421//XM_00645	<i>Traf1</i>	TNF receptor-associated factor 1	0006915 // apoptotic process // inferred from electronic annotation//0007165 // signal transduction // inferred from
1419773_a	0.000837	1.15	1.01	NM_001170489//NM_0_	<i>Aplf</i>	apertaxin and PNKP like factor	0000012 // single strand break repair // not recorded//0000737 // DNA catabolic process, endonucleolytic // not
1416024_x	0.000678	1.15	-1.00	NM_009836	<i>Cct3</i>	chaperonin containing Tcp1, subunit 3 (gamma)	0006457 // protein folding // inferred from electronic annotation//0007339 // binding of sperm to zona pellucida // inferred
1426736_a	0.001309	1.15	1.04	NM_001130008//NM_1_	<i>Gspt1</i>	G1 to S phase transition 1	0000184 // nuclear-transcribed mRNA catabolic process, nonsense-mediated decay // inferred from electronic
1451391_a	0.001076	1.15	1.04	NM_145995//NM_1781_	<i>Edrf1</i>	erythroid differentiation regulatory factor 1	0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 // regulation of transcription, DNA-
1420849_a	0.000115	1.15	1.07	NM_025820	<i>Crnk1</i>	Crn, crooked neck-like 1 (Drosophila)	0000245 // spliceosomal complex assembly // not recorded//0000398 // mRNA splicing, via spliceosome // not
1417773_a	0.000291	1.15	-1.02	NM_053179	<i>Nans</i>	N-acetylneuraminic acid synthase (sialic acid synthase)	016051 // carbohydrate biosynthetic process // inferred from electronic annotation
1434246_a	0.000225	1.15	1.09	NM_172787//XM_00651	<i>L3mbt13</i>	l(3)mbt-like 3 (Drosophila)	0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 // regulation of transcription, DNA-
1423884_a	0.000140	1.15	-1.13	NM_011574//XM_00653	<i>Cirh1a</i>	cirrhosis, autosomal recessive 1A (human)	0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 // regulation of transcription, DNA-
1424831_a	0.000246	1.15	-1.01	NM_153507//XM_00653	<i>Cpne2</i>	copine II	
1429561_a	0.001881	1.15	1.08	NM_025686//XM_0065C	<i>Brf2</i>	BRF2, subunit of RNA polymerase III transcription initiation factor, BRF1-	0006351 // transcription, DNA-templated // inferred from electronic annotation//0006352 // DNA-templated transcription,
1422022_a	0.002388	1.15	1.05	NM_024467	<i>Zfp319</i>	zinc finger protein 319	0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 // regulation of transcription, DNA-
1425119_a	0.000733	1.15	-1.08	NM_001083925//NR_00_	<i>Oas1b</i>	2'-5' oligoadenylate synthetase 1B	0002376 // immune system process // inferred from electronic annotation//0006955 // immune response // inferred from
1428353_a	0.000132	1.15	1.02	NM_001080932//XM_0_	<i>Foxk2</i>	forkhead box K2	0000122 // negative regulation of transcription from RNA polymerase II promoter // ---//0006351 // transcription, DNA-
1424343_a	0.000522	1.15	-1.01	NM_010120//XM_00652	<i>Eif1a</i>	eukaryotic translation initiation factor 1A//expressed sequence	0006412 // translation // inferred from electronic annotation//0006413 // translational initiation // inferred from electronic
142167_a	0.000688	1.14	1.31	NM_009154//XM_00652	<i>Sema5a</i>	sema domain, seven thrombospondin repeats (type 1 and type 1-like),	0001659 // patterning of blood vessels // inferred from mutant phenotype//0001938 // positive regulation of endothelial cell
1416415_a	0.000816	1.14	-1.03	NM_016750//XR_10501_	<i>Gm8203</i>	predicted pseudogene 8203//H2A histone family, member Z	0006334 // nucleosome assembly // inferred from electronic annotation//0007275 // multicellular organismal development
1420579_s	0.001420	1.14	-1.09	NM_021050//XM_0065C	<i>Cfr</i>	cystic fibrosis transmembrane conductance regulator	0006200 // ATP catabolic process // inferred from electronic annotation//0006695 // cholesterol biosynthetic process //
1423846_x	0.000177	1.14	-1.03	NM_011654//XM_00652	<i>Gm5620</i>	tubulin, alpha 1B pseudogene//tubulin, alpha 1B	0000226 // microtubule cytoskeleton organization // inferred from direct assay//0006184 // GTP catabolic process // inferred
1423846_x	0.000177	1.14	-1.03	NM_011654//XM_00652	<i>Gm5620</i>	tubulin, alpha 1B pseudogene//tubulin, alpha 1B	0000226 // microtubule cytoskeleton organization // inferred from direct assay//0006184 // GTP catabolic process // inferred
1417125_a	0.000572	1.14	-1.03	NM_016661	<i>Ahcy</i>	S-adenosylhomocysteine hydrolase	0002439 // chronic inflammatory response to antigenic stimulus // not recorded//0006730 // one-carbon metabolic process
1434798_a	0.000554	1.14	1.11	NM_175406	<i>Atp6v0d2</i>	ATPase, H+ transporting, lysosomal V0 subunit D2	0006810 // transport // inferred from electronic annotation//0006811 // ion transport // inferred from electronic
1417511_a	0.000838	1.14	1.04	NM_025281//XM_0065C	<i>Lyar</i>	Ly1 antibody reactive clone	
1419031_a	0.000712	1.14	-1.11	NM_019699	<i>Fads2</i>	fatty acid desaturase 2	0006629 // lipid metabolic process // inferred from electronic annotation//0006631 // fatty acid metabolic process //
1419022_a	0.000004	1.14	-1.08	NM_001025388//NM_0_	<i>Eno1</i>	enolase 1, alpha non-neuron//enolase 1B, retrotransposed	0001701 // in utero embryonic development // inferred from mutant phenotype//0006096 // glycolytic process // inferred
1428944_a	0.001197	1.14	-1.02	NM_172712	<i>Uba6</i>	ubiquitin-like modifier activating enzyme 6	0006464 // cellular protein modification process // inferred from electronic annotation//0006511 // ubiquitin-dependent
1419022_a	0.000037	1.14	-1.09	NM_001025388//NM_0_	<i>Eno1</i>	enolase 1, alpha non-neuron//enolase 1B, retrotransposed	0001701 // in utero embryonic development // inferred from mutant phenotype//0006096 // glycolytic process // inferred
1448592_a	0.001215	1.14	1.05	NM_019922	<i>Crtap</i>	cartilage associated protein	0007283 // spermatogenesis // inferred from expression pattern//0018400 // peptidyl-proline hydroxylation to 3-hydroxy-L-
1426726_a	0.000833	1.14	1.01	NM_001163818//NM_1_	<i>Gm8801</i>	protein phosphatase 1, regulatory subunit 10 pseudogene//protein	0006351 // transcription, DNA-templated // inferred from electronic annotation//0043086 // negative regulation of catalytic
1423463_a	0.002079	1.14	-1.07	NM_026412//XM_00645	<i>Knstrn</i>	kinetochore-localized astrin/SPAG5 binding	0000070 // mitotic sister chromatid segregation // not recorded//0000090 // mitotic anaphase // inferred from sequence or
1422155_a	0.000009	1.14	1.28	NM_013548//NM_0540_	<i>Hist1h3b</i>	histone cluster 1, H3b//histone cluster 1, H3c//histone cluster 1,	0000122 // negative regulation of transcription from RNA polymerase II promoter // inferred from direct assay//0006334 //
1417097_a	0.002349	1.13	-1.03	NM_025297//XM_00653	<i>Mecr</i>	mitochondrial trans-2-enoyl-CoA reductase	0006629 // lipid metabolic process // inferred from electronic annotation//0006631 // fatty acid metabolic process // not
1423667_a	0.000786	1.13	-1.13	NM_145569	<i>Mat2a</i>	methionine adenosyltransferase II, alpha	0006556 // S-adenosylmethionine biosynthetic process // inferred from direct assay//0006556 // S-adenosylmethionine
1433962_a	0.001136	1.13	-1.06	NM_001099792//NM_0_	<i>Trmt61a</i>	tRNA methyltransferase 61A	0008033 // tRNA processing // inferred from electronic annotation//0030488 // tRNA methylation // inferred from electronic
1422155_a	0.000036	1.13	1.25	NM_013548//NM_0540_	<i>Hist1h3b</i>	histone cluster 1, H3b//histone cluster 1, H3c//histone cluster 1,	0000122 // negative regulation of transcription from RNA polymerase II promoter // inferred from direct assay//0006334 //
1434113_a	0.000454	1.13	-1.01	NM_207234//XM_00645	<i>Rexa4</i>	REX4, RNA exonuclease 4 homolog (S. cerevisiae)	0008152 // metabolic process // inferred from electronic annotation//0009305 // nucleic acid phosphodiester bond
1423122_a	0.000950	1.13	-1.07	NM_027106//XM_00652	<i>Avp1</i>	arginine vasopressin-induced 1	0000187 // activation of MAPK activity // inferred from direct assay//0007049 // cell cycle // inferred from electronic
1420976_a	0.001372	1.13	1.08	NM_010763	<i>Man1a2</i>	mannosidase, alpha, class 1A, member 2	0006486 // protein glycosylation // inferred from electronic annotation//0007585 // respiratory gaseous exchange // inferred
1422155_a	0.000002	1.13	1.26	NM_013548//NM_0540_	<i>Hist1h3b</i>	histone cluster 1, H3b//histone cluster 1, H3c//histone cluster 1,	0000122 // negative regulation of transcription from RNA polymerase II promoter // inferred from direct assay//0006334 //
1422886_a	0.002015	1.13	-1.01	NM_007714//XM_00653	<i>Clik4</i>	CDC like kinase 4	0006468 // protein phosphorylation // inferred from electronic annotation//0016310 // phosphorylation // inferred from
1416605_a	0.000030	1.13	1.01	NM_026631	<i>Nhp2</i>	NHP2 ribonucleoprotein	0006364 // rRNA processing // inferred from electronic annotation//0031118 // rRNA pseudouridine synthesis // inferred
1422416_s	0.000865	1.13	1.13	NM_016982//NM_0169_	<i>Vpreb1</i>	pre-B lymphocyte gene 1//pre-B lymphocyte gene 2	0000909 // cell morphogenesis // inferred from genetic interaction//0002377 // immunoglobulin production // inferred from
1418174_a	0.000246	1.13	1.30	NM_016974//XM_00654	<i>Dpb</i>	D site albumin promoter binding protein	0001897 // liver development // inferred from electronic annotation//0006351 // transcription, DNA-templated // inferred
1417724_a	0.002636	1.13	-1.06	NM_011568//XR_38840_	<i>Alyref</i>	Aly/REF export factor//Aly/REF export factor 2	0006397 // mRNA processing // inferred from electronic annotation//0006810 // transport // inferred from electronic
1422893_a	0.001660	1.13	1.07	NM_001166531//NM_0_	<i>Sfmbt1</i>	Scm-like with four mbt domains 1	0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 // regulation of transcription, DNA-
1432557_a	0.001582	1.13	-1.05	XR_168656	<i>170004511Rik</i>	RIKEN cDNA 170004511 gene	0006955 // immune response // inferred from electronic annotation//0060326 // cell chemotaxis // inferred from electronic

Table S1

Gene_ID	p	FC-RSV 1 d	FC-RSV 5 d	RefSeq Transcript ID	Gene Symbol	Gene Title	Gene Ontology Biological Process
1426726_a	0.002687	1.13	1.00	NM_001163818//NM_1: Gm8801//Ppp1r1c	protein phosphatase 1, regulatory subunit 10 pseudogene	protein	0006351 // transcription, DNA-templated // inferred from electronic annotation//0043086 // negative regulation of catalytic
1416114_a	0.000685	1.13	1.07	NM_010097//XM_00653 Sparc1	SPARC-like 1		0007165 // signal transduction // inferred from electronic annotation
1454957_a	0.000149	1.13	-1.01	NM_026277 Nob1	NIN1/RPN12 binding protein 1 homolog (S. cerevisiae)		0007601 // visual perception // inferred from mutant phenotype//0030490 // maturation of SSU-rRNA // not
1429017_a	0.001676	1.13	1.05	NM_001085440//NM_1: Smc8r	Smith-Magenis syndrome chromosome region, candidate 8 homolog		
1460351_a	0.000985	1.12	-1.00	NM_016740//XM_00308 Gm12854//Gm50t	predicted gene 12854//predicted gene 5068//S100 calcium binding		0007283 // spermatogenesis // inferred from mutant phenotype//0042127 // regulation of cell proliferation // inferred from
1460351_a	0.000985	1.12	-1.00	NM_016740//XM_00308 Gm12854//Gm50t	predicted gene 12854//predicted gene 5068//S100 calcium binding		0007283 // spermatogenesis // inferred from mutant phenotype//0042127 // regulation of cell proliferation // inferred from
1460351_a	0.000985	1.12	-1.00	NM_016740//XM_00308 Gm12854//Gm50t	predicted gene 12854//predicted gene 5068//S100 calcium binding		0007283 // spermatogenesis // inferred from mutant phenotype//0042127 // regulation of cell proliferation // inferred from
1417058_a	0.002070	1.12	-1.08	NM_025327//XM_0065C Krtcap2	keratinocyte associated protein 2		0018279 // protein N-linked glycosylation via asparagine // inferred by curator
1422671_s	0.000795	1.12	1.01	NM_028279//XM_0065C Naalad2	N-acetylated alpha-linked acidic dipeptidase 2		0006508 // proteolysis // inferred from direct assay//0008152 // metabolic process // inferred from electronic
1416052_a	0.000201	1.12	1.03	NM_021463//NM_0010: Prps1//Prps1l3	phosphoribosyl pyrophosphate synthetase 1//phosphoribosyl		0006015 // 5-phosphoribose 1-diphosphate biosynthetic process // not recorded//0006144 // purine nucleobase metabolic
1418538_a	0.002443	1.12	-1.18	NM_134090//XM_00652 Kdelr3	KDEL (Lys-Asp-Glu-Leu) endoplasmic reticulum protein retention		0006621 // protein retention in ER lumen // inferred from electronic annotation//0006810 // transport // inferred from
1418154_a	0.001105	1.12	-1.12	NM_030563//XM_00653 N4bp1	NEDD4 binding protein 1		0031397 // negative regulation of protein ubiquitination // inferred from direct assay//0032435 // negative regulation of
1417190_a	0.001906	1.12	1.01	NM_021524 Nampt	nicotinamide phosphoribosyltransferase		0007565 // female pregnancy // inferred from electronic annotation//0009435 // NAD biosynthetic process // inferred from
1426575_a	0.000917	1.12	1.03	NM_001168525//NM_0: Sgms1	sphingomyelin synthase 1		0006629 // lipid metabolic process // inferred from electronic annotation//0006665 // sphingolipid metabolic process //
1429306_a	0.002284	1.12	-1.03	NM_026963//XM_00653 Lzic	leucine zipper and CTNNBIP1 domain containing		0007417 // central nervous system development // ---//0010212 // response to ionizing radiation // inferred from electronic
1438717_a	0.000060	1.12	1.23	NM_02190733//NM_0: Oshp6	xysterol binding protein-like 6		0006810 // transport // inferred from electronic annotation//0006869 // lipid transport // inferred from electronic
1417483_a	0.002751	1.12	-1.16	NM_001159394//NM_0: Nfkbiz	nuclear factor of kappa light polypeptide gene enhancer in B cells		0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 // regulation of transcription, DNA-
1417035_a	0.001850	1.12	1.04	NM_133678 Sac3d1	SAC3 domain containing 1		0007049 // cell cycle // inferred from electronic annotation//0007067 // mitotic nuclear division // inferred from electronic
1451908_a	0.001233	1.12	1.03	NM_001166506//NM_0: Sec14l1	SEC14-like 1 (S. cerevisiae)		0006810 // transport // inferred from electronic annotation
1420816_a	0.001193	1.11	1.01	NM_018871 Ywhag	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation		0006605 // protein targeting // inferred from direct assay//0032869 // cellular response to insulin stimulus // not
1416037_a	0.000211	1.11	1.02	NM_007636//XM_00651 Cct2	chaperonin containing Tcp1, subunit 2 (beta)		0006457 // protein folding // inferred from electronic annotation//0007339 // binding of sperm to zona pellucida // inferred
1417056_a	0.002761	1.11	-1.05	NM_011189 Psme1	proteasome (prosome, macropain) activator subunit 1 (PA28 alpha)		0010950 // positive regulation of endopeptidase activity // inferred from physical interaction//0019884 // antigen processing
1424473_a	0.000120	1.11	-1.04	NM_145632//XM_00652 Polr2h	polymerase (RNA) II (DNA directed) polypeptide H		0006351 // transcription, DNA-templated // inferred from electronic annotation//0006360 // transcription from RNA
1420563_a	0.002251	1.11	1.02	NM_001281929//NM_0: Gria3	glutamate receptor, ionotropic, AMPA3 (alpha 3)		0001919 // regulation of receptor recycling // not recorded//0006810 // transport // inferred from electronic
1451978_a	0.000086	1.11	-1.26	NM_010729 Loxl1	lysyl oxidase-like 1		0055114 // oxidation-reduction process // inferred from direct assay
1424759_a	0.000592	1.11	-1.18	NM_001042592//NM_0: Arrdc4	arrestin domain containing 4		0051443 // positive regulation of ubiquitin-protein transferase activity // not recorded
1452734_a	0.000287	1.11	1.04	NM_001083938//NM_0: Rnaset2a//Rnaset	ribonuclease T2A//ribonuclease T2B		0006401 // RNA catabolic process // inferred from sequence or structural similarity//0090305 // nucleic acid phosphodiester
1430053_a	0.002768	1.11	-1.05	NM_025942//NM_0300: Ola1	Obg-like ATPase 1		0006200 // ATP catabolic process // not recorded//0008152 // metabolic process // inferred from electronic
1447886_a	0.001150	1.11	-1.09	XM_006534612//XM_00 Hoxb5os	homeobox B5 and homeobox B6, opposite strand		
1426350_a	0.001855	1.11	1.01	NM_146035 Mgat2	mannoside acetylglucosaminyltransferase 2		0006486 // protein glycosylation // inferred from electronic annotation//0006487 // protein N-linked glycosylation // not
1424023_a	0.000062	1.11	1.01	NM_145582 Ctu1	cytosolic thiouridylase subunit 1 homolog (S. pombe)		0002098 // tRNA wobble uridine modification // inferred from electronic annotation//0008033 // tRNA processing // inferred
1425934_a	0.002410	1.11	1.15	NM_001285793//NM_0: B4galta4	UDP-Gal:betaGlcNAc beta 1,4-galactosyltransferase, polypeptide 4		0005957 // carbohydrate metabolic process // inferred from electronic annotation//0006486 // protein glycosylation //
1425868_a	0.000644	1.11	1.46	NM_175666 Hist2h2bb	histone cluster 2, H2bb		0006334 // nucleosome assembly // inferred from electronic annotation
1419313_a	0.002087	1.11	1.06	NM_009833//XM_00652 Ccnt1	cyclin T1		0000079 // regulation of cyclin-dependent protein serine/threonine kinase activity // inferred from electronic
1420654_a	0.002003	1.11	1.26	NM_028803 Gbe1	glucan (1,4-alpha-), branching enzyme 1		0005975 // carbohydrate metabolic process // inferred from electronic annotation//0005978 // glycogen biosynthetic process
1426187_a	0.001693	1.11	1.02	NM_001282032//NM_0: Hax1	HCLS1 associated X-1		0007166 // cell surface receptor signaling pathway // traceable author statement//0014068 // positive regulation of
1426123_a	0.000229	1.10	-1.06	NM_024281//NM_1336: Rrbp1	ribosome binding protein 1		0006810 // transport // inferred from electronic annotation//0007165 // signal transduction// inferred from sequence or
1423643_a	0.001790	1.10	-1.10	NM_197982//XM_00653 Ddx39	DEAD (Asp-Glu-Ala-Asp) box polypeptide 39		0000398 // mRNA splicing, via spliceosome // not recorded//0006397 // mRNA processing // inferred from electronic
1428255_a	0.001545	1.10	-1.11	NM_025881//NM_0281: Luc7l	Luc7 homolog (S. cerevisiae)-like		0006376 // mRNA splice site selection // inferred from electronic annotation//0045843 // negative regulation of striated
1427462_a	0.002381	1.10	-1.05	NM_001289920//NM_0: Ef2f3	E2F transcription factor 3		0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 // regulation of transcription, DNA-
1416137_a	0.000506	1.10	1.02	NM_001110794//NM_0: Anxa7	annexin A7		0006874 // cellular calcium ion homeostasis // inferred from mutant phenotype//0006914 // autophagy // not
1437390_x	0.000118	1.10	-1.09	NM_016801//XM_0065C Stx1a	syntaxin 1A (brain)		0001956 // positive regulation of neurotransmitter secretion // not recorded//0006810 // transport // inferred from
1416125_a	0.000012	1.10	1.58	NM_010220 Fkbp5	FK506 binding protein 5		0000413 // protein peptidyl-prolyl isomerization // not recorded//0006457 // protein folding // inferred from electronic
1418528_a	0.001278	1.10	-1.04	NM_001113358//NM_0: Dad1	defender against cell death 1		0001824 // blastocyst development // inferred from mutant phenotype//0006486 // protein glycosylation // inferred from
1449139_a	0.000998	1.10	-1.07	NM_025509 Ostc	oligosaccharyltransferase complex subunit		
1435248_a	0.001993	1.09	-1.04	NM_001080706//XM_0C Btaf1	BTAf1 RNA polymerase II, B-TFIID transcription factor-associated,		0008152 // metabolic process // inferred from electronic annotation
1432000_a	0.000584	1.09	1.02	NM_001128609//NM_0: Dedd	death effector domain-containing		0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 // regulation of transcription, DNA-
1448642_a	0.001669	1.09	-1.01	NM_0111865 Pcbp1	poly(rC) binding protein 1		0006397 // mRNA processing // traceable author statement//0045727 // positive regulation of translation // traceable author
1423873_a	0.001020	1.09	-1.07	NM_026032 Lsm1	LSM1 homolog, U6 small nuclear RNA associated (S. cerevisiae)		0006397 // mRNA processing // inferred from electronic annotation//0008380 // RNA splicing // inferred from electronic
1419088_a	0.000848	1.09	1.25	NM_011595 Timp3	tissue inhibitor of metalloproteinase 3		0007269 // neurotransmitter secretion // inferred from electronic annotation//0008152 // metabolic process // inferred from
1428231_a	0.001299	1.09	-1.04	NM_001013391//XM_0C Cpsf6	cleavage and polyadenylation specific factor 6		0006378 // mRNA polyadenylation // not recorded//0006397 // mRNA processing // not recorded//0051262 // protein
1424169_a	0.000868	1.09	1.02	NM_029564//NM_0167: Tax1bp3//Rpl13	Tax1 (human T cell leukemia virus type I) binding protein 3//ribosomal		0007266 // Rho protein signal transduction // not recorded//0008285 // negative regulation of cell proliferation // inferred
1424291_a	0.001813	1.09	-1.03	NM_172410//XM_00653 Nup93	nucleoporin 93		0006810 // transport // inferred from electronic annotation//0015031 // protein transport // inferred from electronic
1428586_a	0.000937	1.09	-1.02	NM_153525 Tmem41b	transmembrane protein 41B		0007399 // nervous system development // inferred from electronic annotation
1425703_a	0.001903	1.09	1.02	NM_011145//XM_00652 Ppard//1810013A	peroxisome proliferator activator receptor delta//RIKEN cDNA		0000122 // negative regulation of transcription from RNA polymerase II promoter // inferred from direct assay//0001890 //
1429006_s	0.001458	1.09	-1.17	NM_001142744//NM_0: Atat1	alpha tubulin acetyltransferase 1		0048666 // neuron development // inferred from electronic annotation//0070507 // regulation of microtubule cytoskeleton
1422155_a	0.000000	1.09	1.27	NM_013548//NM_0540: Hist1h3b//Hist1h3	histone cluster 1, H3b//histone cluster 1, H3c//histone cluster 1,		0000122 // negative regulation of transcription from RNA polymerase II promoter // inferred from direct assay//0006334 //
1423039_a	0.002334	1.09	-1.00	NM_025824//XM_00645 Bzw1	basic leucine zipper and W2 domains 1		0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 // regulation of transcription, DNA-
1434687_a	0.000719	1.09	-1.09	NM_175537//XM_00651 C730026J16//Zbtb	uncharacterized protein C730026J16//zinc finger and BTB domain		0045892 // negative regulation of transcription, DNA-templated // not recorded//0045944 // positive regulation of
1448618_a	0.002653	1.09	-1.03	NM_080638 Mvp	major vault protein		0008283 // cell proliferation // inferred from mutant phenotype//0023057 // negative regulation of signaling // not
1427096_s	0.000019	1.09	-1.00	NM_001166480//NM_0: Ssr4	signal sequence receptor, delta		
1451640_a	0.000544	1.09	1.01	NM_001005523//NM_0: Rsrc2	arginine/serine-rich coiled-coil 2		
1429488_a	0.001779	1.09	1.10	NM_026647//XM_00653 Zdhhc21	zinc finger, DHHC domain containing 21		0001942 // hair follicle development // inferred from mutant phenotype//0018230 // peptidyl-L-cysteine S-palmitoylation //
1426410_a	0.000572	1.09	-1.03	NM_145630 Pdk3	pyruvate dehydrogenase kinase, isoenzyme 3		0005975 // carbohydrate metabolic process // inferred from electronic annotation//0006006 // glucose metabolic process //
1424605_a	0.001321	1.08	-1.14	NM_001163144//NM_0: Pcsk5	proprotein convertase subtilisin/kexin type 5		0001822 // kidney development // inferred from mutant phenotype//0001822 // kidney development // not
1427522_a	0.000442	1.08	-1.21	NM_175535//XM_00651 Arhgap20	Rho GTPase activating protein 20		0007165 // signal transduction // inferred from electronic annotation//0043547 // positive regulation of GTPase activity //

Table S1

Gene_ID	p	FC-RSV 1 d	FC-RSV 5 d	RefSeq Transcript ID	Gene Symbol	Gene Title	Gene Ontology Biological Process
1417871_a	0.002298	1.08	-1.11	NM_010476//XM_00645	Hsd17b7	hydroxysteroid (17-beta) dehydrogenase 7	0006629 // lipid metabolic process // inferred from electronic annotation//0006694 // steroid biosynthetic process // inferred
1433656_a	0.002577	1.08	-1.10	NM_153547//NM_1788	Gnl3	guanine nucleotide binding protein-like 3 (nucleolar)	0006184 // GTP catabolic process // not recorded//0008283 // cell proliferation // not recorded//0042127 // regulation of
1436190_a	0.002474	1.08	-1.12	NM_028326//XM_00653	Zfp618	zinc finger protein 618	0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 // regulation of transcription, DNA-
1431127_a	0.000713	1.08	-1.06	NM_001025594//NM_0:	Zbtb43	zinc finger and BTB domain containing 43	0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 // regulation of transcription, DNA-
1424870_a	0.000359	1.08	1.25	NM_148958//NM_1769	Osbpl10	oxysterol binding protein-like 10	0006810 // transport // inferred from electronic annotation//0006869 // lipid transport // inferred from electronic
1421081_a	0.001639	1.08	-1.10	NM_001038231//NM_0:	Banf1	barrier to autointegration factor 1	0015074 // DNA integration // inferred from direct assay//0075713 // establishment of integrated proviral latency //
1426312_a	0.002070	1.08	-1.08	NM_144541//NM_1812:	Bre	brain and reproductive organ-expressed protein	0006281 // DNA repair // inferred from electronic annotation//0006302 // double-strand break repair // not
1434687_a	0.000579	1.08	-1.12	NM_175537//XM_00651	C73002616//Zbtb	uncharacterized protein C73002616//zinc finger and BTB domain	0045892 // negative regulation of transcription, DNA-templated // not recorded//0045944 // positive regulation of
1435991_a	0.000401	1.08	1.20	NM_001083906//XM_0:	Nr3c2	nuclear receptor subfamily 3, group C, member 2	0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 // regulation of transcription, DNA-
1423207_a	0.001686	1.08	-1.03	NM_025335	Tmem167	transmembrane protein 167	
1423316_a	0.000518	1.08	-1.06	NM_001205286//NM_0:	Tmem39a	transmembrane protein 39a	
1434287_a	0.002174	1.08	-1.04	NM_026792	Agpat5	1-acylglycerol-3-phosphate O-acyltransferase 5 (lysophosphatidic acid	
1420625_a	0.002696	1.07	-1.09	NM_026113//XM_00651	Gtf3c6	general transcription factor IIIC, polypeptide 6, alpha	0002244 // hematopoietic progenitor cell differentiation // inferred from genetic interaction//0006629 // lipid metabolic
1422156_a	0.000783	1.07	-1.01	NM_008503//XM_0010C	Gm10420//Gm61:	predicted gene 10420//predicted gene 6139//predicted gene	0006351 // transcription, DNA-templated // not recorded//0006383 // transcription from RNA polymerase III promoter // not
1420494_x	0.000396	1.07	-1.00	NM_019639	Ubc	ubiquitin C	0000028 // ribosomal small subunit assembly // not recorded//0001731 // formation of translation preinitiation complex //
1418566_s	0.002273	1.07	-1.08	NM_001290697//NM_0:	Nudcd2	NudC domain containing 2	0007141 // male meiosis I // inferred from mutant phenotype//0007144 // female meiosis I // inferred from mutant
1426538_a	0.000089	1.07	-1.49	NM_001127233//NM_0:	Trp53	transformation related protein 53	
1424495_a	0.001346	1.07	-1.12	NM_001037840//NM_0:	Cklf	chemokine-like factor	0000060 // protein import into nucleus, translocation // inferred from direct assay//0000122 // negative regulation of
1415877_a	0.001558	1.07	-1.08	NM_001136086//NM_0:	Dpysl3	dihydropyrimidinase-like 3	0006935 // chemotaxis // inferred from electronic annotation//0008283 // cell proliferation // not recorded//0030593 //
1418898_a	0.002073	1.07	1.14	NM_011699	Lin7c	lin-7 homolog C (C. elegans)	0006208 // pyrimidine nucleobase catabolic process // inferred from electronic annotation//0007399 // nervous system
1426235_a	0.001094	1.07	1.30	NM_008131	Glul	glutamate- ammonia ligase (glutamine synthetase)	0002011 // morphogenesis of an epithelial sheet // not recorded//0006810 // transport // inferred from electronic
1419385_a	0.001844	1.07	1.05	NM_026842//NM_1522:	Ubqln1	ubiquilin 1	0006536 // glutamate metabolic process // not recorded//0006542 // glutamine biosynthetic process // not
1424277_a	0.001067	1.06	-1.21	NM_028633//NM_2071:	Haus7	HAUS augmin-like complex, subunit 7	0006289 // nucleotide-excision repair // inferred from electronic annotation//0031396 // regulation of protein ubiquitination
1418197_a	0.001156	1.06	2.94	NM_009463	Ucp1	uncoupling protein 1 (mitochondrial, proton carrier)	0007049 // cell cycle // inferred from electronic annotation//0007067 // mitotic nuclear division // inferred from electronic
1439333_a	0.001576	1.06	-1.03	NM_026200//XM_00652	Kcnv1	potassium channel, subfamily V, member 1	0006357 // regulation of transcription from RNA polymerase II promoter // inferred from direct assay//0006810 // transport
1427929_a	0.002201	1.06	1.21	NM_172134	Pdxk	pyridoxal (pyridoxin, vitamin B6) kinase	0006810 // transport // inferred from electronic annotation//0006811 // ion transport // inferred from electronic
1422156_a	0.000442	1.06	-1.02	NM_008503//XM_0010C	Gm10420//Gm61:	predicted gene 10420//predicted gene 6139//predicted gene	0008283 // cell proliferation // not recorded//0009443 // pyridoxal 5'-phosphate salvage // inferred from electronic
1422555_s	0.002061	1.06	-1.09	NM_010303//XM_00653	Gna13	guanine nucleotide binding protein, alpha 13	0000208 // ribosomal small subunit assembly // not recorded//0001731 // formation of translation preinitiation complex //
1415721_a	0.000788	1.06	1.13	NM_001290689//NM_0:	Naa60	N(alpha)-acetyltransferase 60, NatF catalytic subunit	0001525 // angiogenesis // inferred from mutant phenotype//0001569 // patterning of blood vessels // inferred from mutant
1422687_a	0.000425	1.06	1.00	NM_010937//XM_0065C	Nras	neuroblastoma ras oncogene	0006334 // nucleosome assembly // not recorded//0007059 // chromosome segregation // inferred from electronic
1424175_a	0.000063	1.06	1.24	NM_017376//NM_1534:	Tef	thyrotroph embryonic factor	0001934 // positive regulation of protein phosphorylation // inferred from electronic annotation//0006184 // GTP catabolic
1428674_a	0.002142	1.05	-1.07	NM_025845//XM_0065C	Prp38b	PRP38 pre-mRNA processing factor 38 (yeast) domain containing B	0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 // regulation of transcription, DNA-
1424913_a	0.000118	1.05	1.25	NM_001289429//NM_0:	Cipc	CLOCK interacting protein, circadian	0006397 // mRNA processing // inferred from electronic annotation//0008380 // RNA splicing // inferred from electronic
1420583_a	0.000495	1.05	1.18	NM_001289916//NM_0:	Rora	RAR-related orphan receptor alpha	0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 // regulation of transcription, DNA-
1434803_a	0.002144	1.05	-1.12	NM_026716	Sycn	syncollin	0001525 // angiogenesis // not recorded//0006351 // transcription, DNA-templated // inferred from electronic
1417447_a	0.002276	1.05	1.35	NM_011545	Tcf21	transcription factor 21	0006887 // exocytosis // inferred from electronic annotation
1433611_s	0.002626	1.05	-1.04	NM_001008705//XM_0:	Bud31	BUD31 homolog (yeast)	0000122 // negative regulation of transcription from RNA polymerase II promoter // inferred from direct assay//0000122 //
1436650_a	0.002758	1.05	1.00	NM_001081243//XM_0:	Filip1	filamin A interacting protein 1	
1430849_a	0.000492	1.05	1.18	NM_026832//XM_00651	Cgrrf1	cell growth regulator with ring finger domain 1	0007049 // cell cycle // inferred from electronic annotation//0007050 // cell cycle arrest // inferred from electronic
1451540_a	0.001330	1.05	-1.14	NM_025837//XM_00651	Mpi	mannose phosphate isomerase	0005975 // carbohydrate metabolic process // inferred from electronic annotation//0006013 // mannose metabolic process
1435642_a	0.001088	1.05	1.35	NM_178774//NLR_02828	Prr18	proline rich 18	
1418230_a	0.000303	1.04	-1.18	NM_001193303//NM_0:	Lims1	LIM and senescent cell antigen-like domains 1	0007160 // cell-matrix adhesion // inferred from mutant phenotype//0007163 // establishment or maintenance of cell
1423531_a	0.001552	1.04	-1.10	NM_001039129//NM_0:	Gm10052//Gm56:	heterogeneous nuclear ribonucleoprotein A1 pseudogene//predicted	0000380 // alternative mRNA splicing, via spliceosome // inferred from direct assay//0006397 // mRNA processing // inferred
1419380_a	0.000912	1.04	-1.15	NM_033327//XM_00653	Zfp423	zinc finger protein 423	0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 // regulation of transcription, DNA-
1431721_a	0.000894	1.04	-1.05	NM_025834//XM_0065C	Proz	protein Z, vitamin K-dependent plasma glycoprotein	0006508 // proteolysis // inferred from electronic annotation//0007596 // blood coagulation // inferred from direct
1424598_a	0.002023	1.03	1.12	NM_001110826//NM_0:	Ddx6	DEAD (Asp-Glu-Ala-Asp) box polypeptide 6	0006200 // ATP catabolic process // inferred from electronic annotation//0008152 // metabolic process // inferred from
1438824_a	0.000515	1.03	-1.10	NM_001159593//NM_0:	Slc20a1	solute carrier family 20, member 1	0006810 // transport // inferred from electronic annotation//0006814 // sodium ion transport // not recorded//0006817 //
1416592_a	0.002190	1.03	-1.15	NM_053108//XM_00651	Glrx	glutaredoxin	0006810 // transport // inferred from electronic annotation//0045454 // cell redox homeostasis // inferred from electronic
1434676_a	0.000641	1.03	1.26	NM_177594	Mtmr9	myotubularin related protein 9	0016311 // dephosphorylation // inferred from electronic annotation//0050790 // regulation of catalytic activity // inferred
1423197_a	0.002639	1.03	1.10	NM_134034//XM_00651	Smek2	SMEK homolog 2, suppressor of mek1 (Dictyostelium)	0006470 // protein dephosphorylation // inferred from mutant phenotype//0019216 // regulation of lipid metabolic process
1426484_a	0.002740	1.02	-1.06	NM_026390//XM_00652	Ubxn4	UBX domain protein 4	0006986 // response to unfolded protein // inferred from electronic annotation
1433873_s	0.000452	1.02	1.18	NM_001282992//NM_0:	Pcnt	pericentrin (kendrin)	0000226 // microtubule cytoskeleton organization // inferred from sequence or structural similarity//0000226 // microtubule
1436870_s	0.000581	1.02	-1.25	NM_001177796//NM_0:	Afpap12	actin filament associated protein 1-like 2	0006954 // chemotaxis // inferred from direct assay//0006954 // inflammatory response // inferred from direct
1445068_a	0.000886	1.02	-1.09	NM_172833//XM_00652	Molt1	mucosa associated lymphoid tissue lymphoma translocation gene 1	0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 // regulation of transcription, DNA-
1421404_a	0.000690	1.01	-1.18	NM_00111339	Cxcl15	chemokine (C-X-C motif) ligand 15	0000122 // negative regulation of transcription from RNA polymerase II promoter // inferred from mutant
1452836_a	0.001899	1.01	1.15	NM_001164885//NM_0:	Lpin2	lipin 2	0006281 // DNA repair // inferred from electronic annotation//0006511 // ubiquitin-dependent protein catabolic process //
1425229_a	0.002285	1.01	1.22	NM_001142918//NM_0:	Tcf7l2	transcription factor 7 like 2, T cell specific, HMG box	0007010 // cytoskeleton organization // not recorded//0016043 // cellular component organization // inferred from
1416577_a	0.001952	1.01	-1.07	NM_019712//XM_00652	Gm9840//Rbx1	predicted gene 9840//ring-box 1	0006166 // purine ribonucleoside salvage // inferred from electronic annotation//0009116 // nucleoside metabolic process //
1428579_a	0.000218	1.01	1.16	NM_172409//XM_00645	Fmnl2	formin-like 2	
1424425_a	0.000212	1.01	-1.08	NM_024433	Mtap	methylthioadenosine phosphorylase	0034613 // cellular protein localization // inferred from direct assay//0045944 // positive regulation of transcription from
1421408_a	0.001852	1.00	-1.27	NM_030691//XM_0065C	Igfb6	immunoglobulin superfamily, member 6	0006260 // DNA replication // inferred from electronic annotation//0006261 // DNA-dependent DNA replication // traceable
1424373_a	0.002033	1.00	-1.11	NM_027870//XM_00652	Armcx3	armadillo repeat containing, X-linked 3	0006810 // transport // inferred from electronic annotation//0006836 // neurotransmitter transport // inferred from direct
1419501_a	0.002705	1.00	1.10	NM_012048//XM_00651	Polk	polymerase (DNA directed), kappa	0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 // regulation of transcription, DNA-
1421641_a	0.000760	1.00	1.27	NM_009209//XM_00653	Slc6a2	solute carrier family 6 (neurotransmitter transporter, noradrenalin),	0006629 // lipid metabolic process // inferred from electronic annotation//0006694 // steroid biosynthetic process // inferred
1421956_a	0.000157	1.00	-1.15	NM_009036//XM_00645	Rbpil	recombination signal binding protein for immunoglobulin kappa J	
1420013_s	0.000818	1.00	-1.09	NM_146006//XM_00651	Lss	lanosterol synthase	

Table S1

Gene_ID	p	FC-RSV 1 d	FC-RSV 5 d	RefSeq Transcript ID	Gene Symbol	Gene Title	Gene Ontology Biological Process
1418722_a	0.000000	-4.73	-2.08	NM_008694	<i>Ngp</i>	neutrophilic granule protein	0006952 // defense response // inferred from electronic annotation///0010951 // negative regulation of endopeptidase
1423226_a	0.000000	-2.97	-1.19	NM_007641	<i>Ms4a1</i>	membrane-spanning 4-domains, subfamily A, member 1	0042113 // B cell activation // inferred from electronic annotation
1419691_a	0.000196	-2.84	-1.77	NM_009921	<i>Camp</i>	cathelicidin antimicrobial peptide	0001934 // positive regulation of protein phosphorylation // not recorded///0002227 // innate immune response in mucosa //
1425289_a	0.000002	-2.60	-1.19	NM_007758///XM_00645	<i>Cr2</i>	complement receptor 2	0002376 // immune system process // inferred from electronic annotation///0002430 // complement receptor mediated
1417640_a	0.000000	-2.58	-1.35	NM_008339	<i>Cd79b</i>	CD79B antigen	0002376 // immune system process // inferred from electronic annotation///0007166 // cell surface receptor signaling
1456328_a	0.000003	-2.46	-1.28	NM_001033350///XM_0C	<i>Bank1</i>	B cell scaffold protein with ankyrin repeats 1	0042113 // B cell activation // inferred from electronic annotation///0043410 // positive regulation of MAPK cascade //
1417065_a	0.000055	-2.45	-1.25	NM_007913	<i>Egr1</i>	early growth inhibitor 1	0000122 // negative regulation of transcription from RNA polymerase II promoter // inferred from direct assay///0001975 //
1429889_a	0.000004	-2.43	-1.25	NM_026976	<i>Faim3</i>	Fas apoptotic inhibitory molecule 3	0002376 // immune system process // inferred from electronic annotation
1416957_a	0.000001	-2.42	-1.23	NM_011136	<i>Pou2af1</i>	POU domain, class 2, associating factor 1	0006351 // transcription, DNA-templated // inferred from electronic annotation///0006355 // regulation of transcription, DNA-
1450570_a	0.000001	-2.36	-1.30	NM_009844///XM_0065C	<i>Cd19</i>	CD19 antigen	0050853 // B cell receptor signaling pathway // inferred from direct assay
1419394_s	0.000004	-2.34	-1.98	NM_013650	<i>S100a8</i>	S100 calcium binding protein A8 (calgranulin A)	0002376 // immune system process // inferred from electronic annotation///0002523 // leukocyte migration involved in
1448756_a	0.000013	-2.30	-2.07	NM_001281852///NM_0C	<i>S100a9</i>	S100 calcium binding protein A9 (calgranulin B)	0002376 // immune system process // inferred from electronic annotation///0002523 // leukocyte migration involved in
1424305_a	0.000781	-2.29	-1.23	NM_152839	<i>Igji</i>	immunoglobulin joining chain	0002376 // adaptive immune response // not recorded///0003094 // glomerular filtration // not recorded///0006959 //
1455656_a	0.000011	-2.26	-1.20	NM_001037719///NM_1:	<i>Btla</i>	B and T lymphocyte associated	0002376 // immune system process // inferred from electronic annotation///0002768 // immune response-regulating cell
1427758_x	0.000011	-2.25	-1.25	XM_006535369///XM_00	<i>Igh-VJ558///Ighg3/</i>	immunoglobulin heavy chain (J558 family)///immunoglobulin heavy	0000187 // activation of MAPK activity // inferred from direct assay///0001788 // antibody-dependent cellular cytotoxicity //
1422775_a	0.000068	-2.23	-1.43	NM_007549	<i>Blk</i>	B lymphoid kinase	0006468 // protein phosphorylation // inferred from electronic annotation///0016310 // phosphorylation // inferred from
1419907_s	0.000010	-2.10	-1.22	NM_001160215///NM_1:	<i>Fcrla</i>	Fc receptor-like A	0030154 // cell differentiation // inferred from electronic annotation
1438527_a	0.000071	-2.09	-1.21	NM_013762///XM_00147	<i>Gm12816///Gm58;</i>	predicted gene 12816///predicted gene 5879///ribosomal protein L3	0006412 // translation // inferred from electronic annotation///0071353 // cellular response to interleukin-4 // inferred from
1460407_a	0.000056	-2.05	-1.10	NM_019866///XM_00654	<i>Spib</i>	Spi-B transcription factor (Spi-1/PU.1 related)	0006351 // transcription, DNA-templated // inferred from electronic annotation///0006355 // regulation of transcription, DNA-
1421653_a	0.001475	-2.04	-1.20	NM_001024700	<i>Igh-VJ558///Igha</i>	immunoglobulin heavy chain (J558 family)///immunoglobulin heavy	0002385 // mucosal immune response // inferred from direct assay///0002455 // humoral immune response mediated by
1422089_a	0.000585	-2.02	-1.21	NM_010746///XM_00653	<i>Ncr1</i>	natural cytotoxicity triggering receptor 1	
1422166_a	0.000726	-2.02	-1.27	NM_001289706///NM_0C	<i>Clec2i</i>	C-type lectin domain family 2, member i	0001765 // membrane raft assembly // non-traceable author statement///0007165 // signal transduction // inferred from
1418480_a	0.000090	-2.02	-1.33	NM_023785	<i>Ppbp</i>	pro-platelet basic protein	0002523 // leukocyte migration involved in inflammatory response // inferred from mutant phenotype///0006955 // immune
1419768_a	0.000000	-1.98	-1.28	NM_001043317///NM_0C	<i>Cd22</i>	CD22 antigen	0007155 // cell adhesion // inferred from electronic annotation///0007166 // cell surface receptor signaling pathway //
1427455_x	0.000002	-1.98	-1.22	<i>Igk-V28///Igkc///Ilg</i>		immunoglobulin kappa chain variable 28 (V28)///immunoglobulin	0030183 // B cell differentiation // inferred from mutant phenotype///0032496 // response to lipopolysaccharide // inferred
1428947_a	0.000227	-1.97	-1.23	NM_027222	<i>Mzb1</i>	marginal zone B and B1 cell-specific protein 1	0002642 // positive regulation of immunoglobulin biosynthetic process // inferred from mutant phenotype///0008284 //
1421653_a	0.001195	-1.97	-1.20	NM_001024700///XM_0C	<i>Igh-VJ558///Igha/</i>	immunoglobulin heavy chain (J558 family)///immunoglobulin heavy	0002385 // mucosal immune response // inferred from direct assay///0002455 // humoral immune response mediated by
1425436_x	0.000056	-1.97	-1.15	NM_001289604///NM_0C	<i>Klra3///Klra9///LOX</i>	killer cell lectin-like receptor, subfamily A, member 3///killer cell lectin-	0007155 // cell adhesion // inferred from electronic annotation
1417556_a	0.000383	-1.96	1.03	NM_017399	<i>Fabp1</i>	fatty acid binding protein 1, liver	0006810 // transport // inferred from electronic annotation///0008284 // positive regulation of cell proliferation // inferred
1422201_a	0.000007	-1.95	-1.28	NM_010389///XM_00652	<i>H2-Ob///LOC10263</i>	histocompatibility 2, O region beta locus///uncharacterized	0002376 // immune system process // inferred from electronic annotation///0002504 // antigen processing and presentation
1444214_a	0.000003	-1.95	-1.21	NM_001080971	<i>Tubb1</i>	tubulin, beta 1 class VI	0006184 // GTP catabolic process // inferred from electronic annotation///0007017 // microtubule-based process // inferred
1460245_a	0.000079	-1.95	-1.26	NM_010654///XM_0065C	<i>Klrd1</i>	killer cell lectin-like receptor, subfamily D, member 1	
1417898_a	0.000021	-1.94	-1.10	NM_010370	<i>Gzma</i>	granzyme A	0006508 // proteolysis // inferred from direct assay///0006915 // apoptotic process // inferred from electronic
1418830_a	0.000053	-1.94	-1.12	NM_007655	<i>Cd79a</i>	CD79A antigen (immunoglobulin-associated alpha)	0002376 // immune system process // inferred from electronic annotation///0007166 // cell surface receptor signaling
1427455_x	0.000005	-1.94	-1.24	<i>Igk-V28///Igkc///Ilg</i>		immunoglobulin kappa chain variable 28 (V28)///immunoglobulin	0030183 // B cell differentiation // inferred from mutant phenotype///0032496 // response to lipopolysaccharide // inferred
1440417_a	0.000002	-1.94	-1.36	<i>D19Ert409e</i>		DNA segment, Chr 19, ERATO Doi 409, expressed	0006044 // N-acetylglucosamine metabolic process // inferred from electronic annotation///0006612 // protein targeting to
1425871_a	0.000003	-1.90	-1.23	<i>Igk-V28///Igkc///Ilg</i>		immunoglobulin kappa chain variable 28 (V28)///immunoglobulin	0030183 // B cell differentiation // inferred from mutant phenotype///0032496 // response to lipopolysaccharide // inferred
1425062_a	0.000009	-1.90	-1.12	NM_001136236///NM_1:	<i>Fcrl1</i>	Fc receptor-like 1	
1427455_x	0.000002	-1.89	-1.21	<i>Igk-V28///Igkc///Ilg</i>		immunoglobulin kappa chain variable 28 (V28)///immunoglobulin	0030183 // B cell differentiation // inferred from mutant phenotype///0032496 // response to lipopolysaccharide // inferred
1444003_a	0.000139	-1.88	-1.69	NM_153408///XM_00645	<i>Neur13</i>	neuritized homolog 3 homolog (Drosophila)	0016567 // protein ubiquitination // inferred from genetic interaction
1420357_s	0.001006	-1.88	-1.50	NM_001081643///NM_0C	<i>Xlr3a///Xlr3b///Xlr:</i>	X-linked lymphocyte-regulated 3A///X-linked lymphocyte-regulated	0051965 // positive regulation of synapse assembly // inferred from mutant phenotype///0061003 // positive regulation of
1423467_a	0.000123	-1.87	-1.11	NM_021718	<i>Ms4a4b</i>	membrane-spanning 4-domains, subfamily A, member 4B	
1444268_a	0.000197	-1.87	-1.19	NM_030561///XM_00652	<i>BC004004///LOC106</i>	cDNA sequence BC004004///keratin-associated protein 16-1-like	0042060 // wound healing // not recorded///0045787 // positive regulation of cell cycle // not recorded///0050673 //
1435955_a	0.000441	-1.86	-1.17	NM_172900///XM_00654	<i>Siglecg</i>	sialic acid binding Ig-like lectin G	0002244 // hematopoietic progenitor cell differentiation // inferred from mutant phenotype
1419135_a	0.000005	-1.85	-1.14	NM_008518	<i>Ltb</i>	lymphotoxin B	0006955 // immune response // inferred from electronic annotation///0010467 // gene expression // inferred from mutant
1419206_a	0.000004	-1.82	-1.35	NM_001290802///NM_0C	<i>Cd37</i>	CD37 antigen	0002639 // positive regulation of immunoglobulin production // inferred from mutant phenotype///0002920 // regulation of
1420398_a	0.000031	-1.81	-1.09	NM_022881	<i>Rgs18</i>	regulator of G-protein signaling 18	0007186 // G-protein coupled receptor signaling pathway // inferred from physical interaction///0008277 // regulation of G-
1427576_a	0.000150	-1.79	-1.43	<i>Igk-V28///Igkv6-14,</i>		immunoglobulin kappa chain variable 28 (V28)///immunoglobulin	0030183 // B cell differentiation // inferred from mutant phenotype///0032496 // response to lipopolysaccharide // inferred
1454850_a	0.000000	-1.78	-1.24	NM_178650///XM_00653	<i>Tbc1d10c</i>	TBC1 domain family, member 10c	0032313 // regulation of Rab GTPase activity // inferred from electronic annotation///0032851 // positive regulation of Rab
1416332_a	0.000160	-1.78	-1.27	NM_007705///XM_00651	<i>Cirbp</i>	cold inducible RNA binding protein	0006950 // response to stress // inferred from electronic annotation///0009409 // response to cold // inferred from electronic
1425247_a	0.000079	-1.76	-1.21	XM_006535369///XM_00	<i>abParts///Igh///Igh</i>	Parts of antibodies, mostly variable regions.///SubName: Full=Igh	0000187 // activation of MAPK activity // inferred from direct assay///0001788 // antibody-dependent cellular cytotoxicity //
1442339_a	0.000006	-1.76	-1.84	NM_173869	<i>Sfta2l1</i>	stefin A2 like 1	0010951 // negative regulation of endopeptidase activity // inferred from electronic annotation
1440900_a	0.000151	-1.76	-1.14	XR_141234///XR_395858	<i>2410022M11Rik</i>	G protein-coupled receptor 174	0007165 // signal transduction // inferred from electronic annotation///0007186 // G-protein coupled receptor signaling
1425569_a	0.000709	-1.75	-1.06	NM_001033251///NM_0C	<i>Gpr174</i>	signaling lymphocytic activation molecule family member 1	0031338 // regulation of vesicle fusion // inferred from mutant phenotype///0046649 // lymphocyte activation // inferred
1428837_a	0.000088	-1.74	1.11	NM_013730///XM_00645	<i>Slamf1</i>	kelch-like 14	
1419406_a	0.000005	-1.73	-1.18	NM_001081403///XM_0C	<i>Klhl14</i>	B cell CLL/lymphoma 11A (zinc finger protein)	0006351 // transcription, DNA-templated // inferred from electronic annotation///0006355 // regulation of transcription, DNA-
1440865_a	0.000601	-1.73	-1.53	NM_001159289///NM_0C	<i>Bcl11a</i>	interferon induced transmembrane protein 6	0009607 // response to biotic stimulus // inferred from electronic annotation
1448511_a	0.000055	-1.72	-1.12	NM_001033632	<i>Ititm6</i>	protein tyrosine phosphatase, receptor type, C polypeptide-associated	0006468 // protein phosphorylation // inferred from direct assay///0006468 // protein phosphorylation // inferred from
1419307_a	0.000366	-1.71	-1.05	NM_016933	<i>Ptprcap</i>	tumor necrosis factor receptor superfamily, member 13c	0001782 // B cell homeostasis // inferred from mutant phenotype///0002376 // immune system process // inferred from
1423182_a	0.000095	-1.70	-1.12	NM_028075///XM_00652	<i>Tnfrsf13c</i>	tumor necrosis factor receptor superfamily, member 13b	0001782 // B cell homeostasis // inferred from mutant phenotype///0002244 // hematopoietic progenitor cell differentiation
1430404_a	0.001535	-1.70	-1.11	NM_0012349///XM_00653	<i>Tnfrsf13b</i>	uncharacterized LOC75771	0006468 // protein phosphorylation // inferred from electronic annotation///0010611 // regulation of cardiac muscle
1449965_a	0.000269	-1.69	-1.17	NM_008572///XM_00651	<i>Mcpt8</i>	mast cell protease 8	0006508 // proteolysis // not recorded///0008626 // granzyme-mediated apoptotic signaling pathway // not recorded
1450753_a	0.000482	-1.68	-1.07	NM_024253///XM_00654	<i>Nkg7</i>	natural killer cell group 7 sequence	
1449347_a	0.000070	-1.68	-1.28	NM_001081642///NM_0C	<i>Xlr4a///Xlr4b///Xlr:</i>	X-linked lymphocyte-regulated 4A///X-linked lymphocyte-regulated	0051965 // positive regulation of synapse assembly // inferred from mutant phenotype///0061003 // positive regulation of
1418126_a	0.000020	-1.68	-1.01	NM_013653	<i>Ccl5</i>	chemokine (C-C motif) ligand 5	0000165 // MAPK cascade // not recorded///0002230 // positive regulation of defense response to virus // inferred by
1422122_a	0.000483	-1.67	-1.31	NM_001253737///NM_0C	<i>Fcer2a</i>	Fc receptor, IgE, low affinity II, alpha polypeptide	0002925 // positive regulation of humoral immune response mediated by circulating immunoglobulin // inferred from mutant

Table S1

Gene_ID	p	FC-RSV 1 d	FC-RSV 5 d	RefSeq Transcript ID	Gene Symbol	Gene Title	Gene Ontology Biological Process
1419297_a	0.001975	-1.66	-1.19	NM_008206	<i>H2-Oa</i>	histocompatibility 2, O region alpha locus	0002376 // immune system process // inferred from electronic annotation///0002504 // antigen processing and presentation
1421182_a	0.000104	-1.66	-1.09	NM_001204239///NM_01	<i>Clec1b</i>	C-type lectin domain family 1, member b	0007165 // signal transduction // not recorded///0007166 // cell surface receptor signaling pathway // traceable author
1448010_a	0.000016	-1.66	-1.45	NR_029555	<i>A430104N18Rik</i>	RIKEN cDNA A430104N18 gene//microRNA 142	0071391 // cellular response to estrogen stimulus // inferred from direct assay
1423100_a	0.001205	-1.65	-1.02	NM_010234	<i>Fos</i>	FBJ osteosarcoma oncogene	0001661 // conditioned taste aversion // inferred from electronic annotation///0006355 // regulation of transcription, DNA-
1428114_a	0.000987	-1.64	-1.04	NM_001171010///NM_01	<i>Slc14a1</i>	solute carrier family 14 (urea transporter), member 1	0006810 // transport // inferred from electronic annotation///0006833 // water transport // inferred from direct
1426112_a	0.001247	-1.63	-1.07	NM_001110320///NM_01	<i>Cd72</i>	CD72 antigen	
1423478_a	0.000011	-1.62	-1.19	NM_008855///XM_0065C	<i>Prkcb</i>	protein kinase C, beta	0002376 // immune system process // inferred from electronic annotation///0006351 // transcription, DNA-templated //
1419480_a	0.000037	-1.61	-1.30	NM_001164059///NM_01	<i>Sell</i>	selectin, lymphocyte	0007155 // cell adhesion // inferred from electronic annotation///0033198 // response to ATP // inferred from direct
1434873_a	0.000050	-1.61	-1.19	NM_153788///XM_0065C	<i>Acap1</i>	ArfGAP with coiled-coil, ankyrin repeat and PH domains 1	0006629 // lipid metabolic process // inferred from electronic annotation///0007165 // signal transduction // inferred from
1437127_a	0.000007	-1.59	-1.25	NM_001110254///NM_11	<i>Zfp945</i>	zinc finger protein 945	0006355 // regulation of transcription, DNA-templated // inferred from electronic annotation
1421098_a	0.001273	-1.59	-1.25	NM_019992///XM_0065C	<i>Stap1</i>	signal transducing adaptor family member 1	0007169 // transmembrane receptor protein tyrosine kinase signaling pathway // inferred from direct assay///0009967 //
1449393_a	0.000033	-1.58	1.08	NM_0111364	<i>Sh2d1a</i>	SH2 domain protein 1A	0006959 // humoral immune response // inferred from mutant phenotype///0006968 // cellular defense response // inferred
1448713_a	0.001146	-1.58	-1.02	NM_0011487///XM_0064S	<i>Stat4</i>	signal transducer and activator of transcription 4	0006351 // transcription, DNA-templated // inferred from electronic annotation///0006355 // regulation of transcription, DNA-
1418806_a	0.000001	-1.58	-1.70	NM_001252651///NM_01	<i>Csf3r</i>	colony stimulating factor 3 receptor (granulocyte)	0007155 // cell adhesion // inferred from electronic annotation///0019221 // cytokine-mediated signaling pathway // inferred
1425962_a	0.000593	-1.57	-1.07	NM_153094///NR_02426	<i>Klrb1f</i>	killer cell lectin-like receptor subfamily B member 1F	
1450357_a	0.000670	-1.57	-1.09	NM_001190333///NM_01	<i>Ccr6</i>	chemokine (C-C motif) receptor 6	
1422217_a	0.000987	-1.57	-1.39	NM_001136059///NM_01	<i>Cyp1a1</i>	cytochrome P450, family 1, subfamily A, polypeptide 1	0006935 // chemotaxis // inferred from electronic annotation///0006955 // immune response // inferred from electronic
1429319_a	0.000400	-1.56	1.04	NM_001081105	<i>Rhoh</i>	ras homolog gene family, member H	0001666 // response to hypoxia // inferred from electronic annotation///0001889 // liver development // inferred from
1449077_a	0.001953	-1.55	1.20	NM_133245	<i>Ahspl</i>	alpha hemoglobin stabilizing protein	0006184 // GTP catabolic process // inferred from electronic annotation///0007165 // signal transduction // inferred from
1420659_a	0.000431	-1.55	-1.15	NM_030710///XM_0064S	<i>Slamf6</i>	SLAM family member 6	0006457 // protein folding // inferred from direct assay///0020027 // hemoglobin metabolic process // inferred from
1449220_a	0.000594	-1.54	-1.20	NM_031247	<i>Gimap3</i>	GTPase, IMAP family member 3	0033955 // mitochondrial DNA inheritance // inferred from mutant phenotype
1450639_a	0.000911	-1.54	-1.09	NM_001085518///NM_11	<i>Gm14085//Slc28a</i>	predicted gene 14085//solute carrier family 28 (sodium-coupled	0001895 // retina homeostasis // not recorded///0006810 // transport // inferred from electronic annotation///0015860 //
1425226_x	0.000146	-1.54	-1.07	XM_977361	<i>LOC665506//Tcrb</i>	T-cell receptor beta-2 chain C region-like//T cell receptor beta, joining	
1425822_a	0.000615	-1.54	-1.09	NM_008052///XM_0065C	<i>Dxb1</i>	deltex 1 homolog (Drosophila)	0007219 // Notch signaling pathway // inferred from direct assay///0007219 // Notch signaling pathway // inferred from
1449347_a	0.000051	-1.54	-1.25	NM_001081642///NM_01	<i>Xlr4a//Xlr4b//Xlr4c</i>	X-linked lymphocyte-regulated 4A//X-linked lymphocyte-regulated	0051965 // positive regulation of synapse assembly // inferred from mutant phenotype///0061003 // positive regulation of
1420609_a	0.000001	-1.53	-1.13	NM_020575///XM_0064S	<i>7-Mar</i>	membrane-associated ring finger (C3HC4) 7	0016567 // protein ubiquitination // inferred from electronic annotation
1423130_a	0.000023	-1.53	-1.15	NM_001079694///NM_01	<i>Srsf5</i>	serine/arginine-rich splicing factor 5	0006351 // transcription, DNA-templated // inferred from electronic annotation///0006355 // regulation of transcription, DNA-
1418798_s	0.000017	-1.53	-1.20	NM_019684///XM_0065C	<i>Srp3</i>	serine/arginine-rich protein specific kinase 3	0006468 // protein phosphorylation // inferred from direct assay///0007275 // multicellular organismal development //
1417995_a	0.000415	-1.52	-1.07	NM_008979///NR_10407	<i>Ptpn22</i>	protein tyrosine phosphatase, non-receptor type 22 (lymphoid)	0002376 // immune system process // inferred from electronic annotation///0006470 // protein dephosphorylation // inferred
1451780_a	0.002399	-1.51	-1.10	NM_008528	<i>Blnk</i>	B cell linker	0009967 // positive regulation of signal transduction // not recorded///0035556 // intracellular signal transduction // not
1425738_a	0.001914	-1.51	1.06	<i>abParts//Igk//Igk</i>	Parts of antibodies, mostly variable regions.//immunoglobulin kappa		0030183 // B cell differentiation // inferred from mutant phenotype///0032496 // response to lipopolysaccharide // inferred
1427576_a	0.000349	-1.51	-1.29	<i>Igk-V28//Igkv6-14</i>	immunoglobulin kappa chain variable 28 (V28)//immunoglobulin		0030183 // B cell differentiation // inferred from mutant phenotype///0032496 // response to lipopolysaccharide // inferred
1457728_a	0.000994	-1.50	-1.12	NM_001166213///XM_01	<i>Fam129c</i>	family with sequence similarity 129, member C	
1421924_a	0.000262	-1.50	-1.15	NM_011401///XM_0065C	<i>Slc2a3</i>	solute carrier family 2 (facilitated glucose transporter), member 3	0006810 // transport // inferred from electronic annotation///0008643 // carbohydrate transport // inferred from electronic
1434573_a	0.000025	-1.50	-1.13	NM_153137	<i>Traf3ip3</i>	TRAF3 interacting protein 3	
1436033_a	0.000006	-1.50	-1.11	NM_001113283///NM_11	<i>Fam214a</i>	family with sequence similarity 214, member A	
1436649_a	0.001080	-1.49	-1.13	NM_011771///XM_0065C	<i>Ikzf3</i>	IKAROS family zinc finger 3	0006351 // transcription, DNA-templated // inferred from electronic annotation///0006355 // regulation of transcription, DNA-
1422124_a	0.000051	-1.49	-1.12	NM_001113136///NM_01	<i>Ptpnc</i>	protein tyrosine phosphatase, receptor type, C	0000187 // activation of MAPK activity // inferred from mutant phenotype///0001915 // negative regulation of T cell
1456771_a	0.002033	-1.49	-1.48	NM_001290503///NM_11	<i>Zer1</i>	zyg-11 related, cell cycle regulator	0016567 // protein ubiquitination // not recorded///0051438 // regulation of ubiquitin-protein transferase activity // not
1422411_s	0.001293	-1.49	1.08	NM_001012766///NM_01	<i>Ear1//Ear12//Ear</i>	eosinophil-associated, ribonuclease A family, member 1//eosinophil-	0006935 // chemotaxis // inferred from direct assay///0008152 // metabolic process // inferred from electronic
1422411_s	0.001293	-1.49	1.08	NM_001012766///NM_01	<i>Ear1//Ear12//Ear</i>	eosinophil-associated, ribonuclease A family, member 1//eosinophil-	0006935 // chemotaxis // inferred from direct assay///0008152 // metabolic process // inferred from electronic
1460555_a	0.000542	-1.48	-1.15	NM_001080381///NM_01	<i>Fam65b</i>	family with sequence similarity 65, member B	
1422828_a	0.001037	-1.48	-1.01	NM_013487///XM_0065C	<i>Cd3d</i>	CD3 antigen, delta polypeptide	0006461 // protein complex assembly // non-traceable author statement///0007166 // cell surface receptor signaling pathway
1424975_a	0.001050	-1.48	1.09	NM_001271019///NM_11	<i>Siglec5</i>	sialic acid binding Ig-like lectin 5	0007155 // cell adhesion // inferred from electronic annotation
1417758_a	0.000019	-1.48	-1.12	NM_010575///XM_0065C	<i>Itga2b</i>	integrin alpha 2b	0002687 // positive regulation of leukocyte migration // not recorded///0007155 // cell adhesion // inferred from electronic
1419247_a	0.000017	-1.48	-1.12	NM_009061	<i>Rgs2</i>	regulator of G-protein signaling 2	0006417 // regulation of translation // inferred from electronic annotation///0007049 // cell cycle // inferred from electronic
1425005_a	0.002202	-1.48	-1.13	NM_001136068///NM_01	<i>Klrc1</i>	killer cell lectin-like receptor subfamily C, member 1	
1416464_a	0.001907	-1.47	1.12	NM_011403	<i>Slc4a1</i>	solute carrier family 4 (anion exchanger), member 1	0006810 // transport // inferred from electronic annotation///0006811 // ion transport // inferred from electronic
1452205_x	0.000748	-1.47	-1.07	XM_977361	<i>LOC665506//Tcrb</i>	T-cell receptor beta-2 chain C region-like//T cell receptor beta, joining	
1442514_a	0.002260	-1.47	1.02	NM_001025371///NM_11	<i>Elil3//Serinc4</i>	elongation factor RNA polymerase II-like 3//serine incorporator 4	0006351 // transcription, DNA-templated // inferred from electronic annotation///0006354 // DNA-templated transcription,
1427999_a	0.000222	-1.47	-1.21	NM_183316	<i>Snapp5</i>	small nuclear RNA activating complex, polypeptide 5	0006351 // transcription, DNA-templated // inferred from electronic annotation///0006355 // regulation of transcription, DNA-
1419178_a	0.000863	-1.46	-1.01	NM_009850	<i>Cd3g</i>	CD3 antigen, gamma polypeptide	0007163 // establishment or maintenance of cell polarity // not recorded///0007166 // cell surface receptor signaling pathway
1416930_a	0.001692	-1.46	-1.12	NM_010742	<i>Ly6d</i>	lymphocyte antigen 6 complex, locus D	0030098 // lymphocyte differentiation // inferred from expression pattern///0035634 // response to stilbenoid // inferred
1421303_a	0.000878	-1.46	-1.17	NM_001025597///NM_01	<i>Ikzf1</i>	IKAROS family zinc finger 1	0000122 // negative regulation of transcription from RNA polymerase II promoter // inferred from direct assay///0001779 //
1430597_a	0.000647	-1.46	-1.03	NM_178394///XM_0065C	<i>Jakmip1</i>	janus kinase and microtubule interacting protein 1	0006810 // transport // inferred from electronic annotation///0015031 // protein transport // inferred from electronic
1422411_s	0.001710	-1.46	1.07	NM_001012766///NM_01	<i>Ear1//Ear12//Ear</i>	eosinophil-associated, ribonuclease A family, member 1//eosinophil-	0006935 // chemotaxis // inferred from direct assay///0008152 // metabolic process // inferred from electronic
1436040_a	0.000983	-1.45	-1.23	NR_029468	<i>Shng12</i>	small nuclear RNA host gene 12	
1432492_a	0.000166	-1.45	-1.14	NM_025325///XM_0065C	<i>Haa0</i>	3-hydroxyanthranilate 3,4-dioxygenase	0006569 // tryptophan catabolic process // inferred from electronic annotation///0009435 // NAD biosynthetic process //
1416298_a	0.000010	-1.45	-1.42	NM_013599///XM_0064S	<i>Mmp9</i>	matrix metalloproteinase 9	0001501 // skeletal system development // inferred from genetic interaction///0001501 // skeletal system development //
1418998_a	0.000319	-1.45	-1.21	NM_133809	<i>Kmo</i>	kynurenine 3-monooxygenase (kynurenine 3-hydroxylase)	0006569 // tryptophan catabolic process // inferred from electronic annotation///0008152 // metabolic process // inferred
1460218_a	0.000061	-1.45	-1.13	NM_013706	<i>Cd52</i>	CD52 antigen	
1418989_a	0.000340	-1.45	-1.17	NM_007799	<i>Ctse</i>	cathepsin E	0006508 // proteolysis // not recorded///0016540 // protein autoprocessing // not recorded///0019886 // antigen processing
1426158_a	0.000270	-1.45	-1.07	XM_977361	<i>Tcrb-//TCR-beta c</i>	T cell receptor beta, joining region//Murine TCR Cbeta2 chain	
1418907_a	0.000337	-1.45	-1.10	NM_007976	<i>F5</i>	coagulation factor V	0006508 // proteolysis // not recorded///0007155 // cell adhesion // inferred from electronic annotation///0007596 // blood
1422632_a	0.000503	-1.44	-1.11	NM_009985///XM_0065C	<i>Ctsw</i>	cathepsin W	0006508 // proteolysis // inferred from electronic annotation
1421802_a	0.001784	-1.44	1.09	NM_007894///NM_00101	<i>Ear1//Ear12//Ear</i>	eosinophil-associated, ribonuclease A family, member 1//eosinophil-	0008152 // metabolic process // inferred from electronic annotation///0009305 // nucleic acid phosphodiester bond

Table S1

Gene_ID	p	FC-RSV 1 d	FC-RSV 5 d	RefSeq Transcript ID	Gene Symbol	Gene Title	Gene Ontology Biological Process
1455553_a	0.000459	-1.44	-1.13	NM_001142647///NM_1: <i>Tmem194b</i>		transmembrane protein 194B	
1421214_a	0.000015	-1.43	-1.19	NM_001111110///NM_0: <i>Cmah</i>		cytidine monophospho-N-acetylneuraminic acid hydroxylase	0006054 // N-acetylneuraminate metabolic process // inferred from electronic annotation///0006810 // transport // inferred
1421176_a	0.000746	-1.43	-1.06	NM_011246	<i>Rasgrp1</i>	RAS guanyl releasing protein 1	0001816 // cytokine production // inferred from mutant phenotype///0002437 // inflammatory response to antigenic stimulus
1448409_a	0.000033	-1.42	-1.16	NM_001281980///NM_0: <i>Lrmp</i>		lymphoid-restricted membrane protein	0002376 // immune system process // inferred from electronic annotation///0007338 // single fertilization // inferred from
1425396_a	0.000131	-1.42	-1.06	NM_001162432///NM_0: <i>Lck</i>		lymphocyte protein tyrosine kinase	0006468 // protein phosphorylation // inferred from direct assay///0006468 // protein phosphorylation // not
1454897_a	0.001118	-1.41	1.02	NM_177353///XM_00652 6330509M05RIK///		RIKEN cDNA 6330509M05 gene//solute carrier family 9	0006810 // transport // inferred from electronic annotation///0006811 // ion transport // inferred from electronic
1432356_a	0.000956	-1.41	-1.11	1700056N1ORIK		RIKEN cDNA 1700056N10 gene	
1417230_a	0.000204	-1.41	-1.07	NM_001159965///NM_0: <i>Ralgps2</i>		Ral GEF with PH domain and SH3 binding motif 2	0007264 // small GTPase mediated signal transduction // inferred from electronic annotation///0043547 // positive regulation
1426113_x	0.000044	-1.41	1.04	NM_001081280///NM_1: <i>Nlr3</i>		T cell receptor alpha variable 9D-3	0006810 // transport // inferred from electronic annotation///0015031 // protein transport // inferred from electronic
1446689_a	0.000376	-1.41	-1.01	NM_028773///XM_00654 <i>Sash3</i>		NLR family, CARD domain containing 3	0007249 // I-kappaB kinase/NF-kappaB signaling // not recorded///0007249 // I-kappaB kinase/NF-kappaB signaling //
1427007_a	0.000785	-1.41	-1.09	NM_011270	<i>Rhd</i>	SAM and SH3 domain containing 3	0002639 // positive regulation of immunoglobulin production // inferred from mutant phenotype///0002726 // positive
1417049_a	0.000164	-1.39	1.04	NM_001168256///NM_0: <i>Tmem40</i>		Rh blood group, D antigen	0015696 // ammonium transport // inferred from mutant phenotype///0048821 // erythrocyte development // inferred from
1424966_a	0.000305	-1.39	-1.05	5830427D03RIK		transmembrane protein 40	
1430702_a	0.000976	-1.39	-1.13	NM_009898///XM_0065C <i>Coro1a</i>		SubName: Full=Uncharacterized protein; coronin, actin binding protein 1A	0001845 // phagolysosome assembly // not recorded///0006816 // calcium ion transport // inferred from mutant
1416246_a	0.000093	-1.39	-1.17	NM_032540///XM_0065C <i>Kel</i>		Kell blood group	0006508 // proteolysis // inferred from sequence or structural similarity
1449057_a	0.000031	-1.39	-1.06	NM_010576	<i>Itga4</i>	integrin alpha 4	0001974 // blood vessel remodeling // inferred from mutant phenotype///0007155 // cell adhesion // inferred from mutant
1421194_a	0.000035	-1.38	-1.14	NM_001042671///NM_0: <i>Gpcpd1</i>		glycerophosphocholine phosphodiesterase GDE1 homolog (S.	0006071 // glycerol metabolic process // inferred from electronic annotation///0006629 // lipid metabolic process // inferred
1429144_a	0.000056	-1.38	-1.01	NM_001253872///NM_0: <i>Itgal</i>		integrin alpha L	0002291 // T cell activation via T cell receptor contact with antigen bound to MHC molecule on antigen presenting cell // not
1425367_a	0.000044	-1.38	-1.05	NM_146167	<i>Gimap7</i>	GTPase, IMAP family member 7	0006184 // GTP catabolic process // not recorded
1425084_a	0.001898	-1.38	-1.08	NM_001163748///NM_0: <i>Pde9a</i>		phosphodiesterase 9A	0007165 // signal transduction // inferred from electronic annotation///0008152 // metabolic process // not
1449403_a	0.001183	-1.37	-1.03	NR_030711	<i>Mir22hg</i>	Mir22 host gene (non-protein coding)	
1428562_a	0.000250	-1.37	-1.17	NM_001013372	<i>Nrp</i>	neural regeneration protein	
1440263_a	0.000787	-1.37	-1.16	NM_008725	<i>Nppa</i>	natriuretic peptide type A	0001666 // response to hypoxia // inferred from electronic annotation///0003085 // negative regulation of systemic arterial
1456062_a	0.000154	-1.37	36.43	NM_015786	<i>Hist1h1c</i>	histone cluster 1, H1c	0006334 // nucleosome assembly // inferred from electronic annotation///0016584 // nucleosome positioning // inferred
1416101_a	0.000145	-1.37	1.18	NM_009924///XM_00653 <i>Cnr2</i>		cannabinoid receptor 2 (macrophage)	0001975 // response to amphetamine // inferred from electronic annotation///0006954 // inflammatory response // inferred
1450476_a	0.000964	-1.37	-1.10	NM_001163753///NM_0: <i>Rab37</i>		RAB37, member RAS oncogene family	0002184 // GTP catabolic process // inferred from sequence or structural similarity///0006810 // transport // inferred from
1450167_a	0.001574	-1.36	-1.08	NM_178785///XM_00652 <i>Rasal3</i>		RAS protein activator like 3	0007165 // signal transduction // inferred from electronic annotation///0032320 // positive regulation of Ras GTPase activity
1456870_a	0.000813	-1.36	-1.05	NR_110483	<i>Mirlet7bhg</i>	MIRLET7B host gene (non-protein coding)	
1440357_a	0.002239	-1.36	-1.23	NM_009008	<i>Rac2</i>	RAS-related C3 botulinum substrate 2	0006184 // GTP catabolic process // inferred from direct assay///0006886 // intracellular protein transport // inferred from
1417620_a	0.001678	-1.36	-1.12	NM_029385///XM_00651 <i>Nudt16</i>		nudix (nucleoside diphosphate linked moiety X)-type motif 16	0006382 // adenosine to inosine editing // not recorded///0006402 // mRNA catabolic process // inferred from mutant
1421204_a	0.000180	-1.36	-1.06	NM_001109661///NM_0: <i>Bach2</i>		BTB and CNC homology 2	0000122 // negative regulation of transcription from RNA polymerase II promoter // inferred from direct assay///0006351 //
1437667_a	0.000063	-1.36	-1.04	NM_001033499///NM_0: <i>Sh2d1b1</i> /// <i>Sh2d1b</i>		SH2 domain protein 1B1///SH2 domain protein 1B2	0002366 // leukocyte activation involved in immune response // inferred from direct assay///0002717 // positive regulation of
1423024_a	0.002048	-1.35	1.02	NM_001033391///NM_0: <i>Ipce1</i>		interaction protein for cytohesin exchange factors 1	0003126 // positive regulation of GTP catabolic process // not recorded
1439808_a	0.001435	-1.35	-1.11	NM_008360///XM_00651 <i>Il18</i>		interleukin 18	0000165 // MAPK cascade // not recorded///0001525 // angiogenesis // not recorded///0001525 // angiogenesis // inferred
1417932_a	0.001442	-1.34	1.02	NM_013542	<i>Gzmb</i>	granzyme B	0001913 // T cell mediated cytotoxicity // inferred from mutant phenotype///0006508 // proteolysis // not
1419060_a	0.000093	-1.34	1.18	NM_001285785///NM_1: <i>Arhgap9</i>		Rho GTPase activating protein 9	0007165 // signal transduction // inferred from electronic annotation///0043547 // positive regulation of GTPase activity //
1419810_x	0.000178	-1.34	-1.10	NM_001195421///NM_0: <i>Hist1h4a</i> /// <i>Hist1h4</i>		histone cluster 1, H4a///histone cluster 1, H4b///histone cluster 1,	0006334 // nucleosome assembly // inferred from sequence or structural similarity///0006334 // nucleosome assembly //
1422948_s	0.000610	-1.34	1.13	NM_008859///XM_00645 <i>Prkcg</i>		protein kinase C, theta	0002376 // immune system process // inferred from electronic annotation///0006355 // regulation of transcription, DNA-
1426044_a	0.002727	-1.34	-1.02	NR_002904///NR_00327C <i>Snhg3</i>		small nucleolar RNA host gene 3	
1433789_a	0.002204	-1.33	-1.31	NM_001024708///NM_0: <i>2610005L07RIK</i> ///		cadherin 11 pseudogene//cadherin-11-like	0007156 // homophilic cell adhesion // inferred from electronic annotation
1429041_a	0.000666	-1.33	-1.16	NM_013737///XM_00652 <i>Pla2g7</i>		phospholipase A2, group VII (platelet-activating factor acetylhydrolase,	0006508 // proteolysis // inferred from electronic annotation///0006629 // lipid metabolic process // inferred from electronic
1430700_a	0.000239	-1.33	-1.47	NM_153175	<i>Gimap6</i>	GTPase, IMAP family member 6	
1427891_a	0.000548	-1.33	-1.17	NR_040721	<i>Snhg5</i>	small nucleolar RNA host gene 5	
1428529_a	0.000039	-1.33	-1.11	NM_010516	<i>Cyr61</i>	cysteine rich protein 61	0001558 // regulation of cell growth // inferred from electronic annotation///0001649 // osteoblast differentiation // inferred
1416039_x	0.002522	-1.33	-1.00	NM_001004363	<i>Nuak1</i>	NUAK family, SNF1-like kinase, 1	0006468 // protein phosphorylation // not recorded///0006974 // cellular response to DNA damage stimulus // inferred from
1438684_a	0.000037	-1.33	-1.01	NM_010551///XM_0065C <i>Il16</i>		interleukin 16	0006351 // transcription, DNA-templated // inferred from electronic annotation///0006355 // regulation of transcription, DNA-
1417391_a	0.000004	-1.32	-1.13	NM_001159407///NM_0: <i>B3gnt5</i>		UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 5	0006486 // protein glycosylation // inferred from electronic annotation///0007275 // multicellular organismal development //
1420993_a	0.001696	-1.32	-1.05	NM_016811///XM_00651 <i>Dgka</i>		diacylglycerol kinase, alpha	0007205 // protein kinase C-activating G-protein coupled receptor signaling pathway // inferred from electronic
1418578_a	0.000028	-1.32	-1.02	NR_028574///NR_02857: <i>Snhg8</i> /// <i>Snora24</i>		small nucleolar RNA host gene 8///small nucleolar RNA, H/ACA box 24	
1435524_a	0.000011	-1.32	-1.09	NM_008372	<i>Il7r</i>	interleukin 7 receptor	0000902 // cell morphogenesis // inferred from genetic interaction///0001915 // negative regulation of T cell mediated
1448575_a	0.000076	-1.32	1.06	NM_010734	<i>Lst1</i>	leukocyte specific transcript 1	0000902 // cell morphogenesis // inferred from electronic annotation///0002376 // immune system process // inferred from
1425548_a	0.000119	-1.32	-1.37	NM_001197321///NM_0: <i>Foxp1</i>		forkhead box P1	0000122 // negative regulation of transcription from RNA polymerase II promoter // inferred from direct assay///0000122 //
1421140_a	0.000034	-1.31	-1.01	NM_001290303///NM_1: <i>Nrde2</i>		nrde-2 necessary for RNA interference, domain containing	0006396 // RNA processing // inferred from electronic annotation
1451303_a	0.000292	-1.31	-1.08	NM_008359///XM_0065C <i>Il17ra</i>		interleukin 17 receptor A	0002747 // positive regulation of interleukin-23 production // not recorded///0071345 // cellular response to cytokine
1420904_a	0.000030	-1.31	-1.08	NM_001037138///NM_1: <i>Cd300lb</i>		CD300 antigen like family member B	0002376 // immune system process // inferred from electronic annotation///0002446 // neutrophil mediated immunity //
1445882_a	0.000342	-1.31	-1.50	NM_013462///XM_0065C <i>Adrb3</i>		adrenergic receptor, beta 3	0002024 // diet induced thermogenesis // inferred from genetic interaction///0002025 // vasodilation by norepinephrine-
1421555_a	0.000281	-1.31	-1.07	NM_001282064///NM_0: <i>Cyb561a3</i>		cytochrome b561 family, member A3	0006122 // transport // inferred from electronic annotation///0055114 // oxidation-reduction process // inferred from
1434245_a	0.000148	-1.31	-1.07	NM_007486///XM_0065C <i>Arhgd1b</i>		Rho, GDP dissociation inhibitor (GDI) beta	0043547 // positive regulation of GTPase activity // inferred from electronic annotation///0050790 // regulation of catalytic
1426454_a	0.002126	-1.30	-1.13	NM_009531	<i>Xpc</i>	xeroderma pigmentosum, complementation group C	0000075 // cell cycle checkpoint // inferred from electronic annotation///0000715 // nucleotide-excision repair, DNA damage
1425532_a	0.000455	-1.30	-1.17	NM_001079883///NM_0: <i>Bcl11b</i>		B cell leukemia/lymphoma 11B	0003334 // keratinocyte development // inferred from mutant phenotype///0003382 // epithelial cell morphogenesis //
1450339_a	0.002235	-1.30	1.05	NR_028573///NR_02857: <i>Snhg8</i> /// <i>Snora24</i>		small nucleolar RNA host gene 8///small nucleolar RNA, H/ACA box 24	
1447896_s	0.000458	-1.30	-1.11	NM_021028///NR_04564 <i>Tk2</i>		thymidine kinase 2, mitochondrial	0006139 // nucleobase-containing compound metabolic process // inferred from electronic annotation///0006260 // DNA
1426100_a	0.000884	-1.30	-1.06	NM_001077496///NM_1: <i>Evi2a-evi2b</i> /// <i>Evi2t</i>		Evi2a-Evi2b readthrough//ecotropic viral integration site	
1426505_a	0.000007	-1.30	-1.25	NM_019551///XM_00651 <i>Tdp2</i>		tyrosyl-DNA phosphodiesterase 2	0006281 // DNA repair // inferred from electronic annotation///0006302 // double-strand break repair // not
1448706_a	0.002488	-1.30	-1.03	NM_001291114///NM_0: <i>Rbm39</i>		RNA binding motif protein 39	0006351 // transcription, DNA-templated // traceable author statement///0006355 // regulation of transcription, DNA-
1420982_a	0.000095	-1.30	-1.19				

Table S1

Gene_ID	p	FC-RSV 1 d	FC-RSV 5 d	RefSeq Transcript ID	Gene Symbol	Gene Title	Gene Ontology Biological Process
1422808_s	0.000627	-1.29	-1.04	NM_033374	<i>Dock2</i>	dedicator of cyto-kinesis 2	0001766 // membrane raft polarization // inferred from mutant phenotype//0001768 // establishment of T cell polarity //
1454897_a	0.002185	-1.29	1.02	NM_177353//XM_00652	6330509M05Rik//	RIKEN cDNA 6330509M05 gene//solute carrier family 9	0006810 // transport // inferred from electronic annotation//0006811 // ion transport // inferred from electronic
1416714_a	0.000230	-1.29	-1.08	NM_008320//XM_00653	<i>Irf8</i>	interferon regulatory factor 8	0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 // regulation of transcription, DNA-
1452117_a	0.000388	-1.29	-1.18	NM_001278269//NM_0:	<i>Fyb</i>	FYN binding protein	0045576 // mast cell activation // inferred from mutant phenotype
1452389_a	0.002162	-1.29	1.04	NM_001033126//NM_0:	<i>Cd27</i>	CD27 antigen	0006915 // apoptotic process // inferred from electronic annotation//0042100 // B cell proliferation // non-traceable author
1451285_a	0.000141	-1.28	-1.25	NM_139149//XM_0065C	<i>Fus</i>	fused in sarcoma	
1415996_a	0.000267	-1.28	-1.06	NM_001009935//NM_0:	<i>Txnip</i>	thioredoxin interacting protein	0000122 // negative regulation of transcription from RNA polymerase II promoter // inferred from genetic
1421291_a	0.000007	-1.28	-1.12	NM_010553//XM_00645	<i>Il18rap</i>	interleukin 18 receptor accessory protein	0007165 // signal transduction // inferred from electronic annotation//0019221 // cytokine-mediated signaling pathway //
1417597_a	0.002164	-1.28	1.12	NM_007642	<i>Cd28</i>	CD28 antigen	0002863 // positive regulation of inflammatory response to antigenic stimulus // inferred from mutant phenotype//0006955
1418741_a	0.000201	-1.28	-1.11	NM_013566//XM_00652	<i>Itgb7</i>	integrin beta 7	0007155 // cell adhesion // inferred from electronic annotation//0007160 // cell-matrix adhesion // inferred from electronic
1416007_a	0.001249	-1.28	-1.03	NM_001163630//NM_0:	<i>Satb1</i>	special AT-rich sequence binding protein 1	0000122 // negative regulation of transcription from RNA polymerase II promoter // inferred from direct assay//0000122 //
1450816_a	0.000489	-1.28	-1.07	NM_015810//NR_02778	<i>Polg2</i>	polymerase (DNA directed), gamma 2, accessory subunit	0006260 // DNA replication // inferred by curator//0006261 // DNA-dependent DNA replication // inferred from sequence or
1451566_a	0.001911	-1.28	-1.06	NM_145612	<i>Zfp810</i>	zinc finger protein 810	0006355 // regulation of transcription, DNA-templated // inferred from electronic annotation
1421093_a	0.002112	-1.27	-1.28	NM_017394//XM_00654	<i>Slc7a10</i>	solute carrier family 7 (cationic amino acid transporter, y+ system),	0003333 // amino acid transmembrane transport // not recorded//0006810 // transport // inferred from electronic
1428297_a	0.000089	-1.27	-1.14	NM_001291787//NM_0:	<i>Map4k2</i>	mitogen-activated protein kinase kinase kinase kinase 2	0000165 // MAPK cascade // not recorded//0000185 // activation of MAPKKK activity // not recorded//0002376 // immune
1425099_a	0.001710	-1.27	-1.36	NM_001243048//NM_0:	<i>Arntl</i>	aryl hydrocarbon receptor nuclear translocator-like	0000060 // protein import into nucleus, translocation // inferred from direct assay//0006351 // transcription, DNA-templated
1419764_a	0.000913	-1.27	1.14	NM_009892//XM_0065C	<i>Chil3</i> // <i>Chil4</i>	chitinase-like 3//chitinase-like 4	0000272 // polysaccharide catabolic process // inferred from electronic annotation//0005975 // carbohydrate metabolic
1438238_a	0.001336	-1.27	-1.02	NM_001243117//NM_0:	2010315B03Rik	RIKEN cDNA 2010315B03 gene	0006355 // regulation of transcription, DNA-templated // inferred from electronic annotation
1421251_a	0.000420	-1.27	-1.22	NM_009555//XM_00652	<i>Zfp40</i>	zinc finger protein 40	0006355 // regulation of transcription, DNA-templated // not recorded
1421299_a	0.001315	-1.27	1.02	NM_001276402//NM_0:	<i>Lef1</i>	lymphoid enhancer binding factor 1	0000122 // negative regulation of transcription from RNA polymerase II promoter // inferred from direct assay//0001569 //
1421285_a	0.000187	-1.26	-1.01	NM_031376//XM_00652	<i>Pik3ap1</i>	phosphoinositide-3-kinase adaptor protein 1	0014068 // positive regulation of phosphatidylinositol 3-kinase signaling // inferred from mutant phenotype//0034122 //
1431220_a	0.000565	-1.26	-1.10	XM_006543762	<i>LOC102642487</i>	uncharacterized LOC102642487	
1448420_a	0.002340	-1.26	-1.09	NM_001002846//NM_0:	<i>Fbxl12</i>	F-box and leucine-rich repeat protein 12	0006511 // ubiquitin-dependent protein catabolic process // inferred from physical interaction//0016567 // protein
1452151_a	0.000791	-1.26	-1.13	NM_001205353//NM_1:	<i>Gramd4</i>	GRAM domain containing 4	0006915 // apoptotic process // inferred from electronic annotation
1456694_x	0.000400	-1.26	-1.04	NM_001077705//NM_0:	<i>Ptpn6</i>	protein tyrosine phosphatase, non-receptor type 6	0002244 // hematopoietic progenitor cell differentiation // inferred from mutant phenotype//0002924 // negative regulation
1422310_a	0.002619	-1.26	-1.09	NM_009223//XM_00652	<i>Snn</i>	stannin	
1422141_s	0.002088	-1.26	-1.09	NM_001081746//NM_0:	<i>Csprs</i> // <i>Gm15433</i>	component of Sp100-rs//predicted pseudogene 15433//predicted	0007186 // G-protein coupled receptor signaling pathway // inferred from electronic annotation
1422900_a	0.000195	-1.26	-1.13	NM_023799//XM_00652	<i>Mgea5</i>	meningioma expressed antigen 5 (hyaluronidase)	0006044 // N-acetylglucosamine metabolic process // not recorded//0006612 // protein targeting to membrane // not
1428682_a	0.000739	-1.26	1.05	NM_178404//XM_0065C	<i>Zc3h6</i>	zinc finger CCHC type containing 6	
1433963_a	0.000503	-1.26	-1.12	NM_153795//XM_00652	<i>Fermt3</i>	fermitin family homolog 3 (Drosophila)	0007155 // cell adhesion // inferred from electronic annotation//0007159 // leukocyte cell-cell adhesion // inferred from
1438781_a	0.002429	-1.25	-1.12	NM_001040400//NM_1:	<i>Tet2</i>	tet methylcytosine dioxygenase 2	0001822 // kidney development // inferred from mutant phenotype//0006211 // 5-methylcytosine catabolic process // not
1431840_a	0.001837	-1.25	-1.07	NM_153551//XM_00652	<i>Dennd1c</i>	DENN/MADD domain containing 1C	0032313 // regulation of Rab GTPase activity // not recorded//0032851 // positive regulation of Rab GTPase activity //
1460651_a	0.002747	-1.25	1.04	NM_010689//XM_0065C	<i>Lat</i>	linker for activation of T cells	0002260 // lymphocyte homeostasis // inferred from mutant phenotype//0002376 // immune system process // inferred
1424405_a	0.000145	-1.25	1.01	NM_145442//XM_00651	<i>Mbip</i>	MAP3K12 binding inhibitory protein 1	0043966 // histone H3 acetylation // not recorded
1448937_a	0.000012	-1.25	-1.16	NM_001170430//NM_0:	<i>Slc35b3</i>	solute carrier family 35, member B3	0006810 // transport // inferred from electronic annotation//0055085 // transmembrane transport // inferred from
1426258_a	0.001088	-1.24	1.03	NM_011436	<i>Sorl1</i>	soritin-related receptor, LDLR class A repeats-containing	0000042 // protein targeting to Golgi // not recorded//0006605 // protein targeting // not recorded//0006622 // protein
1422140_a	0.001356	-1.24	-1.07	NM_001081746//NM_0:	<i>Csprs</i> // <i>Gm2666</i> //	component of Sp100-rs//predicted gene 2666//predicted pseudogene	0007186 // G-protein coupled receptor signaling pathway // inferred from electronic annotation
1421107_a	0.000855	-1.24	-1.01	NM_021420//XM_00645	<i>Stk4</i>	serine/threonine kinase 4	0000902 // cell morphogenesis // not recorded//0001569 // patterning of blood vessels // inferred from genetic
1427408_a	0.000902	-1.24	-1.20	NM_146153//XM_0065C	<i>Thrap3</i>	thyroid hormone receptor associated protein 3	0000381 // regulation of alternative mRNA splicing, via spliceosome // not recorded//0000956 // nuclear-transcribed mRNA
1419291_x	0.001551	-1.24	-1.13	NR_002840//NR_02854:	<i>Gas5</i> // <i>Snord47</i>	growth arrest specific 5//small nucleolar RNA, C/D box 47	
1431367_a	0.002424	-1.24	-1.06	NM_001166372//NM_0:	<i>1-Mar</i>	membrane-associated ring finger (C3HC4) 1	0000209 // protein polyubiquitination // inferred from direct assay//0000209 // protein polyubiquitination // not
1418980_a	0.000510	-1.24	-1.04	NM_001146318//NM_0:	<i>Cnp</i>	2',3'-cyclic nucleotide 3' phosphodiesterase	0000226 // microtubule cytoskeleton organization // not recorded//0007409 // axonogenesis // inferred from mutant
1437072_a	0.000110	-1.24	-1.07	NM_001037727//NM_0:	<i>Arhgap25</i>	Rho GTPase activating protein 25	0007165 // signal transduction // inferred from electronic annotation//0043547 // positive regulation of GTPase activity //
1429316_a	0.000344	-1.24	-1.10	NM_027526//XM_0065C	<i>Rasgef1a</i>	RasGEF domain family, member 1A	0007264 // small GTPase mediated signal transduction // inferred from electronic annotation//0016477 // cell migration //
1456204_a	0.000708	-1.23	-1.15	NR_024069	<i>Snim4</i>	small integral membrane protein 4	
1436171_a	0.000816	-1.23	-1.12	NM_001005508	<i>Arhgap30</i>	Rho GTPase activating protein 30	0007165 // signal transduction // inferred from electronic annotation//0043547 // positive regulation of GTPase activity //
1422140_a	0.002511	-1.23	-1.08	NM_001081746//NM_0:	<i>Csprs</i> // <i>Gm2666</i> //	component of Sp100-rs//predicted gene 2666//predicted pseudogene	0007186 // G-protein coupled receptor signaling pathway // inferred from electronic annotation//0000723 // telomere
1417061_a	0.001650	-1.23	-1.24	NM_016917//XM_00645	<i>Slc40a1</i>	solute carrier family 40 (iron-regulated transporter), member 1	0002260 // lymphocyte homeostasis // inferred from mutant phenotype//0003158 // endothelium development // inferred
1425602_a	0.000084	-1.23	-1.10	NM_030566//XM_0065C	<i>Rabep2</i>	rabaptin, RAB GTPase binding effector protein 2	0006810 // transport // inferred from electronic annotation//0006897 // endocytosis // inferred from electronic
1425296_a	0.000304	-1.23	-1.05	NM_001081650//NM_0:	<i>Rgs3</i>	regulator of G-protein signaling 3	0007165 // signal transduction // not recorded//0007186 // G-protein coupled receptor signaling pathway // traceable
1433518_a	0.001237	-1.23	-1.04	NM_177846	<i>Lcmt2</i>	leucine carboxyl methyltransferase 2	0006481 // C-terminal protein methylation // not recorded//0008033 // tRNA processing // inferred from electronic
1454975_a	0.001264	-1.23	-1.14	NM_001033261//XM_0:	<i>Zfc3h1</i>	zinc finger, C3H1-type containing	0006396 // RNA processing // inferred from electronic annotation
1418826_a	0.001443	-1.23	-1.12	NM_027209	<i>Ms4a6b</i>	membrane-spanning 4-domains, subfamily A, member 6B	
1422188_s	0.001605	-1.23	1.13	<i>Tcrg</i> // <i>Tcrg-C2</i> // <i>T</i>		Mus musculus 2 days neonate thymus thymic cells cDNA, RIKEN full-	
1438079_a	0.001693	-1.22	1.04	NM_178417	<i>Zfp867</i>	zinc finger protein 867	0006355 // regulation of transcription, DNA-templated // inferred from electronic annotation
1422754_a	0.000962	-1.22	1.15	NM_021883//XM_00653	<i>Tmod1</i>	tropomodulin 1	0006936 // muscle contraction // inferred from mutant phenotype//0008344 // adult locomotory behavior // inferred from
1449463_a	0.001462	-1.22	-1.15	NM_008457//XM_00654	<i>Klik1b8</i>	kalikrein 1-related peptidase b8	0006508 // proteolysis // inferred from electronic annotation
1435697_a	0.002267	-1.22	-1.04	NM_139200//XM_00645	<i>Cytip</i>	cytohesin 1 interacting protein	0030155 // regulation of cell adhesion // not recorded
1418081_a	0.000027	-1.22	-1.04	NM_025362	<i>Dnajc30</i>	DnaJ (Hsp40) homolog, subfamily C, member 30	
1435116_a	0.002491	-1.22	1.06	NM_028908	<i>Map10</i>	microtubule-associated protein 10	0007049 // cell cycle // inferred from electronic annotation//0031122 // cytoplasmic microtubule organization // not
1418394_a	0.001963	-1.22	-1.04	NM_001163029//NM_0:	<i>Cd97</i>	CD97 antigen	0007155 // cell adhesion // inferred from electronic annotation//0007165 // signal transduction // traceable author
1455180_a	0.001516	-1.22	1.01	NM_001033208	<i>Myzap</i>	myocardial zonula adherens protein	0035556 // intracellular signal transduction // inferred from direct assay
1437886_a	0.002586	-1.22	1.00	NM_183390	<i>Klhl6</i>	kelch-like 6	0002467 // germinal center formation // inferred from mutant phenotype//00050853 // B cell receptor signaling pathway //
1439721_a	0.002197	-1.22	-1.28	NM_001033794	<i>Fbxw18</i>	F-box and WD-40 domain protein 18	
1426623_a	0.002355	-1.22	-1.14	NM_001122640//NM_0:	<i>Arhgap17</i>	Rho GTPase activating protein 17	0007015 // actin filament organization // not recorded//0007165 // signal transduction // inferred from electronic
1428062_a	0.000316	-1.21	-1.21	NM_025350	<i>Cpa1</i>	carboxypeptidase A1, pancreatic	0006508 // proteolysis // not recorded

Table S1

Gene_ID	p	FC-RSV 1 d	FC-RSV 5 d	RefSeq Transcript ID	Gene Symbol	Gene Title	Gene Ontology Biological Process
1416083_a	0.000083	-1.21	-1.07	NM_009551//XM_00652	<i>Zfand5</i>	zinc finger, AN1-type domain 5	0001701 // in utero embryonic development // inferred from mutant phenotype//0001944 // vasculature development //
1434607_a	0.001285	-1.21	1.01	NM_030096	<i>Ddx52</i>	DEAD (Asp-Glu-Ala-Asp) box polypeptide 52	0008152 // metabolic process // inferred from electronic annotation
1427301_a	0.001630	-1.21	-1.01	NM_007649//XM_00645	<i>Cd48</i>	CD48 antigen	0007165 // signal transduction // inferred from direct assay//0042110 // T cell activation // inferred from direct
1426806_a	0.000087	-1.21	1.02	NM_028696//XM_00645	<i>Nabp1</i>	nucleic acid binding protein 1	0000075 // cell cycle checkpoint // inferred from sequence or structural similarity//0000724 // double-strand break repair via
1417751_a	0.000260	-1.21	-1.05	NM_009288//XM_00651	<i>Stk10</i>	serine/threonine kinase 10	0006468 // protein phosphorylation // not recorded//0006950 // response to stress // not recorded//0007049 // cell cycle //
1416318_a	0.001041	-1.21	-1.03	NM_025429//XM_00651	<i>Serpinb1a</i>	serine (or cysteine) peptidase inhibitor, clade B, member 1a	0010466 // negative regulation of peptidase activity // inferred from electronic annotation//0010951 // negative regulation
1425128_a	0.002310	-1.21	1.03	NM_001036740//NM_1	<i>B3gnt8</i>	UDP-GlcNAc:beta-Gal beta-1,3-N-acetylglucosaminyltransferase 8	0006486 // protein glycosylation // inferred from electronic annotation//0030311 // poly-N-acetylglucosamine biosynthetic
1431894_a	0.000400	-1.21	1.02	NM_001001738//XM_0	<i>Itprp</i>	inositol 1,4,5-triphosphate receptor interacting protein	0006469 // negative regulation of protein kinase activity // inferred from direct assay//1902042 // negative regulation of
1433933_s	0.000413	-1.21	1.04	NM_001252530//NM_0	<i>Slco2b1</i>	solute carrier organic anion transporter family, member 2b1	0001889 // liver development // inferred from electronic annotation//0006810 // transport // inferred from electronic
1456061_a	0.000387	-1.21	-1.16	NM_001077410//NM_0	<i>Gimap8</i>	GTPase, IMAP family member 8	
1423702_a	0.001462	-1.21	-1.01	NM_008197	<i>H1f0</i>	H1 histone family, member 0	0006334 // nucleosome assembly // inferred from electronic annotation
1416968_a	0.002103	-1.21	-1.01	NM_001040684//NM_1	<i>Hsd3b7</i>	hydroxy-delta-5-steroid dehydrogenase, 3 beta- and steroid delta-	0001558 // regulation of cell growth // not recorded//0006694 // steroid biosynthetic process // inferred from electronic
1426387_x	0.000366	-1.21	-1.05	NM_001004146//NM_1	<i>Pisd//Pisd-ps1//P</i>	phosphatidylserine decarboxylase//phosphatidylserine decarboxylase,	0006629 // lipid metabolic process // inferred from electronic annotation//0006646 // phosphatidylethanolamine
1416206_a	0.000335	-1.20	-1.14	NM_001164480//NM_0	<i>Sipa1</i>	signal-induced proliferation associated gene 1	0042631 // cellular response to water deprivation // not recorded//0043547 // positive regulation of GTPase activity //
1420412_a	0.002343	-1.20	-1.01	NM_009425	<i>Tnfsf10</i>	tumor necrosis factor (ligand) superfamily, member 10	0006915 // apoptotic process // inferred from electronic annotation//0006955 // immune response // inferred from
1428282_a	0.000506	-1.20	-1.17	NM_178337//XM_00651	<i>Tbce</i>	tubulin-specific chaperone E	0000226 // microtubule cytoskeleton organization // inferred from mutant phenotype//0006457 // protein folding //
1426900_a	0.000038	-1.20	-1.07	NM_001242396//NM_2	<i>Umid1c</i>	jumonji domain containing 1C	0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 // regulation of transcription, DNA-
1416207_a	0.001888	-1.20	-1.13	NM_001173547//NM_0	<i>Taz</i>	tafazzin	0006936 // muscle contraction // not recorded//0007507 // heart development // not recorded//0007519 // skeletal muscle
1433597_a	0.001383	-1.20	-1.23	NM_176849//XM_0065C	<i>Argl1</i>	arginine and glutamate rich 1	
1427109_a	0.001479	-1.20	-1.10	NM_001003949//XM_0	<i>Tmem259</i>	transmembrane protein 259	
1435279_a	0.002007	-1.20	-1.15	NM_198170//XM_0065C	<i>Szt2</i>	seizure threshold 2	0007417 // central nervous system development // inferred from mutant phenotype//0009790 // embryo development //
1429264_a	0.000210	-1.20	-1.11	NR_015601	<i>Fam120aas</i>	family with sequence similarity 120A, opposite strand	
1416720_a	0.002131	-1.20	-1.17	NM_026499	<i>Srsf6</i>	serine/arginine-rich splicing factor 6	0000380 // alternative mRNA splicing, via spliceosome // not recorded//0000381 // regulation of alternative mRNA splicing,
1415723_a	0.000046	-1.20	-1.02	NM_173363//NM_1780	<i>Ejif5</i>	eukaryotic translation initiation factor 5	0006412 // translation // not recorded//0006413 // translational initiation // not recorded//0016070 // RNA metabolic
1419221_a	0.000074	-1.20	-1.15	NM_016758	<i>Rgs14</i>	regulator of G-protein signaling 14	0006913 // nucleocytoplasmic transport // inferred from direct assay//0006913 // nucleocytoplasmic transport // not
1417150_a	0.000987	-1.19	1.08	NM_010484//XM_00653	<i>Slc6a4</i>	solute carrier family 6 (neurotransmitter transporter, serotonin),	0001666 // response to hypoxia // inferred from electronic annotation//0006810 // transport // inferred from electronic
1431071_a	0.001598	-1.19	-1.08	NM_001162945//XM_0	<i>Mtx3</i>	metaxin 3	0006626 // protein targeting to mitochondrion // inferred from electronic annotation
1433669_a	0.000883	-1.19	-1.22	NM_019774//XM_00652	<i>Akap8</i>	A kinase (PRKA) anchor protein 8	0007076 // mitotic chromosome condensation // inferred from direct assay//0007076 // mitotic chromosome condensation
1420485_a	0.000735	-1.19	-1.10	NM_023554	<i>Nol7</i>	nucleolar protein 7	
1429237_a	0.001415	-1.19	-1.03	NM_001102423//NM_0	<i>Stx16</i>	syntaxin 16	0006810 // transport // inferred from electronic annotation//0006886 // intracellular protein transport // inferred from
1423191_a	0.000766	-1.19	-1.21	NM_018828//XM_00645	<i>Fnbp4</i>	formin binding protein 4	
1450512_a	0.000513	-1.19	1.07	NM_021320	<i>Ntn4</i>	netrin 4	0016322 // neuron remodeling // inferred from direct assay//0006068 // regulation of branching involved in salivary gland
1418892_a	0.000110	-1.19	-1.17	NM_023275	<i>Rhoj</i>	ras homolog gene family, member J	0006184 // GTP catabolic process // inferred from sequence or structural similarity//0007165 // signal transduction //
1439788_a	0.001096	-1.19	-1.15	NM_001001184//XM_0	<i>Primpol</i>	primase and polymerase (DNA-directed)	0006260 // DNA replication // inferred from electronic annotation//0006264 // mitochondrial DNA replication // inferred
1431147_a	0.001930	-1.19	-1.13	NM_177323//XM_00653	<i>Rint1</i>	RAD50 interactor 1	0006810 // transport // inferred from electronic annotation//0007049 // cell cycle // inferred from electronic
1437270_a	0.000239	-1.19	-1.16	NM_019952	<i>Clcf1</i>	cardiotrophin-like cytokine factor 1	0002639 // positive regulation of immunoglobulin production // inferred from direct assay//0002830 // positive regulation of
1416542_a	0.000107	-1.18	-1.08	NM_009343//XM_00652	<i>Phf1</i>	PHD finger protein 1	0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 // regulation of transcription, DNA-
1434300_a	0.000465	-1.18	-1.06	NM_001114977//NM_0	<i>U2surp</i>	U2 snRNP-associated SURP domain containing	0006396 // RNA processing // inferred from electronic annotation
1422031_a	0.000032	-1.18	-1.09	NM_022985//XM_0065C	<i>Zfand6</i>	zinc finger, AN1-type domain 6	0006625 // protein targeting to peroxisome // inferred from direct assay//0006810 // transport // inferred from electronic
1421628_a	0.000923	-1.18	-1.34	NM_001161842//NM_0	<i>Il18r1</i>	interleukin 18 receptor 1	0007165 // signal transduction // inferred from electronic annotation//0030101 // natural killer cell activation // inferred
1434681_a	0.000820	-1.18	1.01	NM_001290776//NM_0	<i>Tlxng</i>	taxilin gamma	0000122 // negative regulation of transcription from RNA polymerase II promoter // inferred from direct assay//0006260 //
1426420_a	0.000800	-1.18	-1.11	NR_040628//NM_13407	<i>Gm17066//Rbm2E</i>	predicted gene 17066//RNA binding motif protein 26	0006397 // mRNA processing // inferred from electronic annotation//0010923 // negative regulation of phosphatase activity
1419183_a	0.002071	-1.18	-1.00	NM_133905//XM_00651	<i>Papd4</i>	PAP associated domain containing 4	0002244 // hematopoietic progenitor cell differentiation // inferred from mutant phenotype//0006397 // mRNA processing //
1420123_a	0.000663	-1.18	-1.01	NM_133986//XM_00651	<i>Tcta</i>	T cell leukemia translocation altered gene	
1417134_a	0.000093	-1.18	1.04	NM_009274//XM_00653	<i>Srpk2</i>	serine/arginine-rich protein specific kinase 2	0000245 // spliceosomal complex assembly // inferred from direct assay//0000245 // spliceosomal complex assembly // not
1421872_a	0.001860	-1.18	-1.17	NM_009000//XM_00651	<i>Rab24</i>	RAB24, member RAS oncogene family	0006184 // GTP catabolic process // inferred from electronic annotation//0006810 // transport // inferred from electronic
1416892_s	0.000611	-1.18	-1.02	NM_025626//XM_00645	<i>Fam107b</i>	family with sequence similarity 107, member B	0007605 // sensory perception of sound // inferred from mutant phenotype
1417422_a	0.000481	-1.18	1.11	NM_010321//XM_00652	<i>Gnmt</i>	glycine N-methyltransferase	0005977 // glycogen metabolic process // inferred from mutant phenotype//0006111 // regulation of gluconeogenesis //
1424066_a	0.002457	-1.18	-1.08	NM_144858//XM_00652	<i>Dus3l</i>	dihydrouridine synthase 3-like (S. cerevisiae)	0002943 // tRNA dihydrouridine synthesis // inferred from electronic annotation//0008033 // tRNA processing // inferred
1436906_a	0.001936	-1.18	-1.13	NM_001033142//XM_0	<i>Rnf166</i>	ring finger protein 166	
1449852_a	0.000141	-1.18	1.10	NM_133838	<i>Ehd4</i>	EH-domain containing 4	0006184 // GTP catabolic process // inferred from electronic annotation//0006907 // pinocytosis // not recorded//0030100
1424850_a	0.000790	-1.18	-1.04	NM_011945//XM_00651	<i>Map3k1</i>	mitogen-activated protein kinase kinase kinase 1	0000165 // MAPK cascade // not recorded//0000186 // activation of MAPKK activity // not recorded//0003382 // epithelial
1428584_a	0.001453	-1.18	-1.07	NM_001271433//NM_0	<i>Haghl</i>	hydroxyacylglutathione hydrolase-like	0006750 // glutathione biosynthetic process // inferred from electronic annotation//0008152 // metabolic process // inferred
1436395_a	0.001949	-1.17	1.04	NM_001163138//XM_0	<i>Card6</i>	caspase recruitment domain family, member 6	0042981 // regulation of apoptotic process // inferred from electronic annotation//0043122 // regulation of I-kappaB
1448365_a	0.000377	-1.17	-1.13	NM_001081188//XM_0	<i>Exosc7</i>	exosome component 7	0006364 // rRNA processing // inferred from electronic annotation
1427562_a	0.000625	-1.17	1.08	NM_011101	<i>Prkca</i>	protein kinase C, alpha	0000188 // inactivation of MAPK activity // inferred from mutant phenotype//0000302 // response to reactive oxygen species
1423251_a	0.000736	-1.17	-1.09	NM_001170848//NM_0	<i>Luc7l2</i>	LUC7-like 2 (S. cerevisiae)	0006376 // mRNA splice site selection // inferred from electronic annotation
1455610_a	0.000997	-1.17	-1.10	NM_183312//NM_2016	<i>Synn</i>	synemin, intermediate filament protein	
1422599_s	0.001160	-1.17	-1.02	NM_009281//XM_0065C	<i>Zfp143</i>	zinc finger protein 143	0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 // regulation of transcription, DNA-
1420362_a	0.000303	-1.17	-1.13	NM_007546//XM_00652	<i>Bik</i>	BCL2-interacting killer	0006915 // apoptotic process // inferred from electronic annotation//0007283 // spermatogenesis // inferred from genetic
1452202_a	0.001186	-1.17	-1.14	NM_001008548//NM_0	<i>Pde2a</i>	phosphodiesterase 2A, cGMP-stimulated	0000122 // negative regulation of transcription from RNA polymerase II promoter // not recorded//0006198 // cAMP
1428057_a	0.002549	-1.17	1.01	NM_001039959//NM_0	<i>Ahnak</i>	AHNAK nucleoprotein (desmoyokin)	0043484 // regulation of RNA splicing // inferred from direct assay//0051259 // protein oligomerization // inferred from
1448555_a	0.000937	-1.17	-1.01	NM_028003	<i>Rpap3</i>	RNA polymerase II associated protein 3	
1424238_a	0.000300	-1.17	-1.16	NM_153056//XM_00653	<i>Sirt7</i>	sirtuin 7	0000122 // negative regulation of transcription from RNA polymerase II promoter // not recorded//0001701 // in utero
1434753_a	0.000540	-1.17	-1.09	NM_172766//XM_00651	<i>Nfrkb</i>	nuclear factor related to kappa B binding protein	0006281 // DNA repair // inferred from electronic annotation//0006310 // DNA recombination // inferred from electronic
1454980_a	0.000264	-1.17	1.09		<i>AB351656</i>	Mus musculus non-coding RNA, oocyte_piRNA216, complete sequence.	

Table S1

Gene_ID	p	FC-RSV 1 d	FC-RSV 5 d	RefSeq Transcript ID	Gene Symbol	Gene Title	Gene Ontology Biological Process
1429587_a	0.000045	-1.17	-1.00	NM_172762//XM_00653	<i>Rbm34</i>	RNA binding motif protein 34	
1427192_a	0.002397	-1.17	-1.11	NM_001289606//NM_01	<i>Brd8</i>	bromodomain containing 8	0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 // regulation of transcription, DNA-
1426926_a	0.000778	-1.17	-1.06	NM_172285	<i>Plcg2</i>	phospholipase C, gamma 2	0002316 // follicular B cell differentiation // inferred from mutant phenotype//0006629 // lipid metabolic process // inferred
1418659_a	0.000299	-1.17	-1.19	NM_001289826//NM_01	<i>Clock</i>	circadian locomotor output cycles kaput	0000077 // DNA damage checkpoint // not recorded//0006351 // transcription, DNA-templated // inferred from electronic
1418700_a	0.000163	-1.17	-1.03	NM_024471//XM_0065C	<i>Lias</i>	lipic acid synthetase	0001843 // neural tube closure // inferred from mutant phenotype//0006954 // inflammatory response // inferred from
1419273_a	0.000827	-1.16	-1.07	NM_011274//XM_00653	<i>Uri1</i>	URI1, prefoldin-like chaperone	0000122 // negative regulation of transcription from RNA polymerase II promoter // not recorded//0001558 // regulation of
1451006_a	0.000006	-1.16	1.28	NM_011723//XR_38531	<i>Xdh</i>	xanthine dehydrogenase	0001933 // negative regulation of protein phosphorylation // not recorded//0001937 // negative regulation of endothelial
1428637_a	0.000780	-1.16	1.06	NM_001014390//XM_0C	<i>Dyrk2</i>	dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 2	0006468 // protein phosphorylation // not recorded//0006915 // apoptotic process // inferred from electronic
1429881_a	0.000635	-1.16	-1.07	NM_001025377//NM_1	<i>Arhgap15</i>	Rho GTPase activating protein 15	0007165 // signal transduction // inferred from electronic annotation//0008360 // regulation of cell shape // not
1448054_a	0.000377	-1.16	-1.12	NM_133345//NM_1445	<i>Ing4</i> // <i>Acrbp</i>	inhibitor of growth family, member 4//proacrosin binding protein	0006260 // DNA replication // not recorded//0006473 // protein acetylation // not recorded//0006915 // apoptotic process
1418638_a	0.000421	-1.16	-1.08	NM_010387//NM_0103	<i>H2-DMb1</i> // <i>H2-DM</i>	histocompatibility 2, class II, locus Mb1//histocompatibility 2, class II,	0002376 // immune system process // inferred from electronic annotation//0002474 // antigen processing and presentation
1422470_a	0.000175	-1.16	1.14	NM_009760	<i>Bnip3</i>	BCL2/adenovirus E1B interacting protein 3	0001666 // response to hypoxia // not recorded//0006309 // apoptotic DNA fragmentation // inferred from sequence or
1416791_a	0.002565	-1.16	-1.09	NM_001276704//NM_0	<i>Nxf1</i>	nuclear RNA export factor 1	0006405 // RNA export from nucleus // inferred from direct assay//0006406 // mRNA export from nucleus // not
1425014_a	0.002755	-1.16	-1.04	NM_011630//XM_0065C	<i>Nr2c2</i>	nuclear receptor subfamily 2, group C, member 2	0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 // regulation of transcription, DNA-
1425684_a	0.001977	-1.16	-1.04	NM_172398//XM_0065C	<i>Akr1b10</i>	aldo-keto reductase family 1, member B10 (aldose reductase)	0055114 // oxidation-reduction process // not recorded
1430431_a	0.001143	-1.16	-1.10	NM_001081101//XM_0C	<i>Uvssa</i>	UV stimulated scaffold protein A	0006281 // DNA repair // inferred from electronic annotation//0006283 // transcription-coupled nucleotide-excision repair //
1423673_a	0.001058	-1.16	1.08	NM_177630	<i>Ldccl1</i>	leucine zipper, down-regulated in cancer 1-like	
1437395_a	0.002603	-1.16	-1.09	NM_175472//XM_0065C	<i>Zcchc11</i>	zinc finger, CCHC domain containing 11	0001816 // cytokine production // inferred from direct assay//0008152 // metabolic process // inferred from electronic
1451793_a	0.000269	-1.16	1.00	NM_029436//XM_00652	<i>Klhl24</i>	kelch-like 24	
1427014_a	0.000835	-1.16	-1.08	NM_201407//XM_0065C	<i>Dennd4b</i>	DENN/MADD domain containing 4B	0032313 // regulation of Rab GTPase activity // not recorded//0032483 // regulation of Rab protein signal transduction // not
1436832_a	0.000239	-1.15	-1.04	NM_001145433	<i>Ssmi20</i>	small integral membrane protein 20	
1423930_a	0.001351	-1.15	-1.04	NM_024213	<i>Anapc4</i>	anaphase promoting complex subunit 4	0007049 // cell cycle // inferred from electronic annotation//0007067 // mitotic nuclear division // inferred from electronic
1434335_a	0.000329	-1.15	-1.01	NM_001159361//NM_1	<i>Dip2b</i>	DIP2 disco-interacting protein 2 homolog B (Drosophila)	0008152 // metabolic process // inferred from electronic annotation
1418523_a	0.000110	-1.15	-1.12	NM_011790//XM_00651	<i>Arih2</i>	ariadne homolog 2 (Drosophila)	0002009 // protein polyubiquitination // not recorded//0006511 // ubiquitin-dependent protein catabolic process // inferred
1422820_a	0.002361	-1.15	1.11	NM_001039507//NM_0	<i>Lipe</i>	lipase, hormone sensitive	0006361 // transcription initiation from RNA polymerase I promoter // inferred from sequence or structural
1422505_a	0.000134	-1.15	-1.05	NM_053068	<i>Chrac1</i>	chromatin accessibility complex 1	0006261 // DNA-dependent DNA replication // inferred from electronic annotation//0008152 // metabolic process // inferred
1436796_a	0.001435	-1.15	-1.13	NR_038073	<i>Snhg4</i>	small nuclear RNA host gene 4	
1417721_s	0.001475	-1.15	-1.02	NM_010686//XM_00653	<i>Lapmt5</i>	lysosomal-associated protein transmembrane 5	0006810 // transport // inferred from electronic annotation
1420711_a	0.001861	-1.15	-1.06	NM_001163301//NM_01	<i>Pex2</i>	peroxisomal biogenesis factor 2	0000038 // very long-chain fatty acid metabolic process // not recorded//0000122 // negative regulation of transcription
1439460_a	0.000549	-1.15	-1.08	NM_001166024//NM_0	<i>Arfgap2</i>	ADP-ribosylation factor GTPase activating protein 2	0006810 // transport // inferred from electronic annotation//0015031 // protein transport // inferred from electronic
1427245_a	0.000340	-1.15	-1.18	NM_001177706//NM_01	<i>Arfgap1</i>	ADP-ribosylation factor GTPase activating protein 1	0006810 // transport // inferred from electronic annotation//0015031 // protein transport // inferred from electronic
1422060_a	0.001064	-1.15	-1.04	NM_133167//XM_00652	<i>Parvb</i>	parvin, beta	0007155 // cell adhesion // inferred from electronic annotation//0030031 // cell projection assembly // not
1422281_a	0.001142	-1.15	1.01	NM_009219	<i>Sstr4</i>	somatostatin receptor 4	0007165 // signal transduction // inferred from electronic annotation//0007186 // G-protein coupled receptor signaling
1416896_a	0.002558	-1.15	-1.07	NM_001285505//NM_01	<i>Rps6ka1</i>	ribosomal protein S6 kinase polypeptide 1	0006468 // protein phosphorylation // not recorded//0009103 // lipopolysaccharide biosynthetic process // inferred from
1456603_a	0.001775	-1.15	-1.17	NM_029658	<i>Fam101b</i>	family with sequence similarity 101, member B	0001837 // epithelial to mesenchymal transition // inferred from genetic interaction//0030036 // actin cytoskeleton
1434900_a	0.001279	-1.15	1.02	NM_001082536//NM_1	<i>Mkl1</i>	MKL (megakaryoblastic leukemia)/myocardin-like 1	0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 // regulation of transcription, DNA-
1416799_a	0.000579	-1.15	1.02	NM_001164325//NM_0	<i>Trpm7</i>	transient receptor potential cation channel, subfamily M, member 7	0006468 // protein phosphorylation // inferred from direct assay//0006468 // protein phosphorylation // not
1423538_a	0.000756	-1.14	1.00	NM_010946//XM_00652	<i>Ntan1</i> // <i>Il2</i>	N-terminal Asn amidase//interleukin 2	0007613 // memory // inferred from mutant phenotype//0008152 // metabolic process // inferred from direct
1426506_a	0.001916	-1.14	-1.16	NM_001033711//NM_01	<i>Evi2a</i> // <i>Evi2a-evi2b</i>	ecotropic viral integration site 2a//Evi2a-Evi2b	
1442982_a	0.000838	-1.14	-1.10	NM_177111//XM_00651	<i>Ccdc66</i>	coiled-coil domain containing 66	0046548 // retinal rod cell development // inferred from mutant phenotype//0006060 // post-embryonic retina
1426690_a	0.001026	-1.14	-1.08	NM_011480//XM_00653	<i>Sreb1</i>	sterol regulatory element binding transcription factor 1	0000122 // negative regulation of transcription from RNA polymerase II promoter // inferred from direct assay//0000122 //
1426334_a	0.000776	-1.14	-1.11	NM_001284410//NM_01	<i>Bcl2l11</i>	BCL2-like 11 (apoptosis facilitator)	0001701 // in utero embryonic development // inferred from genetic interaction//0001776 // leukocyte homeostasis //
1428332_a	0.000072	-1.14	1.05	NM_178149//XM_00651	<i>Pik3ip1</i>	phosphoinositide-3-kinase interacting protein 1	0014067 // negative regulation of phosphatidylinositol 3-kinase signaling // inferred from direct assay//0014067 // negative
1419558_a	0.000245	-1.14	-1.11	NM_008575//XM_00652	<i>Mdm4</i>	transformed mouse 3T3 cell double minute 4	0000122 // negative regulation of transcription from RNA polymerase II promoter // not recorded//0006461 // protein
1427537_a	0.000972	-1.14	1.15	NM_144848	<i>Eppk1</i>	epiplakin 1	
1416389_a	0.001040	-1.14	1.02	NM_001170694//NM_1	<i>Rcbtb2</i>	regulator of chromosome condensation (RCC1) and BTB (POZ) domain	
1422566_a	0.000176	-1.14	1.07	NM_001161722//NM_01	<i>Tfjeb</i>	transcription factor EB	0001892 // embryonic placenta development // inferred from mutant phenotype//0002376 // immune system process //
1420159_a	0.000551	-1.14	-1.09	NM_181072//XM_00651	<i>Myo1e</i>	myosin IE	0001570 // vasculogenesis // inferred from mutant phenotype//0001701 // in utero embryonic development // inferred from
1418883_a	0.000459	-1.14	1.00	NM_008774	<i>Pabpc1</i>	poly(A) binding protein, cytoplasmic 1	0000184 // nuclear-transcribed mRNA catabolic process, nonsense-mediated decay // inferred from electronic
1421553_a	0.002041	-1.14	1.15	NM_010146//XM_00651	<i>Epm2a</i>	epilepsy, progressive myoclonic epilepsy, type 2 gene alpha	0005975 // carbohydrate metabolic process // inferred from electronic annotation//0005977 // glycogen metabolic process
1416904_a	0.000457	-1.13	-1.02	NM_001253708//NM_01	<i>Mbnl1</i>	muscleblind-like 1 (Drosophila)	0000380 // alternative mRNA splicing, via spliceosome // inferred from mutant phenotype//0000380 // alternative mRNA
1438491_x	0.000310	-1.13	-1.20	NM_183146	<i>A530054K11Rik</i>	RIKEN cDNA A530054K11 gene	0006355 // regulation of transcription, DNA-templated // inferred from electronic annotation
1460271_a	0.000284	-1.13	-1.48	NM_021407//XM_00652	<i>Trem3</i>	triggering receptor expressed on myeloid cells 3	0002374 // cytokine secretion involved in immune response // inferred from genetic interaction//0016477 // cell migration //
1418180_a	0.000113	-1.13	1.00	NM_013672//XM_00652	<i>Sp1</i>	trans-acting transcription factor 1	0001503 // ossification // inferred from genetic interaction//0001701 // in utero embryonic development // inferred from
1428351_a	0.001338	-1.13	-1.08	NM_026447//NM_1989	<i>Ppm1m</i>	protein phosphatase 1M	0006470 // protein dephosphorylation // inferred from direct assay
1448900_a	0.000170	-1.13	1.04	NM_138583//XM_00652	<i>Tango2</i>	transport and golgi organization 2	
1420612_s	0.002270	-1.13	-1.09	NM_001164745//NM_01	<i>Ptp4a2</i>	protein tyrosine phosphatase 4a2	0006470 // protein dephosphorylation // inferred from electronic annotation//0016311 // dephosphorylation // inferred
1460361_a	0.000903	-1.13	-1.17	NM_026362//XM_00652	<i>Plgrkt</i>	plasmogin receptor, C-terminal lysine transmembrane protein	0006935 // chemotaxis // inferred from electronic annotation//0006954 // inflammatory response // inferred from electronic
1434650_a	0.001285	-1.13	-1.06	NM_001165948//NM_1	<i>Pogz</i>	pogo transposable element with ZNF domain	0007049 // cell cycle // inferred from electronic annotation//0007064 // mitotic sister chromatid cohesion // not
1443490_a	0.000404	-1.13	-1.25		<i>D3Erd34e</i>	DNA segment, Chr 3, ERATO Doi 34, expressed	
1426983_a	0.001970	-1.13	-1.09	NM_001038700//NM_01	<i>Fbnp1</i>	formin binding protein 1	0006897 // endocytosis // inferred from electronic annotation//0007165 // signal transduction // inferred from electronic
1426030_a	0.001220	-1.13	-1.05	NM_146226//XM_00651	<i>Apeh</i>	acylpeptide hydrolase	0006508 // proteolysis // not recorded//0050435 // beta-amyloid metabolic process // not recorded
1424309_a	0.001633	-1.13	-1.00	NM_001113374//NM_01	<i>Mocs2</i>	molybdenum cofactor synthesis 2	0006777 // Mo-molybdopter cofactor biosynthetic process // not recorded
1425180_a	0.001463	-1.13	-1.12	NM_001285852//NM_01	<i>Gsp1p</i> // <i>BC094435</i>	SH3-domain GRB2-like (endophilin) interacting protein 1//cDNA	0002021 // response to dietary excess // not recorded//0006886 // intracellular protein transport // inferred from electronic
1435634_a	0.000443	-1.12	-1.04	NM_183028//XM_00645	<i>Pcmt1d</i>	protein-L-isoaspartate (D-aspartate) O-methyltransferase domain	0006464 // cellular protein modification process // inferred from electronic annotation//0006479 // protein methylation //
1454628_a	0.001613	-1.12	-1.13	NM_001039669//NM_1	<i>Iffo1</i>	intermediate filament family orphan 1	

Table S1

Gene_ID	p	FC-RSV 1 d	FC-RSV 5 d	RefSeq Transcript ID	Gene Symbol	Gene Title	Gene Ontology Biological Process
1426072_a	0.001946	-1.12	-1.19	NM_008153//XM_00653 <i>Cmklr1</i>		chemokine-like receptor 1	0006935 // chemotaxis // not recorded//0007165 // signal transduction // inferred from electronic annotation//0007186 //
1424646_a	0.000458	-1.12	-1.11	NM_026765//XM_0065C <i>Uck1</i>		uridine-cytidine kinase 1-like 1	0008152 // metabolic process // inferred from electronic annotation//0016310 // phosphorylation // inferred from electronic
1434330_a	0.000603	-1.12	1.08	NM_173038//XM_00651 <i>Tbcel</i>		tubulin folding cofactor E-like	
1427177_a	0.002587	-1.12	1.06	NM_001110253//NM_1_1 <i>Fyco1</i>		FVFE and coiled-coil domain containing 1	0006810 // transport // inferred from electronic annotation//0072383 // plus-end-directed vesicle transport along
1424997_a	0.002656	-1.12	-1.12	NM_001035259//NM_1_1 <i>Sfswap</i>		splicing factor, suppressor of white-apricot homolog (Drosophila)	0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 // regulation of transcription, DNA-
1416812_a	0.000120	-1.12	-1.18	NM_001164078//NM_0_1 <i>Tia1</i>		cytotoxic granule-associated RNA binding protein 1	0006915 // apoptotic process // inferred from electronic annotation//0017148 // negative regulation of translation //
1418296_a	0.002236	-1.12	-1.06	NM_001111073//NM_0_1 <i>Fxyd5</i>		FXYD domain-containing ion transport regulator 5	0006810 // transport // inferred from electronic annotation//0006811 // ion transport // inferred from electronic
1426250_s	0.000343	-1.12	1.00	NM_001167939//NM_0_1 <i>Mau2</i>		MAU2 chromatin cohesion factor homolog (C. elegans)	0007049 // cell cycle // inferred from electronic annotation//0007059 // chromosome segregation // inferred from electronic
1432144_a	0.000384	-1.12	-1.08	NM_001271797//NM_0_1 <i>Rchy1</i>		ring finger and CHY zinc finger domain containing 1	0016567 // protein ubiquitination // not recorded//0031398 // positive regulation of protein ubiquitination // not
1428337_a	0.001681	-1.12	-1.10	NM_023397//NR_02831 <i>Mdp1</i>		magnesium-dependent phosphatase 1	0016311 // dephosphorylation // not recorded//0030389 // fructosamine metabolic process // not recorded//0035335 //
1422874_a	0.002667	-1.12	-1.10	NM_001127340//NM_0_1 <i>Acrbp</i> //Ing4		proacrosin binding protein//inhibitor of growth family, member 4	0007286 // spermatid development // not recorded//0010952 // positive regulation of peptidase activity // not
1449990_a	0.001576	-1.12	-1.02	NM_008366//NM_0109_1 <i>IL2</i> //Ntan1		interleukin 2//N-terminal Asn amidase	0001933 // negative regulation of protein phosphorylation // not recorded//0001934 // positive regulation of protein
1436009_a	0.001793	-1.12	-1.04	NM_001033202 <i>Usp30</i>		ubiquitin specific peptidase 30	0000422 // mitochondrion degradation // inferred from sequence or structural similarity//0006508 // proteolysis // inferred
1438712_a	0.000861	-1.12	-1.07	NM_001093754//NM_0_1 <i>Dennd2d</i>		DENN/MADD domain containing 2D	0032313 // regulation of Rab GTPase activity // not recorded//0032851 // positive regulation of Rab GTPase activity //
1454646_a	0.001358	-1.12	1.04	NM_146008 <i>Tcp112</i>		t-complex 11 (mouse) like 2	
1421388_a	0.000727	-1.12	-1.01	NM_133665//XM_0065C <i>Mef2d</i>		myocyte enhancer factor 2D	0001649 // osteoblast differentiation // inferred from genetic interaction//0001958 // endochondral ossification // inferred
1416307_a	0.001114	-1.12	-1.04	NM_007456//XM_0065C <i>Ap1m1</i>		adaptor-related protein complex AP-1, mu subunit 1	0006810 // transport // inferred from electronic annotation//0006886 // intracellular protein transport // traceable author
1426531_a	0.000575	-1.12	-1.02	NM_001199141//NM_1_1 <i>Zmynd11</i> ///AK2152		zinc finger, MYND domain containing 11//Mus musculus cDNA,	0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 // regulation of transcription, DNA-
1448025_a	0.001626	-1.11	-1.21	NM_001002898//NM_0_1 <i>LOC100038947</i> ///S		signal-regulatory protein beta 1-like//signal-regulatory protein beta	0035556 // intracellular signal transduction // inferred from direct assay//0050766 // positive regulation of phagocytosis //
1421385_a	0.001680	-1.11	1.13	NM_001256081//NM_0_1 <i>Myo7a</i>		myosin VIIA	0001845 // phagolysosome assembly // inferred from mutant phenotype//0006200 // ATP catabolic process // not
1456480_a	0.001091	-1.11	1.09	NM_172887//NM_1787_1 <i>Fry</i>		furry homolog (Drosophila)	
1423902_s	0.000058	-1.11	1.05	NM_027144//XM_00651 <i>Arhgef12</i>		Rho guanine nucleotide exchange factor (GEF) 12	0007186 // G-protein coupled receptor signaling pathway // not recorded//0032321 // positive regulation of Rho GTPase
1452820_a	0.001285	-1.11	-1.02	NM_172255//XR_37822_1 <i>Wdr11</i>		WD repeat domain 11	
1423436_a	0.000570	-1.11	1.26	NM_001077353//NM_0_1 <i>Gsta3</i>		glutathione S-transferase, alpha 3	0001657 // ureteric bud development // inferred from expression pattern//0006749 // glutathione metabolic process //
1417662_a	0.002406	-1.11	-1.15	NM_001282967//NM_0_1 <i>Elk3</i>		ELK3, member of ETS oncogene family	0001525 // angiogenesis // inferred from mutant phenotype//0006351 // transcription, DNA-templated // inferred from
1416535_a	0.001323	-1.11	-1.05	NM_001164156//NM_0_1 <i>Mcrs1</i>		microspherule protein 1	0006281 // DNA repair // inferred from electronic annotation//0006310 // DNA recombination // inferred from electronic
1415763_a	0.000947	-1.11	-1.05	NM_029748//XM_0065C <i>Tmem234</i>		transmembrane protein 234	
1452796_a	0.001601	-1.11	1.06	NM_027185 <i>Def6</i>		differentially expressed in FDCP 6	
1426207_a	0.000185	-1.11	-1.11	NM_001159774//NM_0_1 <i>Ikkb</i>		inhibitor of kappaB kinase beta	0001782 // B cell homeostasis // inferred from mutant phenotype//0006468 // protein phosphorylation // inferred from
1428141_a	0.000955	-1.11	-1.01	NM_028758 <i>Gga2</i>		golgi associated, gamma adaptin ear containing, ARF binding protein 2	0006810 // transport // inferred from electronic annotation//0006886 // intracellular protein transport // inferred from
1426614_a	0.001188	-1.11	-1.02	NM_001252584//NM_0_1 <i>Zmynd8</i>		zinc finger, MYND-type containing 8	0016310 // phosphorylation // inferred from electronic annotation
1417329_a	0.001419	-1.11	1.21	NM_018824//XM_00645 <i>Slc23a2</i>		solute carrier family 23 (nucleobase transporters), member 2	0006810 // transport // inferred from electronic annotation//0006811 // ion transport // inferred from electronic
1419874_x	0.000026	-1.11	1.65	NM_001033324//XM_0C <i>Zbtb16</i>		zinc finger and BTB domain containing 16	0001501 // skeletal system development // inferred from mutant phenotype//0001823 // mesonephros development //
1422581_a	0.002156	-1.10	1.05	NM_019663//XM_00651 <i>Pias1</i>		protein inhibitor of activated STAT 1	0000122 // negative regulation of transcription from RNA polymerase II promoter // inferred from mutant
1437844_x	0.000798	-1.10	1.03	NM_013581//XM_00653 <i>Cog1</i> ///LOC102641		component of oligomeric golgi complex 1//conserved oligomeric Golgi	0006810 // transport // inferred from electronic annotation//0015031 // protein transport // inferred from electronic
1427016_a	0.001772	-1.10	1.02	NM_172679//NM_17261 <i>4932438A13Rik</i>		RIKEN cDNA 4932438A13 gene	0001558 // regulation of cell growth // non-traceable author statement//0006629 // lipid metabolic process // non-traceable
1451098_a	0.001793	-1.10	-1.09	NM_145606 <i>Chmp1a</i>		charged multivesicular body protein 1A	0009010 // cytokinesis // not recorded//0006351 // transcription, DNA-templated // inferred from electronic
1428109_a	0.001545	-1.10	-1.00	NM_027889//XM_00651 <i>Vps11</i>		vacuolar protein sorting 11 (yeast)	0006810 // transport // inferred from electronic annotation//0006886 // intracellular protein transport // inferred from
1422837_a	0.001166	-1.10	1.30	NM_022886//XM_00651 <i>Scel</i>		scieillin	0008544 // epidermis development // inferred from direct assay//0009790 // embryo development // inferred from direct
1443932_a	0.000625	-1.10	1.07	NM_178253//XM_00651 <i>Kilhd1</i>		kelch domain containing 1	
1451812_a	0.000607	-1.10	1.23	NM_001007220//NM_0_1 <i>Adam22</i>		a disintegrin and metallopeptidase domain 22	0006508 // proteolysis // inferred from electronic annotation//0007229 // integrin-mediated signaling pathway // inferred
1416674_a	0.000297	-1.10	1.22	NM_001083119//NM_0_1 <i>Ptprr</i>		protein tyrosine phosphatase, receptor type, U	0006470 // protein dephosphorylation // not recorded//0007155 // cell adhesion // inferred from electronic
1429722_a	0.002520	-1.10	-1.00	NM_029348//XM_00653 <i>Zbtb4</i>		zinc finger and BTB domain containing 4	0006974 // cellular response to DNA damage stimulus // not recorded//0045892 // negative regulation of transcription, DNA-
1442085_a	0.001693	-1.10	-1.07	NM_001001735//NM_0_1 <i>Whsc1l1</i>		Wolf-Hirschhorn syndrome candidate 1-like 1 (human)	0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 // regulation of transcription, DNA-
1430185_a	0.001524	-1.10	1.18	NM_029332//XM_00654 <i>Akap13</i>		A kinase (PRKA) anchor protein 13	0006468 // protein phosphorylation // inferred from electronic annotation//0010611 // regulation of cardiac muscle
1434329_s	0.000323	-1.10	1.05	NM_197985//XM_0065C <i>Adipor2</i>		adiponectin receptor 2	0006629 // lipid metabolic process // inferred from electronic annotation//0006631 // fatty acid metabolic process //
1438069_a	0.000223	-1.10	-1.18	NM_148930//XM_00651 <i>Rbm5</i>		RNA binding motif protein 5	0000245 // spliceosomal complex assembly // not recorded//0000381 // regulation of alternative mRNA splicing, via
1449958_a	0.000955	-1.10	-1.01	NM_010201//NM_20761 <i>Fgf14</i>		fibroblast growth factor 14	0007254 // JNK cascade // not recorded//0007268 // synaptic transmission // inferred from genetic interaction//0007399 //
1419255_a	0.002700	-1.10	-1.03	NM_009260//NM_1758: <i>Sptbn1</i>		spectrin beta, non-erythrocytic 1	0000281 // mitotic cytokinesis // not recorded//0007009 // plasma membrane organization // not recorded//0007182 //
1427202_a	0.001201	-1.10	1.12	NM_001252094//NM_0_1 <i>Mettl20</i>		methyltransferase like 20	0006479 // protein methylation // inferred from electronic annotation//0032259 // methylation // inferred from electronic
1438774_s	0.000172	-1.10	1.19	NM_027629//XM_0065C <i>Pgm2l1</i>		phosphoglucomutase 2-like 1	0005975 // carbohydrate metabolic process // inferred from electronic annotation//0006006 // glucose metabolic process //
1416906_a	0.000531	-1.09	-1.11	NM_001042491//NM_0_1 <i>Anapc5</i>		anaphase-promoting complex subunit 5	0007049 // cell cycle // inferred from electronic annotation//0007067 // mitotic nuclear division // inferred from electronic
1433478_a	0.001464	-1.09	-1.15	NM_001005767//XM_0C <i>Parl</i>		presenilin associated, rhomboid-like	0006508 // proteolysis // inferred from electronic annotation//0090201 // negative regulation of release of cytochrome c
1421759_a	0.000967	-1.09	1.06	NM_010812//NM_1990: <i>Foxk1</i>		forkhead box K1	0000122 // negative regulation of transcription from RNA polymerase II promoter // ---//0006351 // transcription, DNA-
1428758_a	0.001471	-1.09	1.08	NM_026436 <i>Tmem86a</i>		transmembrane protein 86A	
1456371_a	0.000562	-1.09	1.09	NM_001290789//NM_0_1 <i>Shroom1</i>		shroom family member 1	0000902 // cell morphogenesis // inferred from direct assay//0051017 // actin filament bundle assembly // inferred from
1449354_a	0.002235	-1.09	1.09	NM_011663 <i>Zrsr1</i>		zinc finger (CCCH type), RNA binding motif and serine/arginine rich 1	
1436953_a	0.000454	-1.09	1.03	NM_001289722//NM_0_1 <i>Wipf1</i>		WAS/WASL interacting protein family, member 1	0008154 // actin polymerization or depolymerization // inferred from electronic annotation//0030036 // actin cytoskeleton
1453496_a	0.001920	-1.09	1.19	NM_029894//XM_00651 <i>Fam162b</i>		family with sequence similarity 162, member B	
1417410_s	0.000067	-1.09	1.06	NM_008857//XM_00653 <i>Prkci</i>		protein kinase C, iota	0006468 // protein phosphorylation // inferred from direct assay//0006468 // protein phosphorylation // not
1424826_s	0.000746	-1.09	-1.12	NM_001146180//NM_1_1 <i>Mtss1</i>		metastasis suppressor 1	0001701 // in utero embryonic development // inferred from genetic interaction//0007015 // actin filament organization //
1440247_a	0.000279	-1.09	-1.01	NM_001168382//NM_0_1 <i>Phf14</i>		PHD finger protein 14	0000122 // negative regulation of transcription from RNA polymerase II promoter // inferred from direct assay//0008285 //
1437773_x	0.001970	-1.09	-1.15	NM_001040187//NM_1_1 <i>Ddx17</i>		DEAD (Asp-Glu-Ala-Asp) box polypeptide 17	0006200 // ATP catabolic process // inferred from electronic annotation//0006351 // transcription, DNA-templated //
1450499_a	0.001823	-1.09	1.08	NM_001199304//NM_0_1 <i>Atn1</i>		ataxin 1	0000122 // negative regulation of transcription from RNA polymerase II promoter // inferred from genetic
1452809_a	0.002448	-1.09	-1.27	NM_027829//XM_00651 <i>Izum4</i>		IZUMO family member 4	
1419526_a	0.001270	-1.09	-1.30	NM_010208//XM_00653 <i>Fgr</i>		Gardner-Rasheed feline sarcoma viral (Fgr) oncogene homolog	0002376 // immune system process // inferred from electronic annotation//0006468 // protein phosphorylation // inferred

Table S1

Gene ID	p	FC-RSV 1 d	FC-RSV 5 d	RefSeq Transcript ID	Gene Symbol	Gene Title	Gene Ontology Biological Process
1422673_a	0.000344	-1.09	1.09	NM_008858//XM_00651 Prkd1	protein kinase D1	0001525 // angiogenesis // inferred from electronic annotation//0001938 // positive regulation of endothelial cell	
1419110_a	0.000946	-1.09	-1.07	NM_024242//XM_00651 Rio1	RIO kinase 1 (yeast)	0006468 // protein phosphorylation // inferred from electronic annotation//0016310 // phosphorylation // inferred from	
1423687_a	0.001286	-1.08	-1.15	NM_028636//XM_00651 Man2c1	mannosidase, alpha, class 2C, member 1	0005975 // carbohydrate metabolic process // inferred from electronic annotation//0006013 // mannose metabolic process	
1417955_a	0.000550	-1.08	1.09	NM_133744//XM_00651 Ccdc71	coiled-coil domain containing 71		
1433877_a	0.000600	-1.08	1.25	NM_175307 Fam46b	family with sequence similarity 46, member B		
1432543_a	0.002172	-1.08	1.06	NM_021366 Klf13	Kruppel-like factor 13	0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 // regulation of transcription, DNA-	
1434919_a	0.000425	-1.08	-1.06	NM_172666 Agps	alkylglycerone phosphate synthase	0006629 // lipid metabolic process // inferred from electronic annotation//0008610 // lipid biosynthetic process // not	
1423200_a	0.000632	-1.08	1.04	NM_001252313//NM_0: Ncor1	nuclear receptor co-repressor 1	0000122 // negative regulation of transcription from RNA polymerase II promoter // inferred from genetic	
1453576_a	0.000087	-1.08	1.04	NM_027707//NM_2012: Nipbl	Nipped-B homolog (Drosophila)	0000122 // negative regulation of transcription from RNA polymerase II promoter // not recorded//0003007 // heart	
1446820_a	0.001827	-1.08	1.01	NM_001013387//NM_0C Zfp182	zinc finger protein 182	0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 // regulation of transcription, DNA-	
1451500_a	0.000973	-1.08	-1.17	NM_181418//XM_0065C Ushbp1	Usher syndrome 1C binding protein 1		
1428903_a	0.000354	-1.08	-1.12	NM_001160043//NM_0: Exo5	exonuclease 5	0000738 // DNA catabolic process, exonucleolytic // not recorded//0006281 // DNA repair // inferred from electronic	
1423028_a	0.002537	-1.08	1.22	NM_010503 Ifna2	interferon alpha 2	0002250 // adaptive immune response // not recorded//0002286 // T cell activation involved in immune response // not	
1417941_a	0.000257	-1.08	1.13	NM_026086//XM_0065C Nanp	N-acetylneuraminic acid phosphatase	0005975 // carbohydrate metabolic process // inferred from electronic annotation//0006045 // N-acetylglucosamine	
1416276_a	0.002475	-1.08	1.01	NM_009094 Rps4x	ribosomal protein S4, X-linked	0006412 // translation // not recorded//0007275 // multicellular organismal development // not recorded//0008284 //	
1427074_a	0.000764	-1.08	1.12	NM_001291211//NM_1: Pcmdt2	protein-L-isopartate (D-aspartate) O-methyltransferase domain	0006464 // cellular protein modification process // inferred from electronic annotation//0006479 // protein methylation //	
1427987_a	0.001235	-1.08	-1.19	NM_001029979//XM_0C Safb2	scaffold attachment factor B2	0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 // regulation of transcription, DNA-	
1432910_a	0.001195	-1.07	1.15	NM_172806//XM_00651 Btdb7	BTB (POZ) domain containing 7	0007275 // multicellular organismal development // inferred from electronic annotation//0006093 // regulation of branching	
1418354_a	0.002590	-1.07	1.01	NM_013581//XM_00653 Cog1//LOC102641	component of oligomeric golgi complex 1//conserved oligomeric Golgi	0006810 // transport // inferred from electronic annotation//0015031 // protein transport // inferred from electronic	
1417379_a	0.001383	-1.07	1.06	NM_016721//XM_00654 Iqgap1//LOC10264	IQ motif containing GTPase activating protein 1//uncharacterized	0001817 // regulation of cytokine production // inferred from mutant phenotype//0007165 // signal transduction // inferred	
1418768_a	0.000347	-1.07	1.01	NM_001199177//NM_1: Opa1	optic atrophy 1	0001843 // neural tube closure // inferred from mutant phenotype//0006184 // GTP catabolic process // traceable author	
1444028_s	0.000535	-1.07	1.12	NM_001081039//NM_0C Dock9	dedicator of cytokinesis 9	0007264 // small GTPase mediated signal transduction // inferred from electronic annotation//0032319 // regulation of Rho	
1452246_a	0.002246	-1.07	-1.12	NM_017375 Ostf1	osteoclast stimulating factor 1		
1420972_a	0.000352	-1.07	1.15	NM_023598//XM_00651 Arid5b	AT rich interactive domain 5B (MRF1-like)	0001822 // kidney development // inferred from mutant phenotype//0006351 // transcription, DNA-templated // inferred	
1421563_a	0.000861	-1.07	1.16	NM_007511//XM_0065C Atp7b	ATPase, Cu++ transporting, beta polypeptide	0006200 // ATP catabolic process // inferred from mutant phenotype//0006810 // transport // inferred from electronic	
1434931_a	0.002604	-1.07	1.04	NM_001042752//NM_0C Neo1	neogenin	0006355 // regulation of transcription, DNA-templated // inferred from direct assay//0007155 // cell adhesion // inferred	
1420495_a	0.000082	-1.07	1.08	NM_001113355//NM_1: Vps26a	vacuolar protein sorting 26 homolog A (yeast)	0006810 // transport // inferred from electronic annotation//0007034 // vacuolar transport // inferred from electronic	
1435089_a	0.000245	-1.06	-1.25	NM_001289924//NM_0C 201011101Rik	RIKEN cDNA 201011101 gene	0006508 // proteolysis // not recorded//0006508 // proteolysis // inferred from sequence or structural similarity//0019370	
1455750_a	0.000285	-1.06	1.19	NM_001033348//XM_0C Ralgapa2	Ral GTPase activating protein, alpha subunit 2 (catalytic)	0032484 // Ral protein signal transduction // inferred from mutant phenotype//0032859 // activation of Ral GTPase activity	
1426525_a	0.002610	-1.06	1.04	NM_175251 Arid2	AT rich interactive domain 2 (ARID, RFX-like)	0006337 // nucleosome disassembly // not recorded//0006355 // regulation of transcription, DNA-templated // inferred from	
1417615_a	0.002429	-1.06	-1.10	NM_025919//XM_00653 Rpl11//Gm5093	ribosomal protein L11//predicted gene 5093	0006364 // rRNA processing // not recorded//0006412 // translation // inferred from electronic annotation//0006605 //	
1429139_a	0.000196	-1.06	1.10	NM_001025613//NM_0C Otud7b	OTU domain containing 7B	0000122 // negative regulation of transcription from RNA polymerase II promoter // inferred from direct assay//0002376 //	
1435169_a	0.000228	-1.06	1.08	NM_029870//XM_00652 Crebfr	CREB3 regulatory factor	0000122 // negative regulation of transcription from RNA polymerase II promoter // not recorded//0006351 // transcription,	
1422869_a	0.001401	-1.06	1.18	NM_008587//XM_00645 Mertk	c-met proto-oncogene tyrosine kinase	0001779 // natural killer cell differentiation // inferred from genetic interaction//0006468 // protein phosphorylation // not	
1431665_a	0.002126	-1.06	1.02	NM_013897 Timm8b	translocase of inner mitochondrial membrane 8B	0006810 // transport // inferred from electronic annotation//0015031 // protein transport // inferred from electronic	
1417854_a	0.002528	-1.06	1.04	NM_011840//XM_00651 Map2k5	mitogen-activated protein kinase kinase 5	0000122 // negative regulation of transcription from RNA polymerase II promoter // not recorded//0000165 // MAPK cascade	
1448521_a	0.001976	-1.06	1.04	NM_012047//XM_00653 Brd7	bromodomain containing 7	0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 // regulation of transcription, DNA-	
1431890_a	0.000364	-1.06	1.17	NM_001286158//NM_0: Mllt3	myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog,	0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 // regulation of transcription, DNA-	
1419328_a	0.000257	-1.06	1.13	NM_001113481//NM_0: Sema4f	sema domain, immunoglobulin domain (Ig), TM domain, and short	0007275 // multicellular organismal development // inferred from electronic annotation//0007399 // nervous system	
1427947_a	0.000668	-1.05	1.13	NM_172148//XM_00653 B9d2	B9 protein domain 2	0007300 // cell projection organization // inferred from electronic annotation//0042384 // cilium assembly // inferred from	
1416926_a	0.001919	-1.05	1.07	NM_001199105//NM_0: Trp53inp1	transformation related protein 53 inducible nuclear protein 1	0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 // regulation of transcription, DNA-	
1419748_a	0.002237	-1.05	1.09	NM_011994//XM_00652 Abcd2	ATP-binding cassette, sub-family D (ALD), member 2	0000038 // very long-chain fatty acid metabolic process // not recorded//0006200 // ATP catabolic process // inferred from	
1436785_a	0.000309	-1.05	1.05	NM_001029937 Sec14l3	SEC14-like 3 (S. cerevisiae)	0006810 // transport // inferred from electronic annotation	
1431188_a	0.002702	-1.05	1.01	NM_001136259//NM_0: Tom1	target of myb1 homolog (chicken)	0006810 // transport // inferred from electronic annotation//0006886 // intracellular protein transport // inferred from	
1420962_a	0.000300	-1.05	1.09	NM_022031//XM_0065C Hapln2	hyaluronan and proteoglycan link protein 2	0007155 // cell adhesion // inferred from electronic annotation//0008065 // establishment of blood-nerve barrier // inferred	
1424895_a	0.002012	-1.05	-1.18	NM_029522//XM_0065C Gpsm2	G-protein signalling modulator 2 (AGS3-like, C. elegans)	0000132 // establishment of mitotic spindle orientation // inferred from mutant phenotype//0008277 // regulation of G-	
1431177_a	0.000356	-1.05	1.04	NM_011287//XM_00652 Rpl10a	ribosomal protein L10A	0006412 // translation // inferred from electronic annotation	
1451335_a	0.001923	-1.05	-1.36	NM_139198 Plac8	placenta-specific 8	0008284 // positive regulation of cell proliferation // inferred from direct assay//0009409 // response to cold // inferred from	
1421101_a	0.001359	-1.05	-1.16	NM_001077398//NM_0C Ldb2	LIM domain binding 2	0001942 // hair follicle development // inferred from genetic interaction//0010669 // epithelial structure maintenance //	
1440194_a	0.001861	-1.04	1.17	NM_001291292//NR_03 2210011C24Rik//RIKEN cDNA 2210011C24 gene//microRNA 1199			
1424569_a	0.000687	-1.04	-1.19	NM_001282055//NM_1: Ddx46	DEAD (Asp-Glu-Ala-Asp) box polypeptide 46	0006200 // ATP catabolic process // inferred from electronic annotation//0006397 // mRNA processing // inferred from	
1421215_a	0.000111	-1.04	1.07	NM_032008//XM_00651 Slmap	sarcolemma associated protein		
1427345_a	0.000517	-1.04	1.31	NM_133670//XM_0065C Sult1a1	sulfotransferase family 1A, phenol-preferring, member 1	0006584 // catecholamine metabolic process // not recorded//0006629 // lipid metabolic process // inferred from electronic	
1432120_a	0.000732	-1.04	1.12	NM_201361//XM_00652 Rmdn2	regulator of microtubule dynamics 2		
1456602_a	0.000413	-1.04	1.14	NM_001033321//XM_0C Tmem231	transmembrane protein 231	0001701 // in utero embryonic development // inferred from mutant phenotype//0001944 // vasculature development //	
1460601_a	0.001090	-1.03	1.15	NM_144557//XM_00651 Myrip	myosin VIIA and Rab interacting protein	0006886 // intracellular protein transport // inferred from electronic annotation//0030050 // vesicle transport along actin	
1437362_a	0.001772	-1.03	-1.11	NM_030016//XM_0065C Trmt13	tRNA methyltransferase 13	0008033 // tRNA processing // inferred from electronic annotation//0032259 // methylation // inferred from electronic	
1448529_a	0.000835	-1.03	1.13	NM_009378 Thbd	thrombomodulin	0007165 // signal transduction // inferred from electronic annotation//0007565 // female pregnancy // inferred from mutant	
1435261_a	0.000111	-1.03	1.26	NM_198967//XM_0065C Tmtc1	transmembrane and tetratricopeptide repeat containing 1	0006396 // RNA processing // inferred from electronic annotation	
1428492_a	0.000205	-1.03	-1.26	NM_027450 Glipr2	GLI pathogenesis-related 2	0010634 // positive regulation of epithelial cell migration // not recorded//0010718 // positive regulation of epithelial to	
1422499_a	0.002041	-1.03	1.05	NM_001113545//NM_0: Lima1	LIM domain and actin binding 1	0030835 // negative regulation of actin filament depolymerization // not recorded//0031529 // ruffle organization // not	
1451142_a	0.000191	-1.03	-1.06	NM_001289770//NM_0C Exoc1	exocyst complex component 1	0006810 // transport // inferred from electronic annotation//0006887 // exocytosis // inferred from electronic	
1425652_s	0.002258	-1.03	1.08	NM_001042674//NM_0C Rbpms	RNA binding protein gene with multiple splicing	0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 // regulation of transcription, DNA-	
1419898_s	0.001897	-1.03	-1.09	NM_145931//NR_02750 Zc3h7a	zinc finger CCCH type containing 7 A		
1424686_a	0.002675	-1.03	-1.09	NM_145432//XM_00653 Heatr6	HEAT repeat containing 6//Mus musculus HEAT repeat containing 6		
1428883_a	0.000717	-1.03	1.10	NM_025382//XM_00653 Tmem57	transmembrane protein 57	0007420 // brain development // inferred from expression pattern	

Table S1

Gene_ID	p	FC-RSV 1 d	FC-RSV 5 d	RefSeq Transcript ID	Gene Symbol	Gene Title	Gene Ontology Biological Process
1417935_a	0.002542	-1.03	1.04	NM_023290	<i>Mkrr2</i>	makorin, ring finger protein, 2	0016567 // protein ubiquitination // inferred from electronic annotation
1434202_a	0.000010	-1.03	1.78	NM_183187//XM_00651	<i>Fam107a</i>	family with sequence similarity 107, member A	0001558 // regulation of cell growth // not recorded
1422615_a	0.000052	-1.02	-1.15	NM_001252200//NM_01	<i>Map4k4</i>	mitogen-activated protein kinase kinase kinase kinase 4	0006468 // protein phosphorylation // not recorded//0006468 // protein phosphorylation // inferred from direct
1458792_a	0.001504	-1.02	1.11		<i>D12Ert208e</i>	DNA segment, Chr 12, ERATO Doi 208, expressed	
1424669_a	0.000066	-1.02	1.20	NM_026752//XM_00651	<i>Zfyve21</i>	zinc finger, FYVE domain containing 21	
1425522_a	0.002082	-1.02	-1.15	NM_027349//XM_00651	<i>Rbm25</i>	RNA binding motif protein 25	0000381 // regulation of alternative mRNA splicing, via spliceosome // inferred from electronic annotation//0000381 //
1417220_a	0.002703	-1.02	-1.16	NM_010176	<i>Fah</i>	fumarylacetoacetate hydrolase	0006527 // arginine catabolic process // inferred from mutant phenotype//0006559 // L-phenylalanine catabolic process //
1432415_a	0.001461	-1.02	1.66	NM_023852//XM_00651	<i>Rab3c</i>	RAB3C, member RAS oncogene family	0006810 // transport // inferred from electronic annotation//0007264 // small GTPase mediated signal transduction //
1451467_s	0.000021	-1.02	-1.11	NM_001083328//NM_01	<i>Mtg2</i>	mitochondrial ribosome associated GTPase 2	0006184 // GTP catabolic process // not recorded//0007264 // small GTPase mediated signal transduction // inferred from
1439197_a	0.000940	-1.02	1.13	NM_001293715//NM_01	<i>Pl4kb</i>	phosphatidylinositol 4-kinase, catalytic, beta polypeptide	0006661 // phosphatidylinositol biosynthetic process // inferred from electronic annotation//0016310 // phosphorylation //
1435394_s	0.001689	-1.02	-1.11	NM_001291859//NM_01	<i>Rhoc</i>	ras homolog gene family, member C	0000910 // cytokinesis // not recorded//0006184 // GTP catabolic process // inferred from electronic annotation//0007165
1420391_a	0.001587	-1.01	1.10	NM_001013580//NM_01	<i>Pard3</i>	par-3 family cell polarity regulator	0000226 // microtubule cytoskeleton organization // inferred from mutant phenotype//0003383 // apical constriction //
1420854_a	0.000072	-1.01	-1.21	NM_007925//XM_00651	<i>Elm</i>	elastin	0001974 // blood vessel remodeling // inferred from electronic annotation//0007519 // skeletal muscle tissue development
1434038_a	0.000393	-1.01	1.07	NM_001163026//XM_01	<i>Dnajc13</i>	DnaJ (Hsp40) homolog, subfamily C, member 13	0001649 // osteoblast differentiation // not recorded
1418895_a	0.001013	-1.01	-1.09	NM_018773	<i>Skap2</i>	src family associated phosphoprotein 2	0008285 // negative regulation of cell proliferation // inferred from mutant phenotype//0042113 // B cell activation //
1424269_a	0.002529	-1.01	-1.05	NM_010860//XM_00651	<i>Gm5526</i>	myosin, light polypeptide 6, alkali, smooth muscle and non-muscle	0006200 // ATP catabolic process // inferred from sequence or structural similarity//0006936 // muscle contraction //
1418072_a	0.000172	-1.01	1.17	NM_001177653//NM_01	<i>Hist1h2bc</i>	histone cluster 1, H2bc//histone cluster 1, H2bc//histone cluster 1,	0002227 // innate immune response in mucosa // not recorded//0006334 // nucleosome assembly // inferred from electronic
1418072_a	0.000172	-1.01	1.17	NM_001177653//NM_01	<i>Hist1h2bc</i>	histone cluster 1, H2bc//histone cluster 1, H2bc//histone cluster 1,	0002227 // innate immune response in mucosa // not recorded//0006334 // nucleosome assembly // inferred from electronic
1418072_a	0.000172	-1.01	1.17	NM_001177653//NM_01	<i>Hist1h2bc</i>	histone cluster 1, H2bc//histone cluster 1, H2bc//histone cluster 1,	0002227 // innate immune response in mucosa // not recorded//0006334 // nucleosome assembly // inferred from electronic
1428844_a	0.000255	-1.01	-1.08	NM_001025392//NM_01	<i>Bclaf1</i>	BCL2-associated transcription factor 1	0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 // regulation of transcription, DNA-
1420864_a	0.000756	-1.01	1.25	NM_009547//XM_00652	<i>Zbtb14</i>	zinc finger and BTB domain containing 14	0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 // regulation of transcription, DNA-
1417860_a	0.000241	-1.01	-1.44	NM_133903//XM_00651	<i>Spon2</i>	spondin 2, extracellular matrix protein	0002376 // immune system process // inferred from electronic annotation//0002448 // mast cell mediated immunity //
1416659_a	0.000538	-1.01	-1.08	NM_010123	<i>Eif3a</i>	eukaryotic translation initiation factor 3, subunit A	0001731 // formation of translation preinitiation complex // inferred from electronic annotation//0001732 // formation of
1422461_a	0.002153	-1.00	-1.11	NM_179203//XM_00653	<i>Atad3a</i>	ATPase family, AAA domain containing 3A	0008152 // metabolic process // inferred from electronic annotation//0016049 // cell growth // not recorded//0043066 //
1420402_a	0.001624	-1.00	1.36	NM_001036684//NM_01	<i>Atp2b2</i>	ATPase, Ca++ transporting, plasma membrane 2	0000902 // cell morphogenesis // inferred from mutant phenotype//0006200 // ATP catabolic process // inferred from
1433482_a	0.000202	-1.00	-1.21	NM_057172//XM_00651	<i>Fubp1</i>	far upstream element (FUSE) binding protein 1	0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 // regulation of transcription, DNA-
1426744_a	0.000881	-1.00	-1.11	NM_033218//XM_00652	<i>Sreb2</i>	sterol regulatory element binding factor 2	0000122 // negative regulation of transcription from RNA polymerase II promoter // not recorded//0006351 // transcription,
1423679_a	0.001046	-1.00	1.06	NM_025944//XM_00653	<i>Tmem246</i>	transmembrane protein 246	
1434816_a	0.001012	-1.00	1.08	NM_029929//XM_00653	<i>Vps33a</i>	vacuolar protein sorting 33A (yeast)	0006810 // transport // inferred from electronic annotation//0006904 // vesicle docking involved in exocytosis // inferred
1422264_s	0.000330	-1.00	1.26	NM_010638	<i>Klf9</i>	Kruppel-like factor 9	0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 // regulation of transcription, DNA-
1417214_a	0.001054	-1.00	-1.14	NM_001082553//NM_01	<i>Rab27b</i>	RAB27B, member RAS oncogene family	0006184 // GTP catabolic process // inferred from direct assay//0006886 // intracellular protein transport // inferred from

Table S2. Lung genes significantly altered by respiratory syncytial virus (RSV) in C3H/HeJ (HeJ) mice (One-Way ANOVA at $p < 0.01$).

Blue(-): fold decrease by RSV vs vehicle. Red : fold increase by RSV vs vehicle.

Gene_ID	p	FC-RSV 1 d	FC-RSV 5 d	RefSeq Transcript ID	Gene Symbol	Gene Title	Gene Ontology Biological Process
1450826_a	0.000026	7.25	2.13	NM_011315	<i>Saa3</i>	serum amyloid A 3	0006953 // acute-phase response // inferred from electronic annotation//0035634 // response to stilbenoid // inferred from expression
1427747_a	0.000036	2.35	1.04	NM_008491	<i>Lcn2</i>	lipocalin-2	0002376 // immune system process // inferred from electronic annotation//0006810 // transport // inferred from electronic
1425450_a	0.000507	1.98	1.81	NM_145126//NM_000000	<i>Chil4</i> ///Chil3	chitinase-like 4//chitinase-like 3	0005975 // carbohydrate metabolic process // inferred from electronic annotation//0006032 // chitin catabolic process // inferred from
1419874_x	0.000115	1.91	2.23	NM_001033324//>	<i>Zbtb16</i>	zinc finger and BTB domain containing 16	0001501 // skeletal system development // inferred from mutant phenotype//0001823 // mesonephros development // inferred from
1449227_a	0.000062	1.84	-1.03	NM_009890	<i>Ch25h</i>	cholesterol 25-hydroxylase	0006629 // lipid metabolic process // inferred from electronic annotation//0006633 // fatty acid biosynthetic process // inferred from
1434202_a	0.000296	1.57	1.36	NM_183187//XM_000000	<i>Fam107a</i>	family with sequence similarity 107, member A	0001558 // regulation of cell growth // not recorded
1419208_a	0.000096	1.52	1.13	NM_007746//XM_000000	<i>Map3k8</i>	mitogen-activated protein kinase kinase kinase 8	0000165 // MAPK cascade // not recorded//0000186 // activation of MAPKK activity // not recorded//0002376 // immune system
1437356_a	0.000346	1.51	1.06	NM_183031	<i>Gpr183</i>	G protein-coupled receptor 183	0005975 // mature B cell differentiation involved in immune response // inferred from mutant phenotype//0002376 // immune system
1423602_a	0.000569	1.51	1.05	NM_009421//XM_000000	<i>Traf1</i>	TNF receptor-associated factor 1	0006915 // apoptotic process // inferred from electronic annotation//0007165 // signal transduction // inferred from electronic
1417266_a	0.000450	1.48	1.19	NM_009139	<i>Ccl6</i>	chemokine (C-C motif) ligand 6	0006935 // chemotaxis // inferred from electronic annotation//0006955 // immune response // inferred from electronic
1419764_a	0.000043	1.47	1.39	NM_009892//XM_000000	<i>Chil3</i> ///Chil4	chitinase-like 3//chitinase-like 4	0000272 // polysaccharide catabolic process // inferred from electronic annotation//0005975 // carbohydrate metabolic process //
1416286_a	0.000639	1.38	1.16	NM_009062//XM_000000	<i>Rgs4</i>	regulator of G-protein signaling 4	0007186 // G-protein coupled receptor signaling pathway // traceable author statement//0009968 // negative regulation of signal
1424794_a	0.000237	1.38	-1.04	NM_025786	<i>Rnf186</i>	ring finger protein 186	
1416318_a	0.000580	1.34	1.06	NM_025429//XM_000000	<i>Serpinb1a</i>	serine (or cysteine) peptidase inhibitor, clade B, member 1a	0010466 // negative regulation of peptidase activity // inferred from electronic annotation//0010951 // negative regulation of
1451537_a	0.000202	1.33	-1.04	NM_007695//XM_000000	<i>Chil1</i>	chitinase-like 1	0005975 // carbohydrate metabolic process // inferred from electronic annotation//0006032 // chitin catabolic process // inferred from
1422642_a	0.000033	1.32	-1.03	NM_026514//XM_000000	<i>Cdc42ep3</i>	CDC42 effector protein (Rho GTPase binding) 3	0008360 // regulation of cell shape // inferred from electronic annotation
1439139_a	0.000595	1.32	-1.09		<i>D2Erd640e</i>	DNA segment, Chr 2, ERATO Doi 640, expressed	
1429137_a	0.000543	1.31	-1.17	NM_027279//XM_000000	<i>Mett18</i>	methyltransferase like 18	0006479 // protein methylation // inferred from electronic annotation//0032259 // methylation // inferred from electronic annotation
1428694_a	0.000512	1.31	-1.00	NR_029382//NR_000000	<i>Mir17hg</i> ///Mir92-1	Mir17 host gene 1 (non-protein coding)///microRNA 92-1	0001701 // in utero embryonic development // inferred from genetic interaction//0002329 // pre-B cell differentiation // inferred from
1436594_a	0.000115	1.28	-1.21	NM_172482//XM_000000	<i>Zfp719</i>	zinc finger protein 719	0006355 // regulation of transcription, DNA-templated // inferred from electronic annotation
1452065_a	0.000194	1.27	1.51	NM_001290539//>	<i>Vstm2a</i>	V-set and transmembrane domain containing 2A	
1422411_s	0.000402	1.25	1.30	NM_001012766//>	<i>Eor1</i> ///Eor12//Eor2//Ea	eosinophil-associated, ribonuclease A family, member 1//eosinophil-	0006935 // chemotaxis // inferred from direct assay//0008152 // metabolic process // inferred from electronic annotation//0090305
1437362_a	0.000066	1.23	-1.02	NM_030016//XM_000000	<i>Tmtc13</i>	tRNA methyltransferase 13	0008033 // tRNA processing // inferred from electronic annotation//0032259 // methylation // inferred from electronic annotation
1435261_a	0.000232	1.23	1.19	NM_198967//XM_000000	<i>Tmtc1</i>	transmembrane and tetratricopeptide repeat containing 1	0006396 // RNA processing // inferred from electronic annotation
1449546_a	0.000155	1.22	-1.07	NM_133358	<i>Zfp617</i>	zinc finger protein 617	0006355 // regulation of transcription, DNA-templated // inferred from electronic annotation
1438408_a	0.000028	1.21	1.13	NM_157570	<i>Sowahb</i>	sosondowah ankyrin repeat domain family member B	
1429380_a	0.000503	1.21	1.16	NM_001163512//>	<i>Rgs12</i>	regulator of G-protein signaling 12	0007165 // signal transduction // inferred from electronic annotation//0035556 // intracellular signal transduction // inferred from
1424260_a	0.000318	1.17	1.30	NM_001079690//>	<i>Slc12a1</i>	solute carrier family 12, member 1	0001822 // kidney development // inferred from mutant phenotype//0006810 // transport // inferred from electronic
1445862_a	0.000434	1.17	-1.02	NM_001081154//>	<i>Marf1</i>	meiosis arrest female 1	0006302 // double-strand break repair // inferred from mutant phenotype//0007126 // meiotic nuclear division // inferred from
1429139_a	0.000433	1.17	1.05	NM_001025613//>	<i>Otud7b</i>	OTU domain containing 7B	0000122 // negative regulation of transcription from RNA polymerase II promoter // inferred from direct assay//0002376 // immune
1423663_a	0.000564	1.16	-1.00	NM_001271356//>	<i>Ficn</i>	folliculin	0000122 // negative regulation of transcription from RNA polymerase II promoter // inferred from mutant phenotype//0000122 //
1438849_a	0.000613	1.16	-1.03	NM_212487//XM_000000	<i>Krt78</i>	keratin 78	
1452262_a	0.000580	1.15	-1.06	NM_021296//XR_000000	<i>Grpel2</i>	GrpE-like 2, mitochondrial	0006457 // protein folding // inferred from electronic annotation//00050790 // regulation of catalytic activity // inferred from electronic
1417001_a	0.000118	1.14	-1.05	NM_023665	<i>Rsrp1</i>	arginine/serine rich protein 1	
1435496_a	0.000344	1.13	1.24	NM_029894//XM_000000	<i>Fam162b</i>	family with sequence similarity 162, member B	
1427515_a	0.000312	1.11	-1.02	NM_175437//XM_000000	<i>Gsap</i>	gamma-secretase activating protein	0030162 // regulation of proteolysis // not recorded//1902004 // positive regulation of beta-amyloid formation // inferred from direct
1438322_x	0.000110	1.11	1.01	NM_010191//XM_000000	<i>Fdft1</i>	farnesyl diphosphate farnesyl transferase 1	0006629 // lipid metabolic process // inferred from electronic annotation//0006694 // steroid biosynthetic process // inferred from
1424235_a	0.000312	1.10	1.02	NM_024180//XM_000000	<i>Gm5553</i> ///Ormdl2	predicted gene 5553//ORM1-like 2 (S. cerevisiae)	0006672 // ceramide metabolic process // not recorded//0006810 // transport // inferred from electronic annotation//0015031 //
1460037_a	0.000427	1.10	1.10	NM_026620//XM_000000	<i>Fam98b</i>	family with sequence similarity 98, member B	
1428213_a	0.000409	1.09	1.02	NM_001162855	<i>Nsmce4a</i>	non-SMC element 4 homolog A (S. cerevisiae)	0006281 // DNA repair // inferred from electronic annotation//2001022 // positive regulation of response to DNA damage stimulus //
1423164_a	0.000174	1.09	-1.00	NM_031999//NR_000000	<i>Gpr137b</i> ///Gpr137b-ps	G protein-coupled receptor 137B//G protein-coupled receptor 137B,	
1419574_a	0.000571	1.07	-1.01	NM_013889//XM_000000	<i>Zfp292</i>	zinc finger protein 292	0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 // regulation of transcription, DNA-
1448211_a	0.000609	1.06	1.10	NM_133764//XM_000000	<i>Atp6v0e2</i>	ATPase, H+ transporting, lysosomal V0 subunit E2	0006810 // transport // inferred from electronic annotation//0006811 // ion transport // inferred from electronic
1415689_s	0.000322	1.06	-1.07	NM_001145778//>	<i>Zkscan3</i>	zinc finger with KRAB and SCAN domains 3	0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 // regulation of transcription, DNA-
1425452_s	0.000287	1.06	-1.19	NM_029007	<i>Fam84a</i>	family with sequence similarity 84, member A	
1448812_a	0.000212	1.06	1.19	NM_016677//XM_000000	<i>Hpcal1</i>	hippocalcin-like 1	0007165 // signal transduction // inferred from electronic annotation
1453155_a	0.000558	1.05	1.08	NM_027935//XM_000000	<i>Tmem50a</i>	transmembrane protein 50A	
1435050_a	0.000362	1.05	-1.16	NM_001033258//>	<i>D108wg1379e</i>	DNA segment, Chr 10, Brigham & Women's Genetics 1379 expressed	0010923 // negative regulation of phosphatase activity // not recorded//0016192 // vesicle-mediated transport // not
1416000_a	0.000039	1.05	-1.07	NM_011034	<i>Gm21399</i> ///Prdx1	peroxiredoxin 1 pseudogene//peroxiredoxin 1	0000302 // response to reactive oxygen species // inferred from mutant phenotype//0006979 // response to oxidative stress // inferred
1443640_a	0.000244	1.04	-1.19	NM_001166645	<i>Zfp882</i>	zinc finger protein 882	0006355 // regulation of transcription, DNA-templated // inferred from electronic annotation
1435454_a	0.000550	1.02	1.15	NM_183162//XM_000000	<i>Helz2</i>	helicase with zinc finger 2, transcriptional coactivator	0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 // regulation of transcription, DNA-
1434513_a	0.000096	1.02	-1.07	NM_001128094//>	<i>Atp13a3</i>	ATPase type 13A3	0006200 // ATP catabolic process // inferred from electronic annotation//0006812 // cation transport // inferred from electronic
1417083_a	0.000367	1.01	-1.07	NM_024171//XM_000000	<i>Sec61b</i> ///LOC101055909	Sec61 beta subunit//protein transport protein Sec61 subunit beta-like	0000660 // protein import into nucleus, translocation // not recorded//0006810 // transport // inferred from electronic
1416505_a	0.000010	-5.08	1.28	NM_010444//XM_000000	<i>Nr4a1</i>	nuclear receptor subfamily 4, group A, member 1	0001938 // positive regulation of endothelial cell proliferation // not recorded//0002042 // cell migration involved in sprouting
1450297_a	0.000071	-4.35	-1.01	NM_031168	<i>Il6</i>	interleukin 6	0001781 // neutrophil apoptotic process // inferred from direct assay//0001781 // neutrophil apoptotic process // inferred from
1417065_a	0.000018	-4.07	1.19	NM_007913	<i>Egr1</i>	early growth response 1	0000122 // negative regulation of transcription from RNA polymerase II promoter // inferred from direct assay//0001975 // response to
1417601_a	0.000003	-4.04	1.14	NM_015811	<i>Rgs1</i>	regulator of G-protein signaling 1	0007186 // G-protein coupled receptor signaling pathway // traceable author statement//0009968 // negative regulation of signal
1423100_a	0.000350	-3.81	1.16	NM_010234	<i>Fos</i>	FB1 osteosarcoma oncogene	0001661 // conditioned taste aversion // inferred from electronic annotation//0006355 // regulation of transcription, DNA-templated
1418156_a	0.000017	-3.59	-1.10	NM_021342	<i>Kcne4</i>	potassium voltage-gated channel, Isk-related subfamily, gene 4	0006810 // transport // inferred from electronic annotation//0006811 // ion transport // inferred from electronic
1415899_a	0.000100	-3.58	1.08	NM_008416	<i>Junb</i>	jun B proto-oncogene	0001570 // vasculogenesis // inferred from mutant phenotype//0001649 // osteoblast differentiation // inferred from mutant
1422134_a	0.000386	-3.25	1.90	NM_008036//XM_000000	<i>Fosb</i>	FB1 osteosarcoma oncogene B	0006355 // regulation of transcription, DNA-templated // not recorded//0006366 // transcription from RNA polymerase II promoter //
1441228_a	0.000001	-3.10	1.44	NM_001109914	<i>Apold1</i>	apolipoprotein L domain containing 1	0001525 // angiogenesis // inferred from electronic annotation//0001666 // response to hypoxia // inferred from electronic
1452519_a	0.000034	-3.00	1.19	NM_011756	<i>Zfp36</i>	zinc finger protein 36	0000122 // negative regulation of transcription from RNA polymerase II promoter // inferred from mutant phenotype//0000122 //
1450749_a	0.000032	-2.98	1.17	NM_001139509//>	<i>Nr4a2</i>	nuclear receptor subfamily 4, group A, member 2	0001666 // response to hypoxia // inferred from mutant phenotype//0001764 // neuron migration // inferred from mutant
1416039_x	0.000024	-2.90	1.17	NM_010516	<i>Cyr61</i>	cysteine rich protein 61	0001558 // regulation of cell growth // inferred from electronic annotation//0001649 // osteoblast differentiation // inferred from
1433000_a	0.000007	-2.72	1.43	NM_153287//XM_000000	<i>Csrnp1</i>	cysteine-serine-rich nuclear protein 1	0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 // regulation of transcription, DNA-
1419766_a	0.000044	-2.71	-1.11	NM_010831	<i>Sik1</i>	salt inducible kinase 1	0000122 // negative regulation of transcription from RNA polymerase II promoter // not recorded//0002028 // regulation of sodium ion
1418932_a	0.000187	-2.49	-1.03	NM_017373//XM_000000	<i>Nfil3</i>	nuclear factor, interleukin 3, regulated	0000122 // negative regulation of transcription from RNA polymerase II promoter // not recorded//0006351 // transcription, DNA-
1416442_a	0.000068	-2.48	1.14	NM_010499	<i>Ier2</i>	immediate early response 2	

Table S2

Gene_ID	p	FC-RSV 1 d	FC-RSV 5 d	RefSeq Transcript ID	Gene Symbol	Gene Title	Gene Ontology Biological Process
1448830_a	0.000069	-2.37	1.18	NM_013642	<i>Dusp1</i>	dual specificity phosphatase 1	0000188 // inactivation of MAPK activity // ---//0000188 // inactivation of MAPK activity // inferred from sequence or structural
1420357_s	0.000622	-2.18	1.31	NM_001081643//Xlr3a//Xlr3b//Xlr3c		X-linked lymphocyte-regulated 3A//X-linked lymphocyte-regulated 3B//X-linked lymphocyte-regulated 3C	0051965 // positive regulation of synapse assembly // inferred from mutant phenotype//0061003 // positive regulation of dendritic
1437595_a	0.000207	-2.17	-1.05	NM_183160	<i>Tmem252</i>	transmembrane protein 252	
1423619_a	0.000006	-2.05	1.28	NM_009026	<i>Rasd1</i>	RAS, dexamethasone-induced 1	0006184 // GTP catabolic process // inferred from electronic annotation//0006886 // intracellular protein transport // inferred from
1450698_a	0.000390	-2.04	1.16	NM_010090	<i>Dusp2</i>	dual specificity phosphatase 2	0000188 // inactivation of MAPK activity // ---//0000188 // inactivation of MAPK activity // inferred from electronic
1452815_a	0.000315	-1.99	-1.02	NM_172435//Xm_P2ry10		purinergic receptor P2Y, G-protein coupled 10	0007165 // signal transduction // inferred from electronic annotation//0007186 // G-protein coupled receptor signaling pathway //
1421079_a	0.000226	-1.93	1.34	NM_015743//Xm_Nr4a3		nuclear receptor subfamily 4, group A, member 3	0001707 // mesoderm formation // inferred from mutant phenotype//0006351 // transcription, DNA-templated // inferred from
1453851_a	0.000154	-1.93	-1.03	NM_011817	<i>Gadd45g</i>	growth arrest and DNA-damage-inducible 45 gamma	0000185 // activation of MAPKKK activity // not recorded//0000186 // activation of MAPKK activity // inferred from direct
1450716_a	0.000053	-1.92	1.22	NM_009621	<i>Adamts1</i>	a disintegrin-like and metalloproteinase (reprolysin type) with thrombospondin	0001542 // ovulation from ovarian follicle // inferred from mutant phenotype//0001822 // kidney development // inferred from mutant
1418936_a	0.000002	-1.87	1.29	NM_010755//Xm_Maff		v-maf musculoaponeurotic fibrosarcoma oncogene family, protein F (avian)	0001701 // in utero embryonic development // inferred from genetic interaction//0006351 // transcription, DNA-templated // inferred
1448756_a	0.000029	-1.81	-1.04	NM_001281852//S100a9		S100 calcium binding protein A9 (calgranulin B)	0002376 // immune system process // inferred from electronic annotation//0002523 // leukocyte migration involved in inflammatory
1416129_a	0.000224	-1.78	1.17	NM_133753//Xm_Erff1		ERBB receptor feedback inhibitor 1	0007175 // negative regulation of epidermal growth factor-activated receptor activity // inferred from mutant phenotype//0007175 //
1449363_a	0.000002	-1.72	1.72	NM_007498	<i>Atf3</i>	activating transcription factor 3	0000122 // negative regulation of transcription from RNA polymerase II promoter // inferred from direct assay//0006094 //
1451924_a	0.000363	-1.70	1.08	NM_010104	<i>Edn1</i>	endothelin 1	0000122 // negative regulation of transcription from RNA polymerase II promoter // not recorded//0001501 // skeletal system
1438527_a	0.000476	-1.67	1.23	NM_013762//Xm_Gm12816//Gm5879//R		predicted gene 12816//predicted gene 5879//ribosomal protein L3	0006412 // translation // inferred from electronic annotation//0071353 // cellular response to interleukin-4 // inferred from direct
1448890_a	0.000004	-1.66	1.09	NM_008452	<i>Klf2</i>	Kruppel-like factor 2 (lung)	0000902 // cell morphogenesis // inferred from mutant phenotype//0001701 // in utero embryonic development // inferred from
1455904_a	0.000173	-1.64	1.30	NR_002840//NR_0_Gas5//Snord47		growth arrest specific 5//small nucleolar RNA, C/D box 47	
1448325_a	0.000020	-1.63	1.30	NM_008654	<i>Ppp1r15a</i>	protein phosphatase 1, regulatory (inhibitor) subunit 15A	0006417 // regulation of translation // inferred from electronic annotation//0006915 // apoptotic process // inferred from electronic
1437100_x	0.000223	-1.62	1.05	NM_145478	<i>Pim3</i>	proliferation-inducing myelomonocytic leukemia 3	0006468 // protein phosphorylation // not recorded//0006915 // apoptotic process // inferred from electronic annotation//0007049
1419394_s	0.000053	-1.61	-1.03	NM_013650	<i>S100a8</i>	S100 calcium binding protein A8 (calgranulin A)	0002376 // immune system process // inferred from electronic annotation//0002523 // leukocyte migration involved in inflammatory
1449399_a	0.000081	-1.53	-1.01	NM_008361//Xm_Illb		interleukin 1 beta	0000122 // negative regulation of transcription from RNA polymerase II promoter // not recorded//0000165 // MAPK cascade // not
1416041_a	0.000167	-1.52	-1.01	NM_001161845//Sgk1		serum/glucocorticoid regulated kinase 1	0006468 // protein phosphorylation // inferred from direct assay//0006883 // cellular sodium ion homeostasis // inferred
1444226_a	0.000442	-1.51	1.04	NM_019740//Xm_Foxo3//LOC102636048		forkhead box O3//uncharacterized LOC102636048	0000122 // negative regulation of transcription from RNA polymerase II promoter // not recorded//0001542 // ovulation from ovarian
1422948_s	0.000008	-1.49	1.12	NM_001195421//H1st1h4a//H1st1h4b//H1st1h4c		histone cluster 1, H4a//histone cluster 1, H4b//histone cluster 1, H4c	0006334 // nucleosome assembly // inferred from sequence or structural similarity//0006334 // nucleosome assembly // inferred from
1417483_a	0.000425	-1.49	1.12	NM_001159394//Nfkbiz		nuclear factor of kappa light polypeptide gene enhancer in B cells inhibitor, zeta	0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 // regulation of transcription, DNA-
1444003_a	0.000603	-1.48	1.02	NM_153408//Xm_Neur13		neuronal homolog 3 homolog (Drosophila)	0016567 // protein ubiquitination // inferred from genetic interaction
1421811_a	0.000085	-1.46	1.22	NM_011580//NM_Pald1//Thbs1		phosphatase domain containing, paladin 1//thrombospondin 1	0000187 // activation of MAPK activity // not recorded//0001937 // negative regulation of endothelial cell proliferation // not
1427005_a	0.000161	-1.42	1.26	NM_152804	<i>Plk2</i>	polo-like kinase 2	0000082 // G1/S transition of mitotic cell cycle // not recorded//0000278 // mitotic cell cycle // inferred from mutant
1416101_a	0.000008	-1.40	1.07	NM_015786	<i>Hist1h1c</i>	histone cluster 1, H1c	0006334 // nucleosome assembly // inferred from electronic annotation//0016584 // nucleosome positioning // inferred from mutant
1418901_a	0.000135	-1.39	-1.07	NM_001287738//Cebpb		CCAAT/enhancer binding protein (C/EBP), beta	0001892 // embryonic placenta development // inferred from genetic interaction//0006351 // transcription, DNA-templated // inferred
1417394_a	0.000145	-1.35	1.19	NM_010637	<i>Klf4</i>	Kruppel-like factor 4 (gut)	0000122 // negative regulation of transcription from RNA polymerase II promoter // not recorded//0006351 // transcription, DNA-
1448170_a	0.000188	-1.34	1.09	NM_009174	<i>Siah2</i>	seven in absentia 2	0006511 // ubiquitin-dependent protein catabolic process // inferred from electronic annotation//0006915 // apoptotic process //
1418959_a	0.000384	-1.34	-1.32	NM_030709//Xm_Tmprss5		transmembrane protease, serine 5 (spinesin)	0006508 // proteolysis // not recorded//0006898 // receptor-mediated endocytosis // inferred from electronic annotation
1417409_a	0.000021	-1.33	1.20	NM_010591	<i>Jun</i>	jun proto-oncogene	0001525 // angiogenesis // inferred from mutant phenotype//0001525 // angiogenesis // not recorded//0001774 // microglial cell
1420088_a	0.000544	-1.32	1.15	NM_010907	<i>Nfkbia</i>	nuclear factor of kappa light polypeptide gene enhancer in B cells inhibitor,	0000060 // protein import into nucleus, translocation // inferred from direct assay//0007253 // cytoplasmic sequestration of NF-kappaB
1423013_a	0.000041	-1.30	1.06	NM_010426	<i>Foxf1</i>	forkhead box F1	0000122 // negative regulation of transcription from RNA polymerase II promoter // inferred from mutant phenotype//0001568 //
1428529_a	0.000194	-1.29	-1.01	NR_040721	<i>Snhg5</i>	small nucleolar RNA host gene 5	
1419301_a	0.000482	-1.29	1.11	NM_008055//Xm_Fzd4		frizzled homolog 4 (Drosophila)	0001553 // luteinization // inferred from mutant phenotype//0001568 // blood vessel development // inferred from mutant
1433632_a	0.000183	-1.29	-1.04	NM_001164598	<i>Irf2bp2</i>	interferon regulatory factor 2 binding protein 2	0000122 // negative regulation of transcription from RNA polymerase II promoter // not recorded//0006351 // transcription, DNA-
1428562_a	0.000213	-1.29	1.16	NR_030711	<i>Mir22hg</i>	Mir22 host gene (non-protein coding)	
1425895_a	0.000568	-1.28	1.18	NM_010495//Xm_Id1		inhibitor of DNA binding 1	0000122 // negative regulation of transcription from RNA polymerase II promoter // inferred from direct assay//0000122 // negative
1423622_a	0.000135	-1.27	1.05	NM_001025442//Ccn1		cyclin L1	0000079 // regulation of cyclin-dependent protein serine/threonine kinase activity // inferred from electronic annotation//0006351 //
1421811_a	0.000137	-1.26	1.20	NM_011580//NM_Pald1//Thbs1		phosphatase domain containing, paladin 1//thrombospondin 1	0000187 // activation of MAPK activity // not recorded//0001937 // negative regulation of endothelial cell proliferation // not
1422473_a	0.000078	-1.26	-1.03	NM_001177980//Pde4b		phosphodiesterase 4B, cAMP specific	0001780 // neutrophil homeostasis // inferred from mutant phenotype//0006198 // cAMP catabolic process // inferred from direct
1451808_a	0.000466	-1.25	-1.05	NM_008427//Xm_Kcnj4		potassium inwardly-rectifying channel, subfamily J, member 4	0006810 // transport // inferred from electronic annotation//0006811 // ion transport // inferred from electronic
1422931_a	0.000221	-1.25	1.14	NM_008037	<i>Fosl2</i>	fos-like antigen 2	0001666 // response to hypoxia // not recorded//0006351 // transcription, DNA-templated // inferred from electronic
1421044_a	0.000512	-1.23	1.02	NM_008626//Xm_Mrc2		mannose receptor, C type 2	0001649 // osteoblast differentiation // not recorded//0006897 // endocytosis // inferred from electronic annotation//00030574 //
1429049_a	0.000174	-1.22	1.03	NM_001195025//Nuak2		NUAK family, SNF1-like kinase, 2	0006468 // protein phosphorylation // not recorded//0006915 // apoptotic process // inferred from electronic annotation//0009103
1450829_a	0.000329	-1.21	1.16	NM_001166402//Tnfrsf1a		tumor necrosis factor, alpha-induced protein 3	0001922 // B-1 B cell homeostasis // inferred from mutant phenotype//0002237 // response to molecule of bacterial origin // inferred
1427893_a	0.000048	-1.21	1.13	NM_026784//NM_Pmkv		phosphomevalonate kinase	0006629 // lipid metabolic process // inferred from electronic annotation//0006694 // steroid biosynthetic process // inferred from
1419024_a	0.000326	-1.20	1.03	NM_011200//NR_1_Gm13363//Ptp4a1		predicted gene 13363//protein tyrosine phosphatase 4a1	0006470 // protein dephosphorylation // inferred from electronic annotation//0007049 // cell cycle // inferred from electronic
1426215_a	0.000404	-1.18	1.07	NM_001190448//Ddc		dopa decarboxylase	0006520 // cellular amino acid metabolic process // inferred from electronic annotation//0007623 // circadian rhythm // inferred from
1450125_a	0.000043	-1.18	1.04	NM_008093//Xm_Gata5		GATA binding protein 5	0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 // regulation of transcription, DNA-
1418714_a	0.000356	-1.17	1.11	NM_008748//Xm_Dusp8		dual specificity phosphatase 8	0000188 // inactivation of MAPK activity // ---//0000188 // inactivation of MAPK activity // inferred from electronic
1426934_a	0.000248	-1.16	1.04	NM_001163592//Nhs1		NHS-like 1	
1424326_a	0.000541	-1.15	1.03	NM_146075//Xr_LemD2		LEM domain containing 2	0035914 // skeletal muscle cell differentiation // inferred from mutant phenotype//0035914 // skeletal muscle cell differentiation //
1418507_s	0.000459	-1.14	-1.17	NM_001168655//Socs2		suppressor of cytokine signaling 2	0001558 // regulation of cell growth // inferred from electronic annotation//0007595 // lactation // inferred from genetic
1431079_a	0.000345	-1.14	1.07	NM_026979//Xm_C1qtnf2		C1q and tumor necrosis factor related protein 2	0000187 // activation of MAPK activity // inferred from direct assay//0045725 // positive regulation of glycogen biosynthetic process //
1435808_a	0.000125	-1.14	-1.13	NM_001270791//Iba57		IBA57, iron-sulfur cluster assembly homolog (S. cerevisiae)	0006546 // glycine catabolic process // inferred from electronic annotation//0006783 // heme biosynthetic process // inferred from
1416111_a	0.000240	-1.10	1.10	NM_001289915//Cd83		CD83 antigen	0014070 // response to organic cyclic compound // inferred from mutant phenotype//0032713 // negative regulation of interleukin-4
1423833_a	0.000533	-1.10	-1.16	NM_027430	<i>Mpc2</i>	mitochondrial pyruvate carrier 2	0006090 // pyruvate metabolic process // inferred from genetic interaction//0006810 // transport // inferred from electronic
1424771_a	0.000466	-1.09	-1.12	NM_177688	<i>H2afj</i>	H2A histone family, member J	0006334 // nucleosome assembly // inferred from electronic annotation
1425367_a	0.000274	-1.08	1.13	NM_001253872//Itgal		integrin alpha L	0002291 // T cell activation via T cell receptor contact with antigen bound to MHC molecule on antigen presenting cell // not
1419629_a	0.000272	-1.08	-1.19	NM_008589	<i>Mesp2</i>	mesoderm posterior 2	0001756 // somitogenesis // inferred from genetic interaction//0001756 // somitogenesis // inferred from mutant
1425021_a	0.000032	-1.08	1.07	NM_145122//NR_1_Pex16		peroxisomal biogenesis factor 16	0006625 // protein targeting to peroxisome // not recorded//0007031 // peroxisome organization // not recorded//0016557 //
1433649_a	0.000073	-1.08	-1.12	NM_172262//Xm_Kdm1b		lysine (K)-specific demethylase 1B	0006349 // regulation of gene expression by genetic imprinting // inferred from mutant phenotype//0006351 // transcription, DNA-
1449511_a	0.000214	-1.07	1.07	NM_133772//Xm_Ssbp4		single stranded DNA binding protein 4	
1419747_a	0.000527	-1.07	-1.22	NM_007493//Xm_Asg2		asialoglycoprotein receptor 2	0006897 // endocytosis // inferred from electronic annotation//0009100 // glycoprotein metabolic process // inferred from mutant
1425598_a	0.000582	-1.05	1.04	NM_00111096//Gm11787//Lyn		predicted gene 11787//Yamaguchi sarcoma viral (v-yes-1) oncogene homolog	0001782 // B cell homeostasis // inferred from mutant phenotype//0001817 // regulation of cytokine production // inferred from
1418269_a	0.000279	-1.05	1.11	NM_013586	<i>Lox13</i>	lysyl oxidase-like 3	0001837 // epithelial to mesenchymal transition // not recorded//0006898 // receptor-mediated endocytosis // inferred from
1440887_a	0.000317	-1.04	-1.18	NM_175319//Xm_Papl		iron/zinc purple acid phosphatase-like	0008152 // metabolic process // inferred from electronic annotation//0016311 // dephosphorylation // inferred from electronic

Table S2

Gene_ID	p	FC-RSV 1 d	FC-RSV 5 d	RefSeq Transcript ID	Gene Symbol	Gene Title	Gene Ontology Biological Process
1448855_a	0.000053	-1.04	1.12	NM_001243748//t_Rassf1		Ras association (RalGDS/AF-6) domain family member 1	0006974 // cellular response to DNA damage stimulus // not recorded//0007049 // cell cycle // inferred from electronic
1422568_a	0.000245	-1.04	1.09	NM_023668//XM_Ndel1		nuclear distribution gene E-like homolog 1 (A. nidulans)	0000226 // microtubule cytoskeleton organization // inferred from genetic interaction//0001764 // neuron migration // inferred from
1426659_a	0.000460	-1.04	-1.03	NM_207523//XM_Gm3362//Gm6177//Gm		predicted pseudogene 3362//ribosomal protein L23A pseudogene//predicted	0006412 // translation // inferred from electronic annotation
1425548_a	0.000472	-1.02	1.21	NM_010734	Lst1	leukocyte specific transcript 1	0000902 // cell morphogenesis // inferred from electronic annotation//0002376 // immune system process // inferred from electronic
1418523_a	0.000197	-1.02	1.14	NM_011790//XM_Arih2		ariadne homolog 2 (Drosophila)	0000209 // protein polyubiquitination // not recorded//0006511 // ubiquitin-dependent protein catabolic process // inferred from
1449234_a	0.000192	-1.02	1.15	NM_030558//XM_Car15		carbonic anhydrase 15	0008152 // metabolic process // inferred from direct assay//0008152 // metabolic process // inferred from electronic annotation
1422893_a	0.000502	-1.01	1.10	NM_001166531//t_Sfmbt1		Scm-like with four mbt domains 1	0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 // regulation of transcription, DNA-
1448025_a	0.000580	-1.01	1.31	NM_001002898//LOC100038947//Sirpb1a		signal-regulatory protein beta 1-like//signal-regulatory protein beta	0035556 // intracellular signal transduction // inferred from direct assay//0050766 // positive regulation of phagocytosis // inferred
1417556_a	0.000310	-1.01	1.33	NM_017399	Fabp1	fatty acid binding protein 1, liver	0006810 // transport // inferred from electronic annotation//0008284 // positive regulation of cell proliferation // inferred from
1444268_a	0.000408	-1.00	-1.33	NM_030561//XM_BC004004//LOC1026396		cDNA sequence BC004004//keratin-associated protein 16-1-like	0042060 // wound healing // not recorded//0045787 // positive regulation of cell cycle // not recorded//0050673 // epithelial cell

2-Way ANOVA 855 genes ($p < 0.01$). Blue(-): fold lower in HeJ vs corresponding OuJ. Red : fold higher in HeJ vs corresponding OuJ

[illegible]

Table S3

Gene ID	p (Corr) (Treatment-Strain)	FD (Vehicle)	FD (1 day)	FD (5 day)	RefSeq Transcript ID	Gene Symbol	Gene Title	Gene Ontology Biological Process
1453196_i	0.009319	1.10	-1.69	1.36	NM_011854	<i>Oos2</i>	2'-5' oligoadenylate synthetase-like 2	0006164 // purine nucleotide biosynthetic process // inferred from direct assay//0006955 // immune response // inferred from electronic annotation//0008152 // metabolic process
1419573_i	0.000994	-1.18	-1.69	-1.17	NM_008495	<i>Lgals1</i>	lectin, galactose binding, soluble 1	0002317 // plasma cell differentiation // inferred from direct assay//0007157 // heterophilic cell-cell adhesion // non-traceable author statement//0007165 // signal transduction //
1439327_i	0.002269	-1.21	-1.67	-1.18	NM_001013378//NM_001159367//NM_01159367	<i>Usp1</i>	ubiquitin specific peptidase like 1	0006508 // proteolysis // inferred from electronic annotation//0006511 // ubiquitin-dependent protein catabolic process // inferred from electronic annotation//0008283 // cell
1449851_i	0.005173	1.37	-1.67	1.26	NM_001159367//NM_01159367	<i>Per1</i>	period circadian clock 1	0000322 // negative regulation of transcription from RNA polymerase II promoter // inferred from direct assay//0006351 // transcription, DNA-dependent // inferred from electronic
1454742_i	0.000025	1.20	-1.66	1.09	NM_145839//NM_18_0010850//NM_0010850	<i>Rasgef1b</i>	RasGEF domain family, member 18	0007264 // small GTPase mediated signal transduction // inferred from electronic annotation//0005106 // regulation of small GTPase mediated signal transduction // inferred from
1418322_i	0.002460	-1.02	-1.66	-1.14	NM_0010850//NM_0010850	<i>Calm</i>	calmodulin responsive element modulator	0006006 // glucose metabolic process // inferred from electronic annotation//0006351 // transcription, DNA-dependent // inferred from electronic annotation//0006355 //
1451064_i	0.002599	-1.01	-1.66	-1.13	NM_001205339//NM_001205339	<i>Phosphoserine aminotransferase 1</i>	phosphoserine aminotransferase 1	0006564 // L-serine biosynthetic process // inferred from electronic annotation//0008152 // metabolic process // inferred from electronic annotation//0008615 // pyridoxine
1451909_i	0.007690	1.13	-1.66	-1.26	NM_016737	<i>Slp1</i>	stress-induced phosphoprotein 1	
1425888_i	0.000991	-1.69	-1.66	-1.09	NM_133203	<i>Kira17</i>	killer cell lectin-like receptor, subfamily A, member 17	
1450716_i	0.000014	2.02	-1.63	2.31	NM_009621	<i>Adamts1</i>	a disintegrin-like and metalloproteinase (reprolysin type) with thrombospondin type	0001542 // ovulation from ovarian follicle // inferred from mutant phenotype//0001822 // kidney development // inferred from mutant phenotype//0006508 // proteolysis //
1416600_i	0.000282	1.02	-1.62	1.06	NM_001081549//NM_001081549	<i>Rcan1</i>	regulator of calcineurin 1	0007519 // skeletal muscle tissue development // inferred from electronic annotation//0009612 // response to mechanical stimulus // inferred from electronic annotation//0001972
1427510_i	0.009935	-1.31	-1.61	-1.37	NM_010305	<i>Gnai1</i>	guanine nucleotide binding protein (G protein), alpha inhibiting 1	0006184 // GTP catabolic process // traceable author statement//0007049 // cell cycle // inferred from electronic annotation//0007165 // signal transduction // inferred from
1448475_i	0.004813	-1.17	-1.61	-1.17	NM_133859	<i>Olfml3</i>	olfactomedin-like 3	0007275 // multicellular organismal development // inferred from electronic annotation
1424010_i	0.007297	-1.12	-1.61	-1.07	NM_029568	<i>Mtsp4</i>	microfibrillar-associated protein 4	0007155 // cell adhesion // inferred from electronic annotation//0007165 // signal transduction // inferred from electronic annotation
1419004_i	0.007502	-1.41	-1.61	-1.09	NM_007534//NM_00_007534//NM_00_007534	<i>Bcl2a1a//Bcl2a1b</i>	B cell leukemia/lymphoma 2 related protein A1a//B cell leukemia/lymphoma 2	0001782 // cell homeostasis // inferred from direct assay//0002903 // negative regulation of B cell apoptotic process // inferred from direct assay//0006915 // apoptotic process
1440216_i	0.002796	-1.05	-1.60	1.00	NM_053088	<i>Ifitm5</i>	interferon induced transmembrane protein 5	0007275 // multicellular organismal development // traceable author statement//0009607 // response to biotic stimulus // inferred from electronic annotation//0003082 // bone
1424671_i	0.004012	1.07	-1.59	-1.22	NM_024413	<i>Plekhl7</i>	pleckstrin homology domain containing, family F (with FYVE domain) member 1	0006915 // apoptotic process // inferred from electronic annotation//0006917 // induction of apoptosis // inferred from direct assay//0007032 // endosome organization // not
1451340_i	0.000969	1.06	-1.59	1.17	NM_001172205//NM_001172205	<i>Arnd5a</i>	AT rich interactive domain 5A (MRF1-like)	0002062 // chondrocyte differentiation // inferred from direct assay//0006351 // transcription, DNA-dependent // inferred from electronic annotation//0006355 // regulation of
1421260_i	0.001157	1.72	-1.59	-1.23	NM_009272	<i>Srm</i>	spermidine synthase	0007519 // metabolic process // inferred from electronic annotation//0008295 // spermidine biosynthetic process // not recorded
1435470_i	0.001479	-1.06	-1.58	1.00	NM_00107189//NM_00107189	<i>Farg2b</i>	Fc receptor, γ 2, low affinity IIB	0001811 // negative regulation of type I hypersensitivity // inferred from mutant phenotype//0002538 // negative regulation of immunoglobulin production // inferred from mutant
1435945_i	0.007336	1.03	-1.58	1.04	NM_008566	<i>Mcm5</i>	minichromosome maintenance deficient 5, cell division cycle 46 (S. cerevisiae)	0006240 // DNA replication // inferred from electronic annotation//0006270 // DNA replication initiation // inferred from electronic annotation//0007049 // cell cycle // inferred
1421486_i	0.003170	-1.27	-1.58	1.20	NM_018781	<i>Egr3</i>	early growth response 3	0001938 // positive regulation of endothelial cell proliferation // not recorded//0002042 // cell migration involved in sprouting angiogenesis // not recorded//0006351 //
1418340_i	0.005389	-1.46	-1.58	-1.04	NM_010185	<i>Fcgr1g</i>	Fc receptor, γ 2, high affinity I, gamma polypeptide	0001798 // positive regulation of type II hypersensitivity // inferred from mutant phenotype//0001805 // positive regulation of type II hypersensitivity // inferred from mutant
1419410_i	0.007411	-1.21	-1.57	-1.09	NM_016767	<i>Botf1</i>	basic leucine zipper transcription factor, ATF-like	0001816 // cytokine production // inferred from mutant phenotype//0002320 // lymphoid progenitor cell differentiation // inferred from mutant phenotype//0006351 //
1417406_i	0.001264	-1.11	-1.57	1.08	NM_018820	<i>Sertad1</i>	SERTA domain containing 1	0006351 // transcription, DNA-dependent // inferred from electronic annotation//0006355 // regulation of transcription, DNA-dependent // inferred from electronic
1431808_i	0.004673	1.01	-1.56	1.14	NM_001159299//NM_001159299	<i>Rth4</i>	inter alpha-trypsin inhibitor, heavy chain 4	0006953 // acute-phase response // inferred from electronic annotation//0010466 // negative regulation of peptidase activity // inferred from electronic annotation//0030212 //
1450165_i	0.002846	-1.21	-1.56	-1.01	NM_011408	<i>Slfn2</i>	schlafen 2	0008285 // negative regulation of cell proliferation // inferred from direct assay
1426215_i	0.001248	-1.25	-1.55	1.09	NM_001190448//NM_001190448	<i>Ddc</i>	dopa decarboxylase	0006520 // cellular amino acid metabolic process // inferred from electronic annotation//0007623 // circadian rhythm // inferred from electronic annotation//0009636 // response
1421408_i	0.000275	-1.54	-1.55	1.10	NM_030691	<i>Igsf1</i>	immunoglobulin superfamily, member 6	
1419519_i	0.000210	1.28	-1.55	1.19	NM_001111274//NM_001111274	<i>Igf1</i>	insulin-like growth factor 1	0001649 // osteoblast differentiation // inferred from expression pattern//0001932 // regulation of protein phosphorylation // inferred from direct assay//0001974 // blood vessel
1455263_i	0.000903	-1.09	-1.54	-1.09	NM_172488	<i>Lacc1</i>	laccase (multicopper oxidoreductase) domain containing 1	
1416129_i	0.000970	1.72	-1.54	-1.27	NM_133753	<i>Ernf1</i>	ENB receptor feedback inhibitor 1	
1448429_i	0.004912	-1.11	-1.54	-1.01	NM_013755	<i>Gwp</i>	glycogen	0006260 // DNA replication // inferred from electronic annotation//0006270 // DNA replication initiation // inferred from electronic annotation//0007049 // cell cycle // inferred
1416575_i	0.005196	1.00	-1.54	1.02	NM_001161623//NM_001161623	<i>Cdk45</i>	cell division cycle 45	0007165 // signal transduction // inferred from electronic annotation//0043547 // positive regulation of GTPase activity // inferred from electronic annotation
1451320_i	0.001206	-1.20	-1.54	-1.11	NM_001164627//NM_001164627	<i>Arhgap8</i>	Rho GTPase activating protein 8	0000660 // protein import into nucleus, translocation // inferred from mutant phenotype//0000165 // MAPK cascade // not recorded//0001818 // negative regulation of cytokine
1420361_i	0.001047	-1.25	-1.53	1.12	NM_013612	<i>Ct1101</i>	solute carrier family 11 (proton-coupled 7) HAUS augmin-ion transporter complexes, member 1	0007049 // cell cycle // inferred from electronic annotation//0007067 // mitosis // inferred from electronic annotation//0051225 // spindle assembly // not recorded//00051297 //
1424777_i	0.001901	-1.31	-1.53	-1.10	NM_028633//NM_02_028633//NM_02_028633	<i>Huau1//LOC1004</i>	HAUS augmin-like complex, subunit 7//HAUS augmin-like complex subunit 7	0001501 // skeletal system development // inferred from mutant phenotype//0007165 // signal transduction // inferred from electronic annotation//0030199 // collagen fibril
1422437_i	0.000124	-1.02	-1.52	1.01	NM_007737	<i>Col5a2</i>	collagen, type V, alpha 2	0007059 // chromosome segregation // inferred from electronic annotation//0007067 // mitosis // inferred from electronic annotation//0034508 // centromere complex assembly
1427105_i	0.006857	-1.25	-1.52	-1.07	NM_028131	<i>Cenpn</i>	centromere protein N	0000122 // negative regulation of transcription from RNA polymerase II promoter // inferred from direct assay//0001022 // negative regulation of transcription from RNA polymerase
1425895_i	0.002597	1.11	-1.52	1.25	NM_010495	<i>Id1</i>	inhibitor of DNA binding 1	0001774 // microglial cell activation // non-traceable author statement//0001934 // positive regulation of protein phosphorylation // not recorded//0006911 // phagocytosis,
1418204_i	0.001411	1.03	-1.52	1.27	NM_019467	<i>Aif1</i>	allograft inflammatory factor 1	
1418206_i	0.000169	-1.01	-1.51	-1.29	NM_022324	<i>Sd211</i>	stromal cell-derived factor 2-like 1	
1437165_i	0.004678	-1.11	-1.51	-1.28	NM_008788	<i>Pcalce</i>	procollagen C-endopeptidase enhancer protein	
1422899_i	0.002645	-1.17	-1.51	-1.16	NM_001098271//NM_001098271	<i>Trnm176a</i>	transmembrane protein 176A	
1428069_i	0.003236	-1.06	-1.50	-1.15	NM_025866	<i>Ckcz7</i>	cell division cycle associated 7	
1426351_i	0.000489	-1.01	-1.50	-1.20	NM_010477//NM_01_010477//NM_01_010477	<i>Hspd1//LOC10105</i>	heat shock protein 1 (chaperonin)//60 kDa heat shock protein, mitochondrial-like	
1448380_i	0.000781	-1.04	-1.50	1.30	NM_011150	<i>Lgals3bp</i>	lectin, galactose-binding, soluble, 3 binding protein	
1422002_i	0.000209	-1.10	-1.49	-1.01	NM_010751	<i>Mxd1</i>	MAX dimerization protein 1	
1417009_i	0.002269	1.15	-1.49	1.09	NM_001113356//NM_001113356	<i>C1ra//C1rb</i>	complement component 1, r subcomponent A//complement component 1, r	
1425545_i	0.007481	-1.27	-1.48	-1.05	NM_001267808//NM_001267808	<i>H2-D1//H2-L</i>	histocompatibility 2, D region locus 1//histocompatibility 2, D region locus 1	
1428776_i	0.000606	1.05	-1.48	1.01	NM_029415	<i>Ct10a6</i>	solute carrier family 10 (sodium/bile acid cotransporter family), member 6	
1425968_i	0.009311	-1.08	-1.48	-1.15	NM_026778	<i>Ctnc1</i>	collagen triple helix repeat containing 1	
1460271_i	0.000224	-1.42	-1.48	1.27	NM_021407	<i>Trem3</i>	triggering receptor expressed on myeloid cells 3	
1417633_i	0.002444	-1.09	-1.48	-1.08	NM_011435	<i>Sod3</i>	superoxide dismutase 3, extracellular	
1417300_i	0.006750	-1.08	-1.47	-1.13	NM_133888	<i>Smpd3b</i>	sphingomyelin phosphodiesterase, acid-like 3B	
1415922_i	0.000330	1.53	-1.47	1.35	NM_010807	<i>Marcks1</i>	MARCKS-like 1	
1418421_i	0.000853	-1.01	-1.47	1.31	NM_007528	<i>Bcl6b</i>	B cell CLL/lymphoma 6, member B	
1424147_i	0.001190	1.01	-1.47	-1.27	NM_146036	<i>Aha1</i>	AHA1, activator of heat shock protein ATPase 1	
1430530_i	0.007295	-1.07	-1.46	-1.16	NM_026393	<i>Nmr1</i>	NmrA-like family domain containing 1	
1418547_i	0.002642	1.10	-1.46	1.03	NM_009364	<i>Tjp2</i>	tissue factor pathway inhibitor 2	
1416514_i	0.000700	1.22	-1.46	1.20	NM_007984	<i>Fxn1</i>	fascin homolog 1, actin bundling protein (Strongylocentrotus purpuratus)	
1421653_i	0.005116	-4.43	-1.45	-3.67	NM_001024700	<i>Igh-V558//Igha</i>	immunoglobulin heavy chain (V558 family)//immunoglobulin heavy constant alpha	
1429209_i	0.006750	-1.13	-1.45	-1.24	NM_153393	<i>Col23a1</i>	collagen, type XXIII, alpha 1	
1422041_i	0.005544	-1.36	-1.45	-1.03	NM_133209	<i>Pilrb1</i>	paired immunoglobulin-like type 2 receptor beta 1	
1416362_i	0.005478	-1.03	-1.44	-1.24	NM_010219	<i>Fkbp4</i>	FK506 binding protein 4	
1449449_i	0.005965	-1.19	-1.44	1.06	NM_022415	<i>Ptges</i>	prostaglandin H synthase	
1421653_i	0.005096	-4.23	-1.44	-3.52	NM_001024700//NM_001024700	<i>Igh-V558//Igha</i>	immunoglobulin heavy chain (V558 family)//immunoglobulin heavy constant	
1420444_i	0.001427	1.15	-1.44	1.33	NM_011395	<i>Ct22a3</i>	solute carrier family 22 (organic cation transporter), member 3	
1421402_i	0.001423	-1.44	-1.43	-1.05	NM_053191	<i>Pil5</i>	peptidase inhibitor 5	
1417601_i	0.000124	2.37	-1.43	1.31	NM_015811	<i>Rgs1</i>	regulator of G-protein signaling 1	
1421217_i	0.002250	-1.04	-1.43	1.20	NM_001159301//NM_001159301	<i>Lgals9</i>	lectin, galactose binding, soluble 9	
1450749_i	0.000245	3.02	-1.43	2.78	NM_001139509//NM_001139509	<i>Nr4a2</i>	nuclear receptor subfamily 4, group A, member 2	
1451415_i	0.003529	-1.02	-1.43	-1.07	NM_026931	<i>1810011O10Rik</i>	RIKEN cDNA 1810011O10 gene	
1440215_i	0.004678	-1.17	-1.43	-1.05	NM_001171801//NM_001171801	<i>Triak</i>	triple Qxx/R motif containing	
1418936_i	0.000004	3.02	-1.43	2.49	NM_010755	<i>Moff</i>	v-maf musculoaponeurotic fibrosarcoma oncogene family, protein F (avian)	
1428255_i	0.009935	-1.19	-1.43	-1.10	NM_025881//NM_02_025881	<i>Luc71</i>	Luc7 homolog (S. cerevisiae)-like	
1435626_i	0.004474	1.03	-1.42	-1.20	NM_022331	<i>Hspu1</i>	homoysteine-inducible, endoplasmic reticulum stress-inducible, ubiquitin-like	
1420622_i	0.003922	1.19	-1.42	-1.20	NM_031165	<i>Hspu8</i>	heat shock protein 8	
1435851_i	0.000511	1.38	-1.42	1.57	NM_011817	<i>Gadd45g</i>	growth arrest and DNA-damage-inducible 45 gamma	
1448830_i	0.000162	1.39	-1.42	2.15	NM_013642	<i>Dusp1</i>	dual specificity phosphatase 1	
1418939_i	0.001536	1.52	-1.42	1.50	NM_008250	<i>Hlx</i>	H2.0-like homeobox	
1415923_i	0.006082	-1.11	-1.41	-1.21	NM_010882	<i>Ndn</i>	nanos	
1427298_i	0.003272	1.21	-1.41	1.31	NR_002870	<i>Dnm3os</i>	dynamitin 3, opposite strand	
1437140_i	0.007545	-1.22	-1.40	1.03	NM_175517	<i>Fam221b</i>	family with sequence similarity 221, member B	
1418465_i	0.000139	-1.30	-1.40	-1.01	NM_008677	<i>Ncf4</i>	neutrophil cytosolic factor 4	
1416880_i	0.001186	-1.05	-1.40	-1.07	NM_008562	<i>Mcl1</i>	myeloid cell leukemia sequence 1	
1424542_i	0.009797	-1.19	-1.40	1.14	NM_011311	<i>S100a4</i>	S100 calcium binding protein A4	
1422020_i	0.001391	1.29	-1.40	1.34	NM_011898	<i>Spry4</i>	sprouty homolog 4 (Drosophila)	
1422790_i	0.006256	1.03	-1.40	1.09	NM_010933	<i>Nppc</i>	natriuretic peptide type C	
1429056_i	0.000337	-1.10	-1.40	1.08	NM_025832	<i>Naa16</i>	N(alpha)-acetyltransferase 16, NatA auxiliary subunit	

Table S3

Gene ID	p (Cort) (Treatment-Strain)	FD (Vehicle)	FD (1 day)	FD (5 day)	RefSeq Transcript ID	Gene Symbol	Gene Title	Gene Ontology Biological Process
1427916_i	0.009498	-1.07	-1.40	-1.15	NM_001253702//NM	<i>Scf7</i>	suppression of tumorigenicity 7-like	0030198 // extracellular matrix organization // non-traceable author statement//00030308 // negative regulation of cell growth // inferred from direct assay//00045595 // regulation
1417836_i	0.007962	-1.11	-1.40	-1.05	NM_024198	<i>Gpx7</i>	glutathione peroxidase 7	0006979 // response to oxidative stress // inferred from electronic annotation//00055114 // oxidation-reduction process // inferred from electronic annotation
1416303_i	0.001157	-1.05	-1.39	1.02	NM_019980	<i>Liifaf</i>	LYI-induced TN factor	0001817 // regulation of cytokine production // inferred from mutant phenotype//0006351 // transcription, DNA-dependent // inferred from electronic annotation//0006355 //
1417968_i	0.002252	-1.06	-1.38	-1.01	NM_013594	<i>Mbd1</i>	methy1-CpG binding domain protein 1	0006306 // DNA methylation // traceable author statement//0006351 // transcription, DNA-dependent // inferred from electronic annotation//0006355 // regulation of
1418714_i	0.000096	1.18	-1.38	1.28	NM_008748	<i>Dusp8</i>	dual specificity phosphatase 8	0000188 // inactivation of MAPK activity // not recorded//0006470 // protein dephosphorylation // not recorded//00016311 // dephosphorylation // inferred from electronic
1421811_i	0.000072	3.02	-1.38	2.45	NM_011580//NM_01	<i>Pold1//Thbs1</i>	phosphatase domain containing, paladin 1//thrombospondin 1	0000187 // activation of MAPK activity // not recorded//0001937 // negative regulation of endothelial cell proliferation // not recorded//0001953 // negative regulation of cell-
1420113_i	0.007679	-1.06	-1.38	-1.17	NM_025556	<i>Cops2</i>	coordinator of PRMT5, differentiation stimulator	0006351 // transcription, DNA-dependent // inferred from electronic annotation//0006355 // regulation of transcription, DNA-dependent // inferred from electronic
1429568_i	0.006463	-1.11	-1.38	-1.16	NM_026454	<i>Ube2f</i>	ubiquitin-conjugating enzyme E2F (putative)	0008152 // metabolic process // inferred from electronic annotation//00045116 // protein neddylation // inferred from mutant phenotype//00045116 // protein neddylation // not
1426381_i	0.002640	1.13	-1.38	1.04	NM_01081214//NM	<i>Pprc1</i>	peroxisome proliferative activated receptor, gamma, coactivator-related 1	0006351 // transcription, DNA-dependent // inferred from electronic annotation//0006355 // regulation of transcription, DNA-dependent // inferred from electronic annotation
1428593_i	0.002052	1.02	-1.38	-1.14	NM_029368	<i>Tesb30</i>	testis expressed 30	
1415871_i	0.007429	-1.00	-1.38	1.11	NM_009369	<i>Tgfb1</i>	transforming growth factor, beta induced	0001525 // angiogenesis // inferred from electronic annotation//0002062 // chondrocyte differentiation // inferred from electronic annotation//0007155 // cell adhesion // inferred
1424314_i	0.003203	-1.08	-1.38	-1.12	NM_027541	<i>Ppf3</i>	PRP3 pre-mRNA processing factor 3 homolog (yeast)	0000398 // mRNA splicing, via spliceosome // inferred from electronic annotation//0006397 // mRNA processing // inferred from electronic annotation//0008380 // RNA splicing //
1425154_i	0.008651	-1.13	-1.37	-1.01	NM_001113529//NM	<i>Cpf1</i>	colony stimulating factor 1 (macrophage)	0001503 // ossification // not recorded//0001954 // positive regulation of cell-matrix adhesion // inferred from genetic interaction//0002158 // osteoclast proliferation // inferred
1423125_i	0.000703	1.34	-1.36	1.11	NM_001111051//NM	<i>Dck1</i>	doublecortin-like kinase 1	0001764 // neuron migration // inferred from genetic interaction//0006468 // protein phosphorylation // inferred from electronic annotation//0007275 // multicellular organismal
1426519_i	0.002616	1.16	-1.36	-1.12	NM_011030	<i>Ptha1</i>	procollagen-proline, 2-oxoglutarate 4-dioxygenase (proline 4-hydroxylase), alpha 1	00018401 // peptidyl-proline hydroxylation to 4-hydroxy-L-proline // inferred from direct assay//00030199 // collagen fibril organization // inferred from mutant phenotype//00055114
1454617_i	0.001242	1.18	-1.36	-1.13	NM_001042591	<i>Ardc3</i>	arrestin domain containing 3	0001699 // temperature homeostasis // inferred from mutant phenotype//0007165 // signal transduction // inferred from electronic annotation//00031651 // negative regulation of
1425137_i	0.004334	-1.43	-1.36	-1.01	NM_010391	<i>H2-Q10</i>	histocompatibility 2, Q region locus 10	0001916 // positive regulation of T cell mediated cytotoxicity // inferred from electronic annotation//0002474 // antigen processing and presentation of peptide antigen via MHC class
1451978_i	0.003585	1.08	-1.35	1.21	NM_010729	<i>Lod1</i>	lysyl oxidase-like 1	00055114 // oxidation-reduction process // inferred from direct assay
1428661_i	0.003767	-1.11	-1.34	-1.04	NM_001049397//NM	<i>Filip1</i>	filipin A interacting protein 1-like	
1416414_i	0.006750	-1.02	-1.34	1.03	NM_133918	<i>Emilin1</i>	elastin microfibril interface 1	0007155 // cell adhesion // inferred from electronic annotation//0010811 // positive regulation of cell-substrate adhesion // inferred from direct assay//00030198 // extracellular
1424972_i	0.001186	1.03	-1.34	-1.11	NM_001205052//NM	<i>Jdp2</i>	Jm1 dimerization protein 2	0000122 // negative regulation of transcription from RNA polymerase II promoter // inferred from direct assay//0000122 // negative regulation of transcription from RNA polymerase
1450808_i	0.008138	-2.00	-1.34	-1.69	NM_013521	<i>Fpr1</i>	formyl peptide receptor 1	0006935 // chemotaxis // traceable author statement//0007165 // signal transduction // inferred from electronic annotation//0007186 // G-protein coupled receptor signaling
1416121_i	0.008294	-1.08	-1.34	1.17	NM_010728	<i>Lox</i>	lysyl oxidase	0001568 // blood vessel development // inferred from mutant phenotype//0009725 // response to hormone stimulus // not recorded//00030199 // collagen fibril organization //
1438992_i	0.002050	-1.01	-1.34	1.04	NM_009716	<i>Atf4</i>	activating transcription factor 4	0006094 // gluconeogenesis // inferred from direct assay//0006351 // transcription, DNA-dependent // inferred from electronic annotation//0006355 // regulation of transcription,
1433610_i	0.000088	1.33	-1.34	-1.19	NM_177604	<i>AA986860</i>	expressed sequence AA986860	
1419766_i	0.003199	2.17	-1.33	1.91	NM_010831	<i>Sik1</i>	salt inducible kinase 1	0000122 // negative regulation of transcription from RNA polymerase II promoter // not recorded//0002028 // regulation of sodium ion transport // not recorded//0006468 //
1446619_i	0.000375	1.81	-1.33	2.10		<i>AL130083B17RIK</i>	RIKEN cDNA AL130083B17 gene	
1423884_i	0.005307	-1.21	-1.32	-1.04	NM_011574	<i>Cirh1a</i>	cirrhosis, autosomal recessive 1A (human)	0006351 // transcription, DNA-dependent // inferred from electronic annotation//0006355 // regulation of transcription, DNA-dependent // not recorded//00030490 // maturation of
1448700_i	0.009155	-1.09	-1.32	1.14	NM_008059	<i>Gob2</i>	G0G1 switch gene 2	0006915 // apoptotic process // not recorded//00043065 // positive regulation of apoptotic process // not recorded//00079191 // extrinsic apoptotic signaling pathway // inferred
1415910_i	0.009255	-1.17	-1.32	-1.11	NM_134141	<i>Copin1</i>	cytokine induced apoptosis inhibitor 1	0006915 // apoptotic process // inferred from electronic annotation//0016226 // iron-sulfur cluster assembly // inferred from electronic annotation//00030097 // hemopoiesis //
1417018_i	0.003767	-1.01	-1.32	-1.11	NM_001043522//NM	<i>Elpmp2</i>	epidermal growth factor-containing fibulin-like extracellular matrix protein 2	0007596 // blood coagulation // inferred from electronic annotation
1430700_i	0.000700	-1.58	-1.32	1.13	NM_013273	<i>Phc2p</i>	phospholipase A2, group VII (platelet-activating factor acetylhydrolase, plasma)	0006508 // proteolysis // inferred from electronic annotation//0006629 // lipid metabolic process // inferred from electronic annotation//0006954 // inflammatory response //
1415940_i	0.002396	-1.09	-1.32	-1.10	NM_01159908//NM	<i>Zfand2a</i>	zinc finger, AN1-type domain 2A	
1423571_i	0.004725	1.15	-1.32	1.17	NM_007901	<i>S1pr1</i>	sphingosine-1-phosphate receptor 1	0001525 // angiogenesis // inferred from direct assay//0003376 // sphingosine-1-phosphate signaling pathway // inferred from electronic annotation//0007165 // signal
1420671_i	0.004754	-1.34	-1.32	1.18	NM_029499	<i>M404c</i>	membrane-spanning 4-domains, subfamily A, member 4C	
1434316_i	0.004475	-1.01	-1.31	1.04	NM_001081163	<i>Chsy1</i>	chondroitin sulfate synthase 1	0030206 // chondroitin sulfate biosynthetic process // not recorded//0030279 // negative regulation of ossification // not recorded//00031667 // response to nutrient levels //
1416072_i	0.004012	1.03	-1.31	-1.00	NM_00111059//NM	<i>Cd34</i>	CD34 antigen	0001894 // tissue homeostasis // not recorded//0001935 // endothelial cell proliferation // not recorded//0003094 // glomerular filtration // inferred from sequence or structural
1452436_i	0.001276	1.04	-1.31	1.03	NM_033325	<i>Loxb2</i>	lysyl oxidase-like 2	0001666 // response to hypoxia // inferred from direct assay//0001837 // epithelial to mesenchymal transition // not recorded//0001935 // endothelial cell proliferation // not
1418901_i	0.000000	1.51	-1.31	1.26	NM_009883	<i>Cebp1</i>	CCAAT/enhancer binding protein (C/EBP), beta	0001892 // embryonic placenta development // inferred from genetic interaction//0006351 // transcription, DNA-dependent // inferred from electronic annotation//0006355 //
1417985_i	0.001426	1.03	-1.31	1.14	NM_025980	<i>Nrap</i>	Notch-regulated ankyrin repeat protein	0000122 // negative regulation of transcription from RNA polymerase II promoter // inferred from genetic interaction//0001569 // patterning of blood vessels // inferred from mutant
1418859_i	0.007125	-1.02	-1.31	-1.07	NM_133231	<i>Rfxap</i>	regulatory factor X-associated protein	0045893 // positive regulation of transcription, DNA-dependent // inferred from direct assay
1448890_i	0.000129	1.91	-1.30	1.86	NM_008452	<i>Klf2</i>	Kruppel-like factor 2 (lung)	0000902 // cell morphogenesis // inferred from mutant phenotype//0001701 // in utero embryonic development // inferred from mutant phenotype//0006351 // transcription, DNA-
1423667_i	0.000166	1.13	-1.30	1.31	NM_145569	<i>Mat2a</i>	methionine adenosyltransferase II, alpha	0006556 // S-adenosylmethionine biosynthetic process // inferred from direct assay//0006556 // S-adenosylmethionine biosynthetic process // not recorded//0006730 // one-
1422452_i	0.000250	1.33	-1.30	1.22	NM_013863	<i>Bug3</i>	BCG2-associated athanogene 3	0006915 // apoptotic process // inferred from reviewed computational analysis//0007420 // brain development // inferred from electronic annotation//0008625 // extrinsic
1422921_i	0.000007	1.41	-1.30	1.35	NM_008037	<i>Foxl2</i>	fox-like antigen 2	0006351 // transcription, DNA-dependent // inferred from electronic annotation//0006355 // regulation of transcription, DNA-dependent // inferred from electronic
1426858_i	0.009255	1.26	-1.30	1.25	NM_008381	<i>Inhbb</i>	inhibin beta-B	0001654 // eye development // traceable author statement//0009267 // cellular response to starvation // inferred from expression pattern//0006905 // response to external
1427883_i	0.001188	1.27	-1.30	1.10	NM_009930	<i>Col3a1</i>	collagen, type III, alpha 1	0001501 // skeletal system development // inferred from electronic annotation//0001568 // blood vessel development // inferred from mutant phenotype//0007160 // cell-matrix
1417598_i	0.009935	-1.06	-1.29	-1.16	NM_001131188//NM	<i>Fxr1</i>	fragile X mental retardation gene 1, autosomal homolog	0007275 // multicellular organismal development // inferred from electronic annotation//0007517 // muscle organ development // inferred from mutant phenotype//0007148 //
1450829_i	0.000089	1.43	-1.29	1.69	NM_001166402//NM	<i>Tnfrsf3</i>	tumor necrosis factor, alpha-induced protein 3	0001922 // B-1 cell homeostasis // inferred from mutant phenotype//0002237 // response to molecule of bacterial origin // inferred from direct assay//0002237 // response to
1435130_i	0.002533	1.03	-1.29	1.03	NM_001013778	<i>Tvp23a</i>	trans-golgi network vesicle protein 23A	0006879 // cellular iron ion homeostasis // not recorded//0006879 // cellular iron ion homeostasis // inferred from electronic annotation//00010826 // negative regulation of
1451983_i	0.008837	1.73	-1.29	1.19	NM_010573	<i>Irx1</i>	Iroquois related homeobox 1 (Drosophila)	0001656 // metanephros development // inferred from expression pattern//0006355 // regulation of transcription, DNA-dependent // inferred from electronic annotation//00072086
1417127_i	0.007360	1.03	-1.29	1.11	NM_010835	<i>Mx1</i>	hemoxob, msh-like 1	0000122 // negative regulation of transcription from RNA polymerase II promoter // inferred from direct assay//0000122 // negative regulation of transcription from RNA polymerase
1434744_i	0.000474	1.06	-1.28	1.13	NM_153566	<i>Yrdc</i>	yrdC domain containing (E.coli)	0051051 // negative regulation of transport // not recorded
1437803_i	0.002709	-1.03	-1.28	1.07	NM_009193	<i>Slbp</i>	stem-loop binding protein	0006397 // mRNA processing // inferred from electronic annotation//0006398 // histone mRNA 3'-end processing // inferred from direct assay//0033260 // nuclear cell cycle DNA
1417056_i	0.002748	-1.08	-1.28	-1.01	NM_011189	<i>Psmc1</i>	proteasome (prosome, macropain) 28 subunit, alpha	0010950 // positive regulation of endopeptidase activity // inferred from physical interaction//0019884 // antigen processing and presentation of exogenous antigen // inferred from
1448416_i	0.000400	-1.04	-1.28	-1.13	NM_008597	<i>Mgp</i>	matrix Gla protein	0001503 // ossification // inferred from electronic annotation//0006464 // protein complex assembly // not recorded//0007275 // multicellular organismal development // inferred
1460282_i	0.000124	-1.06	-1.28	1.11	NM_021408	<i>Tmem1</i>	triggering receptor expressed on myeloid cells 1	
1416740_i	0.003098	1.16	-1.28	1.21	NM_015734	<i>Col5a1</i>	collagen, type V, alpha 1	
1423903_i	0.000070	1.10	-1.28	1.17	NM_027514	<i>Pvr</i>	poliovirus receptor	0001568 // blood vessel development // inferred from mutant phenotype//0003007 // heart morphogenesis // inferred from genetic interaction//0007155 // cell adhesion // not
1448025_i	0.004176	-1.51	-1.28	1.10	NM_001173459//NM	<i>LOC100038947//S</i>	signal-regulatory protein beta 1-like//signal-regulatory protein beta 1B	0009615 // response to virus // not recorded//0016337 // cell-cell adhesion // inferred from direct assay//0016477 // cell migration // inferred from direct assay
1436111_i	0.006256	-1.13	-1.28	-1.14	NM_001008705//NM	<i>Bud31//LOC10004</i>	BUD31 homolog (yeast)//protein BUD31 homolog	
1451815_i	0.006032	-1.04	-1.27	-1.07	NM_009054	<i>Trim27</i>	tripartite motif-containing 27	0000122 // negative regulation of transcription from RNA polymerase II promoter // inferred from genetic interaction//0000122 // negative regulation of transcription from RNA
1428800_i	0.003196	-1.06	-1.27	-1.06	NM_172437	<i>Pua71</i>	psudouridine synthase 7 homolog (S. cerevisiae)-like	0001522 // pseudouridine synthesis // inferred from electronic annotation//0008033 // rRNA processing // inferred from electronic annotation//0009451 // RNA modification //
1434079_i	0.009674	1.26	-1.27	1.08	NM_008564	<i>Mcm2</i>	minichromosome maintenance deficient 2 mitotin (S. cerevisiae)	0006260 // DNA replication // inferred from electronic annotation//0006268 // DNA unwinding involved in replication // inferred from direct assay//0006270 // DNA replication
1416498_i	0.005173	1.02	-1.27	-1.07	NM_008908	<i>Ppic</i>	peptidylprolyl isomerase C	0000413 // protein peptidyl-prolyl isomerization // inferred from electronic annotation//0006457 // protein folding // inferred from electronic annotation
1437100_i	0.000188	1.48	-1.27	1.45	NM_145478	<i>Pim3</i>	provinl integration site 3	0006468 // protein phosphorylation // inferred from electronic annotation//0006468 // protein phosphorylation // not recorded//0006915 // apoptotic process // inferred from
1417574_i	0.000719	-1.01	-1.27	1.10	NM_001012477//NM	<i>Cxd12</i>	chemokine (C-X-C motif) ligand 12	0001569 // patterning of blood vessels // inferred from mutant phenotype//0001666 // response to hypoxia // inferred from electronic annotation//0001667 // ameboidal cell
1438003_i	0.000400	1.04	-1.26	1.05	NM_001169131//NM	<i>Papd7</i>	PAP associated domain containing 7	0006260 // DNA replication // inferred from electronic annotation//0007049 // cell cycle // inferred from electronic annotation//0007067 // mitosis // inferred from electronic
1416125_i	0.001672	1.29	-1.26	1.29	NM_010220	<i>Fkbp5</i>	FKBP5 binding protein 5	0004113 // protein peptidyl-prolyl isomerization // --//0000413 // protein peptidyl-prolyl isomerization // inferred from electronic annotation//0000413 // protein peptidyl-prolyl
1419021_i	0.000573	3.02	-1.26	1.03	NM_019660	<i>Fcd2</i>	fatty acid desaturase 2	0006629 // lipid metabolic process // inferred from electronic annotation//0006631 // fatty acid metabolic process // inferred from electronic annotation//0006633 // fatty acid
1421326_i	0.006032	-1.02	-1.26	1.03	NM_007780//NM_00	<i>Cs2rb//Cs2rb2</i>	colony stimulating factor 2 receptor, beta, low-affinity (granulocyte-	0011921 // cytokine-mediated signaling pathway // inferred from electronic annotation
1439773_i	0.002615	1.03	-1.25	1.25	NM_001164036//NM	<i>Lye</i>	lymphocyte antigen 6 complex, locus E	0001701 // in utero embryonic development // inferred from mutant phenotype//00030325 // adrenal gland development // inferred from mutant phenotype//0035265 // organ
1425649_i	0.002040	1.05	-1.25	1.10	NM_001135151//NM	<i>Slc39a14</i>	solute carrier family 39 (zinc transporter), member 14	0006810 // transport // inferred from electronic annotation//0006811 // ion transport // inferred from electronic annotation//0006826 // iron ion transport // inferred from direct
1452462_i	0.002400	1.27	-1.25	1.07	NM_001110100//NM	<i>Bomp</i>	BTG3 associated nuclear protein	0006351 // transcription, DNA-dependent // inferred from electronic annotation//0006355 // regulation of transcription, DNA-dependent // inferred from electronic
1423316_i	0.002640	-1.05	-1.25	1.03	NM_001205286//NM	<i>Tmem39a</i>	transmembrane protein 39a	
1418230_i	0.002860	-1.07	-1.25	1.06	NM_001193303//NM	<i>Lims1</i>	LM and senescent cell antigen-like domains 1	
1417511_i	0.002001	-1.07	-1.24	-1.11	NM_025281	<i>Lyar</i>	Ly1 antibody reactive clone	
1426726_i	0.001294	-1.00	-1.24	1.05	NM_001163818//NM	<i>Gm8801//Ppp1r1</i>	protein phosphatase 1, regulatory subunit 10 pseudogene//protein phosphatase 1,	0006351 // transcription, DNA-dependent // inferred from electronic annotation//0043086 // negative regulation of catalytic activity // not recorded
1418156_i	0.000041	3.02	-1.24	3.20	NM_021342	<i>Kcne4</i>	potassium voltage-gated channel, isk-related subfamily, gene 4	0006810 // transport // inferred from electronic annotation//0006811 // ion transport // inferred from electronic annotation//0006813 // potassium ion transport // inferred from
1426278_i	0.007329	3.02	-1.24	2.49	NM_029803	<i>Ifi272a</i>	interferon, alpha-inducible protein 27 like 2A	0007568 // tissue // inferred from direct assay//0009615 // response to virus // inferred from direct assay
1422555_i	0.003047	1.05	-1.24	1.07	NM_030303	<i>Gna13</i>	guanine nucleotide-binding protein, alpha 13	0001525 // angiogenesis // inferred from mutant phenotype//0001569 // patterning of blood vessels // inferred from mutant phenotype//0001701 // in utero embryonic
1416700_i	0.000107	3.02	-1.24	1.03	NM_010464	<i>Ndel1</i>	nuclear receptor subfamily 4, group A, member 1	0001938 // positive regulation of endothelial cell proliferation // not recorded//0002042 // cell migration involved in sprouting angiogenesis // not recorded//0006351 //
1423754_i	0.006463	1.05	-1.24	1.11	NM_025378	<i>Ifitm3</i>	interferon induced transmembrane protein 3	0008285 // negative regulation of cell proliferation // inferred from direct assay//0009607 // response to biotic stimulus // inferred from electronic annotation//0009615 // response
1426869_i	0.005196	1.12	-1.24	-1.03	NM_127506	<i>Boc</i>	biglycan cell adhesion molecule-related/down-regulated by oncogenes (Cdon)	0007155 // cell adhesion // inferred from electronic annotation//0007224 // smoothed signaling pathway // inferred from direct assay//0007411 // axon guidance // inferred from
1418115_i	0.001426	1.04	-1.24	-1.04	NM_001160180//NM	<i>Tor1aip2</i>	torsin A interacting protein 2	
1453285_i	0.009099	-1.01	-1					

Table S3

Gene ID	p (Corr) (Treatment-Strain)	FD (Vehicle)	FD (1 day)	FD (5 day)	RefSeq Transcript ID	Gene Symbol	Gene Title	Gene Ontology Biological Process
1415989_i	0.003481	1.17	-1.22	1.15	NM_011693	Vcam1	vascular cell adhesion molecule 1	0001666 // response to hypoxia // inferred from electronic annotation // 0002526 // acute inflammatory response // inferred from electronic annotation // 0002544 // chronic
1432282_i	0.007252	-1.32	-1.22	-1.05	NM_027249	Ticd2	TLC domain containing 2	0000188 // inactivation of MAPK activity // not recorded // 0001933 // negative regulation of protein phosphorylation // inferred from mutant phenotype // 0006470 // protein
1415834_i	0.001240	1.26	-1.22	1.44	NM_026268	Dusp6	dual specificity phosphatase 6	0007155 // cell adhesion // inferred from electronic annotation // 00019221 // cytokine-mediated signaling pathway // inferred from electronic annotation // 00030593 // neutrophil
1418806_i	0.002400	-1.36	-1.22	1.24	NM_001252651//NM_001252651	Csf3r	colony stimulating factor 3 receptor (granulocyte)	0006886 // intracellular protein transport // inferred from electronic annotation // 00007264 // small GTPase mediated signal transduction // inferred from electronic
1418250_i	0.002400	1.34	-1.22	1.58	NM_025404	Ar4ad	ADP-ribosylation factor-like 4D	0000381 // regulation of alternative mRNA splicing, via spliceosome // not recorded // 0006366 // transcription from RNA polymerase II promoter // inferred from sequence or
1416177_i	0.004796	1.03	-1.22	-1.08	NM_001252089//NM_001252089	Rbm11	RNA binding motif protein, X linked-like-1	0006636 // protein targeting to mitochondrion // not recorded // 0006810 // transport // inferred from electronic annotation // 0006811 // ion transport // inferred from electronic
1426118_i	0.003375	-1.01	-1.21	-1.05	NM_00109748//NM_00109748	Tamr40	translocase of outer mitochondrial membrane 40 homolog (yeast)	0001525 // angiogenesis // inferred from electronic annotation // 0006887 // exocytosis // inferred from electronic annotation // 0007275 // multicellular organismal development //
1416273_i	0.002415	1.12	-1.21	1.15	NM_009396	Tafai2	tumor necrosis factor, alpha-induced protein 2	0006810 // transport // inferred from electronic annotation // 0006888 // ER to Golgi vesicle-mediated transport // traceable author statement // 00015031 // protein transport //
1415766_i	0.008278	-1.09	-1.21	-1.10	NM_0011342	Sc22b	SEC22 vesicle trafficking protein homolog B (S. cerevisiae)	0001516 // prostaglandin biosynthetic process // inferred from direct assay // 00001516 // prostaglandin biosynthetic process // not recorded // 0001525 // angiogenesis // not
1417262_i	0.000738	2.19	-1.21	2.02	NM_0011198	Pigs2	prostaglandin-endoperoxide synthase 2	0014070 // response to organic cyclic compound // inferred from mutant phenotype // 0032713 // negative regulation of interleukin-4 production // inferred from mutant
1416111_i	0.006038	-1.03	-1.21	1.04	NM_009856	Ca83	CD83 antigen	0000188 // inactivation of MAPK activity // not recorded // 0002819 // regulation of adaptive immune response // inferred from mutant phenotype // 0006470 // protein
1417163_i	0.001264	1.28	-1.21	1.44	NM_022019	Dusp10	dual specificity phosphatase 10	0002021 // response to dietary excess // inferred from mutant phenotype // 0006810 // transport // inferred from electronic annotation // 00014823 // response to activity // inferred
1424735_i	0.001426	1.09	-1.21	1.24	NM_00164357//NM_00164357	Slc25a25	solute carrier family 25 (mitochondrial carrier, phosphate carrier), member 25	0001122 // negative regulation of transcription from RNA polymerase II promoter // not recorded // 0006351 // transcription, DNA-dependent // inferred from electronic
1417394_i	0.000000	-1.90	-1.21	1.89	NM_010637	Klf4	Kruppel-like factor 4 (gut)	0006810 // transport // inferred from electronic annotation // 00015031 // protein transport // inferred from electronic annotation // 0003030 // cell projection organization // inferred
1417471_i	0.009935	1.01	-1.20	-1.23	NM_133825	E1Erd622e	DNA segment, Chr 1, ERATO Doi 622, expressed	0006260 // DNA replication // inferred from electronic annotation // 0006468 // protein phosphorylation // not recorded // 0007049 // cell cycle // inferred from electronic
1418334_i	0.001703	1.16	-1.20	1.06	NM_001190717//NM_001190717	Dbf4	DBF4 homolog (S. cerevisiae)	0000660 // protein import into nucleus, translocation // inferred from direct assay // 0007253 // cytoplasmic sequestration of NF-kappaB // not recorded // 00010745 // negative
1420088_i	0.000137	1.26	-1.20	1.43	NM_010907	Nfkbia	nuclear factor of kappa light polypeptide gene enhancer in B cells inhibitor, alpha	0006468 // protein phosphorylation // inferred from electronic annotation // 0007229 // integrin-mediated signaling pathway // inferred from mutant phenotype // 0007229 //
1428491_i	0.000341	1.06	-1.20	-1.02	NM_178577	Comm10	COMM domain containing 10	0006468 // protein phosphorylation // not recorded // 0008283 // cell proliferation // not recorded // 0009103 // lipopolysaccharide biosynthetic process // inferred from electronic
1419526_i	0.000250	1.13	-1.20	1.09	NM_012268	Fgr	Gardner-Rasheed feline sarcoma viral (Fgr) oncogene homolog	0001122 // negative regulation of transcription from RNA polymerase II promoter // inferred from direct assay // 0006351 // transcription, DNA-dependent // inferred from electronic
1423006_i	0.000540	1.26	-1.20	1.37	NM_008842	Pim1	proliferin integration site 1	0006546 // glycine catabolic process // inferred from electronic annotation // 0006783 // heme biosynthetic process // inferred from electronic annotation
1421111_i	0.009255	-1.00	-1.20	1.04	NM_019743//NM_019743	Ryb1p	predicted gene 6910//RING1 and YY1 binding protein	0001122 // negative regulation of transcription from RNA polymerase II promoter // not recorded // 0001501 // skeletal system development // inferred from mutant
1435808_i	0.002084	1.08	-1.20	-1.16	NM_001270791//NM_001270791	Irb57	IRB57, iron-sulfur cluster assembly homolog (S. cerevisiae)	0000982 // cell morphogenesis // inferred from electronic annotation // 0006983 // ER overload response // inferred from direct assay // 0006987 // activation of signaling protein
1451924_i	0.001349	1.55	-1.20	1.64	NM_010104	Edn1	endothelin 1	0001184 // nuclear-transcribed mRNA catabolic process, nonsense-mediated decay // not recorded // 0006396 // RNA processing // inferred from electronic annotation // 0006397 //
1425913_i	0.005600	1.02	-1.19	-1.01	NM_001164566//NM_001164566	Spatz1	spermatogenesis associated, serine-rich 2-like	0001764 // neuron migration // not recorded // 0003009 // skeletal muscle contraction // inferred from electronic annotation // 0006200 // ATP catabolic process // not
1416064_i	0.006221	1.22	-1.19	-1.05	NM_001163434//NM_001163434	Hspa5	heat shock protein 5	0006461 // protein complex assembly // not recorded // 0006935 // chemotaxis // inferred from electronic annotation // 0006955 // immune response // not recorded // 00010628 //
1418119_i	0.001100	1.00	-1.19	-1.03	NM_001102407//NM_001102407	Rbm8a	RNA binding motif protein 8a	0006629 // lipid metabolic process // inferred from electronic annotation // 0006694 // steroid biosynthetic process // inferred from electronic annotation // 0006695 // cholesterol
1426465_i	0.000412	1.25	-1.19	-1.10	NM_010480	Hsp90aa1	heat shock protein 90, alpha (cytosolic), class A member 1	0006351 // transcription, DNA-dependent // inferred from electronic annotation // 00043086 // negative regulation of catalytic activity // not recorded // 00071230 // cellular response
1448995_i	0.009515	-1.04	-1.18	1.18	NM_019932	Pf4	platelet factor 4	0006606 // protein import into nucleus // inferred from direct assay // 0006611 // protein export from nucleus // not recorded // 0006810 // transport // inferred from electronic
1427893_i	0.005307	1.10	-1.18	1.18	NM_026784//NM_026784	Pmkv	phosphomevalonate kinase	0006468 // protein phosphorylation // not recorded // 0008283 // cell proliferation // not recorded // 0009103 // lipopolysaccharide biosynthetic process // inferred from electronic
1426726_i	0.002299	-1.03	-1.18	1.04	NM_001163818//NM_001163818	Gm8801	protein phosphatase 1, regulatory subunit 10 pseudogene // protein phosphatase 1, regulatory subunit 10 pseudogene	0000982 // cell morphogenesis // inferred from electronic annotation // 0006983 // ER overload response // inferred from direct assay // 0006987 // activation of signaling protein
1418274_i	0.001118	1.02	-1.18	-1.06	NM_026532//NR_033_033	Gm10349	predicted gene 10349 // predicted pseudogene 9386 // nuclear transport factor	0000184 // nuclear-transcribed mRNA catabolic process, nonsense-mediated decay // not recorded // 0006396 // RNA processing // inferred from electronic annotation // 0006397 //
1435644_i	0.000764	1.13	-1.18	1.10	NM_177268	Sl3p2d2b	Sl3 and PX domains 2b	0001764 // neuron migration // not recorded // 0003009 // skeletal muscle contraction // inferred from electronic annotation // 0006200 // ATP catabolic process // not
1416953_i	0.002724	1.29	-1.18	1.22	NM_010217	Cxgf	connective tissue growth factor	0006461 // protein complex assembly // not recorded // 0006935 // chemotaxis // inferred from electronic annotation // 0006955 // immune response // not recorded // 00010628 //
1418274_i	0.003366	1.02	-1.18	-1.06	NM_026532//NR_033_033	Gm10349	predicted gene 10349 // predicted pseudogene 9386 // nuclear transport factor	0006629 // lipid metabolic process // inferred from electronic annotation // 0006694 // steroid biosynthetic process // inferred from electronic annotation // 0006695 // cholesterol
1423452_i	0.003595	1.15	-1.17	1.35	NM_133810	Slk17b	serine/threonine kinase 17b (apoptosis-inducing)	0006351 // transcription, DNA-dependent // inferred from electronic annotation // 00043086 // negative regulation of catalytic activity // not recorded // 00071230 // cellular response
1424238_i	0.001887	-1.30	-1.17	-1.06	NM_153056	Sirt7	sirtuin 7 (silent mating type information regulation 2, homolog) 7 (S. cerevisiae)	0006606 // protein import into nucleus // inferred from direct assay // 0006611 // protein export from nucleus // not recorded // 0006810 // transport // inferred from electronic
1438578_i	0.006131	1.19	-1.17	1.10	NM_133700	Btdb10	BTB (POZ) domain containing 10	0001501 // skeletal system development // inferred from mutant phenotype // 0001501 // skeletal system development // not recorded // 0001654 // eye development // inferred
1421811_i	0.000129	1.59	-1.17	1.83	NM_011580//NM_011580	Pald1	phosphatase domain containing, paladin 1 // thrombospondin 1	0001502 // cartilage condensation // inferred from direct assay // 0001503 // ossification // inferred from mutant phenotype // 0001525 // angiogenesis // inferred from direct
1438767_i	0.000969	1.20	-1.17	1.46	NM_001013365	Osm	oncostatin M	0006606 // protein import into nucleus // inferred from direct assay // 0006611 // protein export from nucleus // not recorded // 0006810 // transport // inferred from electronic
1426298_i	0.001330	1.42	-1.16	1.20	NM_010574	Irx2	Iroquois related homeobox 2 (Drosophila)	0006468 // protein phosphorylation // not recorded // 0006915 // apoptotic process // inferred from electronic annotation // 0006917 // induction of apoptosis // not
1425548_i	0.000057	-1.39	-1.16	1.22	NM_010734	Lst1	leukocyte specific transcription 1	0001122 // negative regulation of transcription from RNA polymerase II promoter // not recorded // 0001701 // in utero embryonic development // inferred from genetic
1421679_i	0.003154	1.42	-1.16	1.72	NM_001111099//NM_001111099	Cdkn1a	cyclin-dependent kinase inhibitor 1A (P21)	0000187 // activation of MAPK activity // not recorded // 0001937 // negative regulation of endothelial cell proliferation // not recorded // 0001953 // negative regulation of cell-
1418401_i	0.001240	1.18	-1.16	1.09	NM_0011638054//NM_0011638054	Dusp16	dual specificity phosphatase 16	0006915 // apoptotic process // inferred from direct assay // 0006955 // immune response // inferred from electronic annotation // 0007422 // peripheral nervous system
1421151_i	0.001118	-1.00	-1.16	1.19	NM_010139	Ephr2	Eph receptor A2	0001656 // metanephros development // inferred from expression pattern // 0006355 // regulation of transcription, DNA-dependent // inferred from electronic annotation // 00072086
1430498_i	0.002683	-1.25	-1.16	1.01	NM_027193	Dp55	DPS5 homolog (S. cerevisiae)	0009092 // cell morphogenesis // inferred from electronic annotation // 0006955 // immune response // inferred from electronic annotation // 0008360 // regulation of cell shape //
1416213_i	0.009719	1.03	-1.16	-1.04	NM_011512	Surf4	surfactant protein 4	0000079 // regulation of cyclin-dependent protein serine/threonine kinase activity // inferred from mutant phenotype // 0000082 // G1/S transition of mitotic cell cycle // not
1426238_i	0.000707	1.13	-1.16	1.61	NM_009755//NR_033_033	Bmp1	bone morphogenetic protein 1	0000188 // inactivation of MAPK activity // inferred from direct assay // 0006470 // protein dephosphorylation // not recorded // 00016310 // phosphorylation // inferred from
1417724_i	0.004313	1.07	-1.15	1.02	NM_011568//NM_011568	Allyrf2	Allyl/REF export factor // Allyl/REF export factor 2	0001501 // skeletal system development // inferred from mutant phenotype // 0001525 // angiogenesis // inferred from electronic annotation // 0001568 // blood vessel development
1437884_i	0.003884	1.12	-1.15	1.16	NM_029466	Ar5b	ADP-ribosylation factor-like 5B	0006152 // metabolic process // inferred from electronic annotation // 0017183 // peptidyl-dipeptidase biosynthetic process from peptidyl-histidine // inferred from electronic
1451139_i	0.007295	1.12	-1.15	1.11	NM_028064	Sc39a4	solute carrier family 39 (zinc transporter), member 4	0007030 // Golgi organization // not recorded // 00010638 // positive regulation of organelle organization // not recorded
1449110_i	0.001485	1.70	-1.15	1.65	NM_007483	Rhb6	ras homolog gene family, member 8	0001503 // ossification // inferred from electronic annotation // 0006508 // proteolysis // not recorded // 0007275 // multicellular organismal development // inferred from electronic
1416364_i	0.001710	1.26	-1.15	-1.01	NM_008302	Hsp90ab1	heat shock protein 90 alpha (cytosolic), class B member 1	0006397 // mRNA processing // inferred from electronic annotation // 0006406 // mRNA export from nucleus // not recorded // 00006810 // transport // inferred from electronic
1452734_i	0.006790	-1.01	-1.15	-1.06	NM_001083938//NM_001083938	Rnaset2a	ribonuclease 72A // ribonuclease T2B	0006886 // intracellular protein transport // inferred from electronic annotation // 0007186 // G-protein coupled receptor signaling pathway // inferred from electronic
1426597_i	0.008457	1.08	-1.14	1.19	NM_001205173//NM_001205173	Ifj2	intermediate filament family orphan 2	0006810 // transport // inferred from electronic annotation // 0006811 // ion transport // inferred from electronic annotation // 0006829 // zinc ion transport // inferred from direct
1426495_i	0.009605	1.02	-1.14	-1.07	NM_024254	Katnbl1	katanin p80 subunit B like 1	0009010 // cytokinesis // not recorded // 0001525 // angiogenesis // inferred from electronic annotation // 0006184 // GTP catabolic process // inferred from electronic
1423013_i	0.000129	1.33	-1.14	1.45	NM_010426	Foxf1	forkhead box F1	0001890 // placenta development // inferred from mutant phenotype // 0006457 // protein folding // inferred from electronic annotation // 0006950 // response to stress // inferred
1428167_i	0.008926	1.06	-1.14	1.14	NM_00101880//NM_00101880	Myp1l	myosin protein zero-like 1	0006401 // RNA catabolic process // inferred from sequence or structural similarity // 00090305 // nucleic acid phosphodiester bond hydrolysis // inferred from electronic annotation
1437232_i	0.001391	-1.00	-1.14	-1.78	NM_007771	Cry1	cryptochrome 1 (photolyase-like)	0000122 // negative regulation of transcription from RNA polymerase II promoter // not recorded // 0006281 // DNA repair // inferred from electronic annotation // 0006351 //
1430535_i	0.001596	1.29	-1.14	1.23	NM_001081229//NM_001081229	Tsc2d2	TSC2 domain-containing protein, member 2	0006355 // regulation of transcription, DNA-dependent // inferred from electronic annotation // 0006970 // response to osmotic stress // inferred from direct assay
1426722_i	0.002329	1.21	-1.14	1.28	NM_175121	Slc38a2	solute carrier family 38, member 2	0003333 // amino acid transmembrane transport // inferred from direct assay // 0006810 // transport // inferred from electronic annotation // 0006811 // ion transport // inferred
1423619_i	0.005070	1.85	-1.14	2.15	NM_009026	Rsd1	RAS, dexamethasone-induced 1	0006184 // GTP catabolic process // inferred from electronic annotation // 0006886 // intracellular protein transport // inferred from electronic annotation // 0006913 //
1417483_i	0.000041	1.57	-1.13	2.14	NM_001159394//NM_001159394	Nfkbi2	nuclear factor of kappa light polypeptide gene enhancer in B cells inhibitor, zeta	0006351 // transcription, DNA-dependent // inferred from electronic annotation // 0006355 // regulation of transcription, DNA-dependent // inferred from electronic
1422014_i	0.007690	1.09	-1.13	1.03	NM_053242//NM_053242	Foxp2	forkhead box P2	0000122 // negative regulation of transcription from RNA polymerase II promoter // not recorded // 0000122 // negative regulation of transcription from RNA polymerase II promoter
1418280_i	0.001192	1.30	-1.13	1.21	NM_011803	Klf6	Kruppel-like factor 6	0006351 // transcription, DNA-dependent // inferred from electronic annotation // 0006355 // regulation of transcription, DNA-dependent // inferred from electronic
1437649_i	0.001726	1.03	-1.13	-1.01	NM_011149	Ppilb	peptidylprolyl isomerase B	0004413 // protein peptidyl-prolyl isomerization // inferred from electronic annotation // 0006457 // protein folding // inferred from electronic annotation
1416256_i	0.008294	1.10	-1.13	1.13	NM_011655	Tubb5	tubulin, beta 5 class I	0006184 // GTP catabolic process // inferred from electronic annotation // 0006457 // protein folding // traceable author statement // 0007017 // microtubule-based process //
1425364_i	0.003443	1.15	-1.13	1.09	NM_001161413//NM_001161413	Slc3a2	solute carrier family 3 (activators of dibasic and neutral amino acid transport),	0005975 // carbohydrate metabolic process // inferred from electronic annotation // 0006810 // transport // inferred from electronic annotation // 0006865 // amino acid transport //
1433975_i	0.009871	-1.23	-1.12	-1.06	NM_194444//NM_194444	Cdk10	cyclin-dependent kinase 10	0006468 // protein phosphorylation // inferred from electronic annotation // 00061310 // phosphorylation // inferred from electronic annotation
1417409_i	0.000618	1.49	-1.12	1.68	NM_010591	Jul	Juvenile polyposis syndrome 1	0001525 // angiogenesis // inferred from mutant phenotype // 0001525 // angiogenesis // not recorded // 0001774 // microgial cell activation // inferred from mutant
1426262_i	0.003970	1.05	-1.11	1.15	NM_179520	Adnp2	ADNP homeobox 2	0006351 // transcription, DNA-dependent // inferred from electronic annotation // 0006355 // regulation of transcription, DNA-dependent // inferred from electronic
1425891_i	0.007429	-1.32	-1.11	-1.06	NM_025768	Grt1p	GRG regulated TBC protein 1	0032313 // regulation of Rab GTPase activity // inferred from electronic annotation // 0003285 // positive regulation of Rab GTPase activity // inferred from electronic
1418296_i	0.009187	-1.23	-1.11	-1.04	NM_001111073//NM_001111073	Fxyd5	FXD domain-containing ion transport regulator 5	0006810 // transport // inferred from electronic annotation // 0006811 // ion transport // inferred from electronic annotation
1426721_i	0.001264	1.30	-1.11	1.33	NM_178892	Tiparp	TCD-inducible poly(ADP-ribose) polymerase	0001510 // vasculogenesis // inferred from mutant phenotype // 0001832 // kidney development // inferred from mutant phenotype // 0006471 // protein ADP-ribosylation // inferred
1452013_i	0.006082	-1.16	-1.10	-1.41	NM_009728	Atp10a	ATPase, class V, type 10A	0006810 // cation transport // inferred from electronic annotation // 0008152 // metabolic process // inferred from electronic annotation // 00015914 // phospholipid transport //
1424569_i	0.009159	-1.16	-1.10	1.06	NM_145975	Ddx46	DEAD (Asp-Glu-Ala-Asp) box polypeptide 46	0006397 // mRNA processing // inferred from electronic annotation // 0008380 // RNA splicing // inferred from electronic annotation
1423798_i	0.000958	1.08	-1.10	1.05	NM_011508//NM_011508	Ej1	eukaryotic translation initiation factor 1 // predicted pseudogene	0006412 // translation // inferred from electronic annotation // 0006413 // translational initiation // inferred from electronic annotation // 0009048 // dosage compensation by
1435250_i	0.001186	1.16	-1.10	-1.03	NM_001159595//NM_001159595	Ints8	integrator complex subunit 8	0016180 // snRNA processing // not recorded
1450792_i	0.009935	-1.39	-1.10	-1.00	NM_011662	Tyrbp	TYRO protein tyrosine kinase binding protein	0002281 // macrophage activation involved in immune response // inferred from mutant phenotype // 0002283 // neutrophil activation involved in immune response // inferred from
1416851_i	0.001097	1.12	-1.10	-1.11	NM_133726	Slc13	suppression of tumorigenicity 13	0006457 // protein folding // not recorded // 0051260 // protein homooligomerization // not recorded // 0061084 // negative regulation of protein folding // not
1424221_i	0.006256	1.15	-1.10	1.06	NM_144796	Susd4	sushi domain containing 4	0001503 // ossification // inferred from electronic annotation // 0001525 // angiogenesis // inferred from electronic annotation // 0001541 // ovarian follicle development // inferred
1416572_i	0.000638	1.34	-1.09	1.42	NM_008038	Mmp14	matrix metalloprotein	

Table S3

Gene ID	p (Corr) (Treatment-Strain)	FD (Vehicle)	FD (1 day)	FD (5 day)	RefSeq Transcript ID	Gene Symbol	Gene Title	Gene Ontology Biological Process	
1420494_i	0.002989	1.10	-1.07	1.11	NM_019639	<i>Ubc</i>	ubiquitin C	0007141 // male meiosis I // inferred from mutant phenotype // 0007144 // female meiosis I // inferred from mutant phenotype // 0008584 // male gonad development // inferred	
1424605_i	0.001427	1.27	-1.07	1.38	NM_001163144//NM	<i>Pcsk5</i>	proprotein convertase subtilisin/kexin type 5	0001822 // kidney development // inferred from mutant phenotype // 0001822 // kidney development // not recorded // 0002001 // renin secretion into blood stream // inferred from	
1425868_i	0.00621	1.52	-1.07	-1.22	NM_175666	<i>Hist2h2bb</i>	histone cluster 2, H2bb	0000334 // nucleosome assembly // inferred from electronic annotation	
1422054_i	0.003346	1.17	-1.06	1.25	NM_001039090//NM	<i>Skil</i>	SKI-like	0000122 // negative regulation of transcription from RNA polymerase II promoter // inferred from direct assay // 0000122 // negative regulation of transcription from RNA polymerase	
1421186_i	0.006371	-1.35	-1.06	1.02	NM_009915	<i>Cor2</i>	chemokine (C-C motif) receptor 2	0001525 // angiogenesis // traceable author statement // 0001666 // response to hypoxia // inferred from electronic annotation // 0001974 // blood vessel remodeling // inferred	
1448325_i	0.000015	1.72	-1.06	2.13	NM_000654	<i>Ppp1r15a</i>	protein phosphatase 1, regulatory (inhibitor) subunit 15A	0006417 // regulation of translation // inferred from electronic annotation // 0006915 // apoptotic process // inferred from electronic annotation // 0006950 // response to stress //	
1426165_i	0.008860	1.03	-1.06	1.14	NM_008810	<i>Casp2</i>	caspase 3	0001782 // B cell homeostasis // inferred from mutant phenotype // 0001836 // release of cytochrome c from mitochondria // inferred from genetic interaction // 0008309 //	
1417061_i	0.000899	-1.25	-1.06	1.01	NM_016917	<i>Slc40a1</i>	solute carrier family 40 (iron-regulated transporter), member 1	0002260 // lymphocyte homeostasis // inferred from mutant phenotype // 0003158 // endothelium development // inferred from mutant phenotype // 0006810 // transport //	
1422568_i	0.000707	1.02	-1.06	1.12	NM_023668	<i>Ndel1</i>	nuclear distribution gene E-like homolog 1 (A. nidulans)	0000226 // microtubule cytoskeleton organization // inferred from genetic interaction // 0001764 // neuron migration // inferred from genetic interaction // 0001833 // inner cell mass	
1436397_i	0.003150	-1.51	-1.05	-1.26	NM_001168615//NM	<i>Tjfab</i>	TRAF-interacting protein with forkhead-associated domain, family member 8		
1416630_i	0.006857	1.24	-1.04	1.18	NM_008321	<i>Id3</i>	inhibitor of DNA binding 3	0000122 // negative regulation of transcription from RNA polymerase II promoter // inferred from direct assay // 0000122 // negative regulation of transcription from RNA polymerase	
1440235_i	0.002670	-1.36	-1.04	1.10	NM_001081053	<i>Itpa10</i>	integrin, alpha 10	0007155 // cell adhesion // inferred from electronic annotation // 0007229 // integrin-mediated signaling pathway // inferred from electronic annotation	
1452262_i	0.003183	-1.07	-1.04	-1.24	NM_021296	<i>Grpel2</i>	GrPE-like 2, mitochondrial	0006457 // protein folding // inferred from electronic annotation	
1420123_i	0.004067	-1.21	-1.04	-1.17	NM_133986	<i>Tcto</i>	T cell leukemia translocation altered gene		
1452623_i	0.003894	-1.31	-1.04	-1.62	NM_172392	<i>Zfp759</i>	zinc finger protein 759	0006355 // regulation of transcription, DNA-dependent // inferred from electronic annotation	
1425577_i	0.002215	-1.26	-1.03	-1.11	NM_001253752//NM	<i>Zmym5</i>	zinc finger, MYM-type 5		
1430614_i	0.007630	-1.11	-1.03	-1.25	NM_028883	<i>Tidc1</i>	TBC/LysM associated domain containing 1		
1418798_i	0.005533	-1.49	-1.03	-1.32	NM_019584	<i>Srp3</i>	serine/arginine-rich protein specific kinase 3	0006468 // protein phosphorylation // inferred from direct assay // 0006468 // protein phosphorylation // inferred from electronic annotation // 0007275 // multicellular organismal	
1427576_i	0.002040	-1.39	-1.03	-1.41		<i>Igk-v28//Ighv6-14</i>	immunoglobulin kappa chain variable 28 [V28] // immunoglobulin kappa variable 6-		
1429049_i	0.001287	1.16	-1.03	1.29	NM_001195025//NM	<i>Nuak2</i>	NUAK family, SNF1-like kinase, 2	0006468 // protein phosphorylation // inferred from electronic annotation // 0006468 // protein phosphorylation // not recorded // 0006915 // apoptotic process // inferred from	
1421824_i	0.008880	1.16	-1.03	1.02	NM_001145947//NM	<i>Bace1</i>	beta-site APP cleaving enzyme 1	0005608 // proteolysis // inferred from direct assay // 0006508 // proteolysis // not recorded // 0005435 // beta-amyloid metabolic process // not recorded	
1442339_i	0.002712	-1.52	-1.02	1.55	NM_173869	<i>Sfo2l1</i>	sterin a21	0010466 // negative regulation of peptidase activity // inferred from electronic annotation // 0010951 // negative regulation of endopeptidase activity // inferred from electronic	
1444589_i	0.007194	-1.24	-1.02	-1.34	NM_001205095	<i>Gm4944</i>	predicted gene 4944	0006355 // regulation of transcription, DNA-dependent // inferred from electronic annotation	
1452769_i	0.006870	-1.06	-1.02	-1.22	NM_001166553//NM	<i>Rnf145</i>	ring finger protein 145		
1430073_i	0.002748	-1.26	-1.02	-1.30	NM_029116	<i>Kbtbd11</i>	kelch repeat and BTB (POZ) domain containing 11		
1424669_i	0.006322	-1.10	-1.02	-1.32	NM_026752	<i>Zfyve21</i>	zinc finger, FYVE domain containing 21		
1416041_i	0.000642	1.63	-1.02	1.63	NM_001161845//NM	<i>Sgk1</i>	serum/glucocorticoid regulated kinase 1	0006468 // protein phosphorylation // inferred from direct assay // 0006883 // cellular sodium ion homeostasis // not recorded // 0006915 // apoptotic process // inferred from	
1416359_i	0.009197	1.26	-1.01	1.28	NM_130796	<i>Snx18</i>	sorting nexin 18	0006810 // transport // inferred from electronic annotation // 0006897 // endocytosis // not recorded // 0007154 // cell communication // inferred from electronic	
1417465_i	0.008406	1.03	-1.01	-1.09	NM_008033	<i>Fnta</i>	farnesyltransferase, CAAX box, alpha	0007528 // neuromuscular junction development // inferred from mutant phenotype // 0008284 // positive regulation of cell proliferation // not recorded // 0010035 // response to	
1434896_i	0.007826	-1.16	-1.01	-1.37	NM_029952	<i>Zfp955a</i>	zinc finger protein 955A	0006355 // regulation of transcription, DNA-dependent // inferred from electronic annotation	
1448419_i	0.000147	-1.40	-1.01	-1.20	NM_025390	<i>Pap4</i>	processing of precursor 4, ribonuclease P/MRP family, (S. cerevisiae)	0006364 // RNA processing // inferred from electronic annotation // 0006379 // mRNA cleavage // inferred from electronic annotation // 0008033 // RNA processing // inferred from	
1421304_i	0.002967	-1.33	-1.02	-1.55	NM_029385	<i>Nudt16</i>	nucleoside diphosphate-linked moiety X)-type motif 16	0006382 // adenosine to inosine editing // not recorded // 0006402 // mRNA catabolic process // inferred from mutant phenotype // 0006402 // mRNA catabolic process // not	
1418523_i	0.000200	-1.13	-1.01	1.14	NM_0117190	<i>Arh16</i>	aridase homolog 2 (Drosophila)	0000209 // protein polyubiquitination // not recorded // 0006511 // ubiquitin-dependent protein catabolic process // inferred from physical interaction // 0016567 // protein	
1419598_i	0.008294	-1.29	-1.01	-1.28	NM_001040684//NM	<i>Hsd3b7</i>	hydroxy-delta-5-steroid dehydrogenase, 3 beta- and steroid delta-isomerase 7	0001558 // regulation of cell growth // not recorded // 0006694 // steroid biosynthetic process // inferred from electronic annotation // 0008152 // metabolic process // inferred from	
1435261_i	0.002254	-1.29	-1.01	-1.39	NM_198967	<i>Tmtc1</i>	transmembrane and tetratricopeptide repeat containing 1	0006396 // RNA processing // inferred from electronic annotation	
1448010_i	0.001997	-1.61	1.01	-1.02	NR_029555	<i>A430104N18IK1</i>	RIKEN cDNA A430104N18 gene // microRNA 142	0071391 // cellular response to estrogen stimulus // inferred from direct assay	
1448010_i	0.001997	-1.61	1.01	-1.02	NR_029555	<i>A430104N18IK1</i>	RIKEN cDNA A430104N18 gene // microRNA 142	0071391 // cellular response to estrogen stimulus // inferred from direct assay	
1423622_i	0.002737	1.21	1.02	1.49	NM_001025442//NM	<i>Con11</i>	cyclin 11	0000079 // regulation of cyclin-dependent protein serine/threonine kinase activity // inferred from electronic annotation // 0006351 // transcription, DNA-dependent // inferred from	
1436548_i	0.001521	-1.25	1.02	-1.19	NM_001076681	<i>Lymn9</i>	LYR motif containing 9		
1435304_i	0.006256	1.08	1.02	-1.03	NM_011434	<i>Sod1</i>	superoxide dismutase 1, soluble	0000187 // activation of MAPK activity // inferred from direct assay // 0000302 // response to reactive oxygen species // inferred from mutant phenotype // 0000303 // response to	
1416468_i	0.003580	-1.07	1.02	-1.28	NM_013467	<i>Aldh1a1</i>	aldehyde dehydrogenase family 1, subfamily A1	0001822 // kidney development // inferred from electronic annotation // 0001889 // liver development // inferred from electronic annotation // 0002072 // optic cup morphogenesis	
1421304_i	0.006538	-1.38	1.02	-1.05	NM_001170851//NM	<i>Klra2</i>	killer cell lectin-like receptor, subfamily A, member 2	0007155 // cell adhesion // inferred from electronic annotation	
1437362_i	0.003723	-1.31	1.02	-1.16	NM_030016	<i>Tmt13</i>	IRNA methyltransferase 13	0008003 // RNA processing // inferred from electronic annotation // 0032259 // methylation // inferred from electronic annotation	
1444890_i	0.002898	1.51	1.02	1.48	NM_144549	<i>Trib1a1</i>	tribbles homolog 1 (Drosophila)	0006468 // protein phosphorylation // traceable author statement // 0006469 // negative regulation of protein kinase activity // not recorded // 0007254 // JNK cascade // not	
1421129_i	0.006200	-1.59	1.02	-1.55	NM_001094066//NM	<i>Zfp366</i>	zinc finger protein 366 (Kruppel-like)	0006355 // regulation of transcription, DNA-dependent // inferred from electronic annotation // 0051028 // negative regulation of transcription during meiosis // not recorded	
1448252_i	0.007803	1.00	1.02	-1.05	NM_018796	<i>Eof1b2</i>	eukaryotic translation elongation factor 1 beta 2	0006412 // translation // inferred from electronic annotation // 0006414 // translational elongation // inferred from sequence or structural similarity	
1426505_i	0.002647	-1.32	1.03	-1.02	NM_001077496//NM	<i>Ev12a-ev12b//Ev12i</i>	Ev12a-Ev12b readthrough // Ecotropic viral integration site 2b // ecotropic viral		
1425305_i	0.009379	1.25	1.03	1.29	NM_001081684//NM	<i>Zfb212</i>	zinc finger and BTB domain containing 21	0045892 // negative regulation of transcription, DNA-dependent // not recorded	
1418398_i	0.009851	-1.40	1.03	-1.23	NM_001128080//NM	<i>Tspan32</i>	tetraspanin 32	0007010 // cytoskeleton organization // inferred from mutant phenotype // 0007229 // integrin-mediated signaling pathway // inferred from mutant phenotype // 0007596 // blood	
1420993_i	0.003768	-1.49	1.03	-1.52	NM_001159407//NM	<i>B3gn15</i>	UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 5	0006486 // protein glycosylation // inferred from electronic annotation // 0007275 // multicellular organismal development // inferred from electronic annotation // 0007417 //	
1421618_i	0.005868	-1.23	1.03	1.03	NM_053214	<i>Myo1f</i>	myosin IF	0002446 // neutrophil mediated immunity // inferred from mutant phenotype // 0007162 // negative regulation of cell adhesion // inferred from mutant phenotype // 0003035 // cell	
1425450_i	0.001596	-2.34	1.03	-1.42	NM_145126//NM_001	<i>Ch13i4//Ch13i3</i>	chitinase 3-like 4 // chitinase 3-like 3	0005975 // carbohydrate metabolic process // inferred from electronic annotation // 0006032 // chitin catabolic process // inferred from electronic annotation // 0006954 //	
1428239_i	0.004648	-1.35	1.03	-1.03	NM_177268	<i>Ankr16</i>	ankyrin repeat domain 16		
1426506_i	0.005539	-1.33	1.03	-1.03	NM_001033711//NM	<i>Ev12a//Ev12a-ev12i</i>	ecotropic viral integration site 2a // Ev12a-Ev12b readthrough // ecotropic viral		
1432492_i	0.006896	-1.62	1.03	-1.01	NM_025325	<i>Haoa</i>	3-hydroxyanthranilate 3,4-dioxygenase	0009435 // NAD biosynthetic process // inferred from electronic annotation // 0010043 // response to zinc ion // not recorded // 0019363 // pyridine nucleotide biosynthetic process	
1416442_i	0.004016	3.02	1.04	2.75	NM_010499	<i>Ier2</i>	immediate early response 2		
1439810_i	0.006211	-1.15	1.04	-1.03	NM_146011	<i>Arhgap9</i>	Rho GTPase activating protein 9	0007165 // signal transduction // inferred from electronic annotation // 0043547 // positive regulation of GTPase activity // not recorded	
1417142_i	0.002712	-1.01	1.04	-1.15	NM_024202//NR_033	<i>Fam120b</i>	family with sequence similarity 120, member B	0006351 // transcription, DNA-dependent // inferred from electronic annotation // 0006355 // regulation of transcription, DNA-dependent // inferred from electronic	
1419465_i	0.009935	-1.11	1.04	-1.24	NM_028186	<i>Nkd2</i>	naked cuticle 2 homolog (Drosophila)	0006810 // transport // inferred from electronic annotation // 0006887 // exocytosis // inferred from electronic annotation // 0010954 // positive regulation of protein processing //	
1450480_i	0.004607	-1.10	1.04	-1.06	NM_001038018//NM	<i>Grk6</i>	G protein-coupled receptor kinase 6	0002029 // desensitization of G-protein coupled receptor protein signaling pathway // not recorded // 0006468 // protein phosphorylation // inferred from electronic	
1416767_i	0.004813	-1.06	1.04	-1.11	NM_133697	<i>Sam14</i>	small integral membrane protein 14		
1428903_i	0.005443	-1.25	1.05	-1.27	NM_001160043//NM	<i>Exo5</i>	exonuclease 5	0006281 // DNA repair // inferred from electronic annotation // 0006974 // response to DNA damage stimulus // inferred from electronic annotation // 0036297 // interstrand cross-	
1423602_i	0.006016	-1.22	1.05	-1.26	NM_009421	<i>Trsf1</i>	TNF receptor-associated factor 1	0006915 // apoptotic process // inferred from electronic annotation // 0007165 // signal transduction // inferred from electronic annotation // 0042981 // regulation of apoptotic	
1456602_i	0.004114	-1.02	1.05	-1.20	NM_001033321	<i>Tmem231</i>	transmembrane protein 231	0001701 // in utero embryonic development // inferred from mutant phenotype // 0007224 // smoothed signaling pathway // inferred from mutant phenotype // 0030030 // cell	
1421098_i	0.002850	-1.73	1.05	-1.17	NM_019992	<i>Stop1</i>	signal transducing adaptor family member 1	0007169 // transmembrane receptor protein tyrosine kinase signaling pathway // inferred from direct assay // 0030099 // myeloid cell differentiation // traceable author statement	
1418081_i	0.002112	-1.18	1.05	-1.16	NM_025362	<i>Dnaj30</i>	DnaJ (Hsp40) homolog, subfamily C, member 30	0006457 // protein folding // inferred from electronic annotation	
1416200_i	0.006335	1.40	1.05	1.00	NM_001164724//NM	<i>I33</i>	interleukin 33	0002686 // negative regulation of leukocyte migration // inferred from genetic interaction // 0002826 // negative regulation of T-helper 1 type immune response // inferred from	
1455665_i	0.002478	-1.11	1.05	-1.23	NM_001081150	<i>Lor1f1</i>	LON peptidase N-terminal domain and ring finger 1	0006508 // proteolysis // inferred from electronic annotation	
1455820_i	0.001101	-1.11	1.06	-1.05	NM_172255	<i>Wdr11</i>	WD repeat domain 11		
1422357_i	0.003458	-1.13	1.04	-1.28	NM_009099	<i>Cyp2b10</i>	cytochrome P450, family 2, subfamily b, polypeptide 10	0006805 // xenobiotic metabolic process // not recorded // 0008202 // steroid metabolic process // not recorded // 0001714 // drug metabolic process // not recorded // 00042180 //	
1416250_i	0.002745	1.97	1.06	2.38	NM_007570	<i>Bip2</i>	B cell translocation gene 2, anti-proliferative	0006351 // transcription, DNA-dependent // inferred from electronic annotation // 0006355 // regulation of transcription, DNA-dependent // inferred from electronic	
1421003_i	0.008733	-1.07	1.06	1.06	NM_001122992//NM	<i>Gmeb1</i>	glucocorticoid modulatory element binding protein 1	0006351 // transcription, DNA-dependent // inferred from electronic annotation // 0006355 // regulation of transcription, DNA-dependent // inferred from direct assay	
1448310_i	0.008195	-1.16	1.06	-1.03	NM_001163780//NM	<i>Ick</i>	intestinal cell kinase	0006468 // protein phosphorylation // inferred from direct assay // 0006468 // protein phosphorylation // inferred from electronic annotation // 0006468 // protein phosphorylation //	
1418277_i	0.005398	-1.07	1.06	-1.07	NM_018739	<i>Rp9</i>	retinitis pigmentosa 9 (human)		
1436171_i	0.006652	-1.23	1.07	-1.02	NM_001005508	<i>Arhgap30</i>	Rho GTPase activating protein 30	0007165 // signal transduction // inferred from electronic annotation // 0043547 // positive regulation of GTPase activity // inferred from electronic annotation	
1449498_i	0.006371	1.38	1.07	2.20	NM_010766	<i>Marco</i>	macrophage receptor with collagenous structure	0006897 // endocytosis // inferred from mutant phenotype // 0043277 // apoptotic cell clearance // inferred from mutant phenotype // 0045087 // innate immune response //	
1449546_i	0.001596	-1.16	1.07	-1.32	NM_133358	<i>Zfp617</i>	zinc finger protein 617	0006355 // regulation of transcription, DNA-dependent // inferred from electronic annotation	
1427005_i	0.002278	1.46	1.07	1.92	NM_152804	<i>Plk2</i>	polo-like kinase 2	0000082 // G1/S transition of mitotic cell cycle // not recorded // 0000278 // mitotic cell cycle // inferred from mutant phenotype // 0006468 // protein phosphorylation // inferred	
1433963_i	0.007295	-1.13	1.07	1.15	NM_153795	<i>Fermt3</i>	fermitin family homolog 3 (Drosophila)	0007155 // cell adhesion // inferred from electronic annotation // 0007159 // leukocyte cell-cell adhesion // inferred from mutant phenotype // 0007159 // leukocyte cell-cell adhesion	
1420659_i	0.005173	-1.57	1.07	-1.29	NM_030710	<i>Slamf6</i>	SLAM family member 6		
1444003_i	0.000310	-1.37	1.07	1.46	NM_153408	<i>Neur3</i>	neuronal homolog 3 homolog (Drosophila)	0016567 // protein ubiquitination // inferred from electronic annotation // 0016567 // protein ubiquitination // not recorded // 0002544 // chronic inflammatory response // inferred from electronic annotation // 0006914 //	
1448756_i	0.000221	-1.18	1.07	1.68	NM_009114	<i>S100a9</i>	S100 calcium binding protein A9 (calgranulin B)	0002523 // leukocyte migration involved in inflammatory response // not recorded // 0002544 // chronic inflammatory response // inferred from electronic annotation // 0006914 //	
1425896_i	0.008461	1.57	1.07	1.69	NM_007993	<i>Fbn1</i>	fibrillin 1	0001501 // skeletal system development // not recorded // 0001822 // kidney development // not recorded // 0006030 // chitin metabolic process // inferred from electronic	
1455503_i	0.002278	-1.20	1.07	-1.48	NM_001001130//NM	<i>Zfp273//Zfp85-rs1</i>	zinc finger protein 273 // zinc finger protein 85, related sequence 1	0006355 // regulation of transcription, DNA-dependent // inferred from electronic annotation	
1434873_i	0.004274	-1.36	1.07	-1.19	NM_153788	<i>Acap1</i>	ARFAP with coiled-coil, ankyrin repeat and PH domains 1	0006629 // lipid metabolic process // inferred from electronic annotation // 0007165 // signal transduction // inferred from electronic annotation // 0016042 // lipid catabolic process	
1451494_i	0.008195	1.27	1.08	1.15	NM_001146298//NM	<i>LOC101056456//VW</i>	VW domain-containing adapter protein with coiled-coil-like//VW domain	0000075 // cell cycle checkpoint // not recorded // 0006351 // transcription, DNA-dependent // inferred from electronic annotation // 0006355 // regulation of transcription, DNA-	
1421555_i	0.009187	-1.27	1.08	-1.03	NM_013462	<i>Adrb3</i>	adrenergic receptor, beta 3		

Table S3

Gene ID	p (Corr)	(Transcript-Strain)	FD (Vehicle)	FD (1 day)	FD (5 day)	RefSeq	Transcript ID	Gene Symbol	Gene Title	Gene Ontology Biological Process
1422473_i	0.00084	2.03	1.08	1.96	NM_001177980//NM	<i>Pde4b</i>		phosphodiesterase 4B, cAMP specific	0001780 // neutrophil homeostasis // inferred from mutant phenotype//0006198 // cAMP catabolic process // not recorded//0006939 // smooth muscle contraction // inferred	
1440865_i	0.000319	-1.46	1.08	1.56	NM_001033632	<i>Ifitm6</i>		interferon induced transmembrane protein 6	0009607 // response to biotic stimulus // inferred from electronic annotation	
1452588_i	0.009935	-1.14	1.08	-1.19	NM_026999	<i>Zfp688</i>		zinc finger protein 688	0006355 // regulation of transcription, DNA-dependent // inferred from electronic annotation	
1451364_i	0.000873	-1.20	1.09	-1.10	NM_027241	<i>Polr3gl</i>		polymerase (RNA) III (DNA directed) polypeptide G like		
1435524_i	0.003236	-1.06	1.09	1.05	NR_028574	<i>Smhg8</i>		small nuclear RNA host gene 8		
1423441_i	0.009319	-1.13	1.09	-1.10	NM_009249	<i>Tp2tm</i>		transcription factor b2, mitochondrial	0001554 // rRNA modification // inferred from electronic annotation//0006351 // transcription, DNA-dependent // inferred from electronic annotation//0006355 // regulation of	
1421656_i	0.009388	1.49	1.09	1.47	NM_011897	<i>Spry2</i>		sprouty homolog 2 (Drosophila)	0007275 // multicellular organismal development // inferred from electronic annotation//0007605 // sensory perception of sound // inferred from mutant phenotype//0008285 //	
1427192_i	0.002533	-1.10	1.09	1.10	NM_030147	<i>Brd8</i>		bromodomain containing 8	0006351 // transcription, DNA-dependent // inferred from electronic annotation//0006355 // regulation of transcription, DNA-dependent // inferred from electronic	
1434161_i	0.009871	-1.01	1.09	-1.14	NM_173756//XM_894	<i>Gm7020//Lin52</i>		predicted gene 7020//lin-52 homolog (C. elegans)		
1471931_i	0.004012	-1.17	1.10	-1.04	NM_010811	<i>Nds1c</i>		N-deacetylase/h-sulfotransferase (heparan glucosaminyl) 2	0002002 // regulation of angiotensin levels in blood // inferred from mutant phenotype//0006024 // glycosaminoglycan biosynthetic process // traceable author	
1457266_i	0.002968	-1.18	1.10	-1.03	NM_001037717	<i>Slc38a6</i>		solute carrier family 38, member 6		
1422470_i	0.003457	-1.12	1.10	-1.27	NM_009760	<i>Bnip3</i>		BCL2/adenovirus E1B interacting protein 3	0001666 // response to hypoxia // not recorded//0006309 // apoptotic DNA fragmentation // not recorded//0006338 // chromatin remodeling // not recorded//0006915 //	
1421603_i	0.002750	-1.14	1.10	1.06	NM_001113368//NM	<i>Ceacam2//Ceacam</i>		carcinoembryonic antigen-related cell adhesion molecule 2//carcinoembryonic	0019048 // virus-host interaction // inferred from electronic annotation//0009615 // response to virus // inferred from electronic annotation//0043406 // positive regulation of MAP	
1437356_i	0.000107	-1.55	1.10	-1.56	NM_183031	<i>Gpr183</i>		G protein-coupled receptor 183	0002313 // mature B cell differentiation involved in immune response // inferred from mutant phenotype//0006959 // humoral immune response // inferred from mutant	
1436054_i	0.000781	-1.08	1.10	1.00	NM_027143	<i>Khny1</i>		KH and NYN domain containing		
1439141_i	0.004475	-1.77	1.11	-1.64	NM_182806	<i>Gpr18</i>		G protein-coupled receptor 18	0007165 // signal transduction // inferred from electronic annotation//0007186 // G-protein coupled receptor signaling pathway // inferred from electronic annotation	
1454850_i	0.003443	-1.50	1.11	-1.30	NM_178650	<i>Tbc1d10c</i>		TBC1 domain family, member 10c	0032313 // regulation of Rab GTPase activity // inferred from electronic annotation//0032851 // positive regulation of Rab GTPase activity // inferred from electronic	
1425361_i	0.000938	-1.25	1.11	-1.33	NM_027007	<i>Zfp397</i>		zinc finger protein 397	0006351 // transcription, DNA-dependent // inferred from electronic annotation//0006355 // regulation of transcription, DNA-dependent // inferred from electronic	
1424142_i	0.008646	-1.06	1.11	1.06	NM_026079	<i>Ikkap</i>		inhibitor of kappa light polypeptide enhancer in B cells, kinase complex-associated	0006351 // transcription, DNA-dependent // inferred from electronic annotation//0006355 // regulation of transcription, DNA-dependent // inferred from electronic	
1415723_i	0.009935	-1.06	1.11	-1.07	NM_173633//NM_171	<i>EFS//LOC000476</i>		eukaryotic translation initiation factor 5//eukaryotic translation initiation factor 5-	0006412 // translation // inferred from electronic annotation//0006413 // translational initiation // inferred from electronic annotation//0016070 // RNA metabolic process //	
1420999_i	0.000277	1.30	1.11	1.20	NM_00116441//NM	<i>Cnot4</i>		CCR4-NOT transcription complex, subunit 4	0006351 // transcription, DNA-dependent // inferred from electronic annotation//0006355 // regulation of transcription, DNA-dependent // inferred from electronic	
1428636_i	0.009455	-1.04	1.12	-1.11	NM_001103156//NM	<i>Steap2</i>		5 transmembrane epithelial antigen of prostate 2	0006810 // transport // inferred from electronic annotation//0006811 // ion transport // inferred from electronic annotation//0006893 // Golgi to plasma membrane transport //	
1424012_i	0.006439	-1.45	1.12	-1.35	NM_030188	<i>Txc30a1</i>		tetratricopeptide repeat domain 30A1	0030300 // cell projection organization // inferred from electronic annotation	
1434607_i	0.000250	-1.21	1.12	-1.11	NM_030096	<i>Dks52</i>		DEAD (Asp-Glu-Ala-Asp) box polypeptide 52		
1435134_i	0.003991	-1.16	1.12	-1.06	NM_178772	<i>Nceh1</i>		neutral cholesterol ester hydrolase 1	0006470 // protein dephosphorylation // inferred from direct assay//0006629 // lipid metabolic process // inferred from electronic annotation//0006805 // xenobiotic metabolic	
1415899_i	0.001521	3.02	1.12	3.98	NM_008416	<i>Jumb</i>		Jun-B oncogene	0001570 // vasculogenesis // inferred from mutant phenotype//0001649 // osteoblast differentiation // inferred from mutant phenotype//0001701 // in utero embryonic	
1427007_i	0.000820	-1.17	1.12	-1.09	NM_028773	<i>Sash3</i>		SAM and SH3 domain containing 3	0002639 // positive regulation of immunoglobulin production // inferred from mutant phenotype//0002726 // positive regulation of T cell cytokine production // inferred from mutant	
1433442_i	0.002831	1.11	1.12	-1.03	NM_172871	<i>Klhl9</i>		kelch-like 9	0000910 // cytokinesis // not recorded//0007049 // cell cycle // inferred from electronic annotation//0007067 // mitosis // inferred from electronic annotation//0016567 //	
1434675_i	0.009871	-1.19	1.13	-1.47	NM_028543	<i>Zfp763</i>		zinc finger protein 763	0006355 // regulation of transcription, DNA-dependent // inferred from electronic annotation	
1416318_i	0.003867	-1.42	1.13	-1.31	NM_025429	<i>Serpinb1a</i>		serine (or cysteine) peptidase inhibitor, clade B, member 1a	0010466 // negative regulation of peptidase activity // inferred from electronic annotation//00010951 // negative regulation of endopeptidase activity // not recorded//0030162 //	
1448511_i	0.005297	-1.35	1.13	-1.20	NM_016933	<i>Piprcap</i>		protein tyrosine phosphatase, receptor type, C polypeptide-associated protein		
1430170_i	0.006150	-1.32	1.14	-1.52	NM_027914	<i>Bcl6l10</i>		Bardet-Biedl syndrome 10 (human)		
1425738_i	0.006171	-1.41	1.14	-1.41	1.41			immunoglobulin kappa chain complex	0001895 // retina homeostasis // not recorded//00035058 // nonmotile primary cilium assembly // not recorded//0043254 // regulation of protein complex assembly // not	
1422089_i	0.006171	-1.86	1.14	-1.22	NM_010746	<i>Nect1</i>		natural cytotoxicity triggering receptor 1	0003183 // B cell differentiation // inferred from mutant phenotype//0032496 // response to lipopolysaccharide // inferred from direct assay//0042493 // response to drug //	
1428083_i	0.006131	-1.29	1.14	-1.20	NR_003513	<i>Nect1</i>		nuclear paraspeckle assembly transcript 1 (non-protein coding)	0043954 // cellular component maintenance // inferred from direct assay//0043954 // cellular component maintenance // inferred from mutant phenotype	
1471955_i	0.002115	1.06	1.14	-1.11	NM_133744	<i>Ccdc71</i>		coiled-coil domain containing 71		
1423182_i	0.003768	-1.50	1.14	-1.34	NM_021349	<i>Tnfrsf13b</i>		tumor necrosis factor receptor superfamily, member 13b	0001782 // B cell homeostasis // inferred from mutant phenotype//0030889 // negative regulation of B cell proliferation // inferred from mutant phenotype	
1420864_i	0.000524	1.02	1.14	-1.19	NM_009547	<i>Zbtb14</i>		zinc finger and BTB domain containing 14	0006351 // transcription, DNA-dependent // inferred from electronic annotation//0006355 // regulation of transcription, DNA-dependent // inferred from electronic	
1433632_i	0.003197	1.52	1.15	1.35	NM_001164598	<i>Ifi2b2p</i>		interferon regulatory factor 2 binding protein 2	0001122 // negative regulation of transcription from RNA polymerase II promoter // not recorded//0006351 // transcription, DNA-dependent // inferred from electronic	
1428297_i	0.000188	-1.19	1.15	1.02	NM_009006	<i>Mapk2k</i>		mitogen-activated protein kinase kinase kinase 2	0006468 // protein phosphorylation // inferred from electronic annotation//0006468 // protein phosphorylation // not recorded//0006903 // vesicle targeting // inferred from direct	
1435169_i	0.001709	-1.06	1.15	-1.08	NM_029870	<i>Creb1</i>		CREB3 regulatory factor	0001122 // negative regulation of transcription from RNA polymerase II promoter // not recorded//0006351 // transcription, DNA-dependent // inferred from electronic	
1434202_i	0.000331	-1.35	1.16	-1.81	NM_183187	<i>Fam107a</i>		family with sequence similarity 107, member A	0001558 // regulation of cell growth // not recorded	
1451819_i	0.005827	1.43	1.16	1.49	NM_145456	<i>Zswim6</i>		zinc finger SWIM-type containing 6	0048812 // neuron projection morphogenesis // inferred from mutant phenotype//2001222 // regulation of neuron migration // inferred from mutant phenotype	
1451566_i	0.006221	-1.15	1.16	-1.06	NM_145612	<i>Zfp810</i>		zinc finger protein 810	0006355 // regulation of transcription, DNA-dependent // inferred from electronic annotation	
1426806_i	0.000215	-1.53	1.16	-1.43	NM_028696	<i>Hnbp1</i>		nucleic acid binding protein 1	0000075 // cell cycle checkpoint // not recorded//0007074 // double-strand break repair via homologous recombination // not recorded//0006281 // DNA repair // not	
1434245_i	0.003761	-1.12	1.17	-1.06	NM_201351	<i>Cy55a1a3</i>		cytochrome b561 family, member A3	0006810 // transport // inferred from electronic annotation//0022900 // electron transport chain // inferred from electronic annotation//0055114 // oxidation-reduction process //	
1423191_i	0.003203	1.01	1.17	1.23	NM_018828	<i>Fnhp4</i>		formin binding protein 4		
1429587_i	0.005389	-1.02	1.17	-1.02	NM_172762	<i>Rbm34</i>		RNA binding motif protein 34		
1427163_i	0.009287	-1.01	1.18	1.08	NM_001177374//NM	<i>Ubr2</i>		ubiquitin protein ligase E3 component n-recognin 2	0006342 // chromatin silencing // inferred from direct assay//0006511 // ubiquitin-dependent protein catabolic process // inferred from direct assay//0007141 // male meiosis I //	
1455700_i	0.006249	-1.34	1.18	-1.30	NM_028832	<i>Mterf1d3</i>		MTERF domain containing 3	0006351 // transcription, DNA-dependent // inferred from mutant phenotype//0006355 // regulation of transcription, DNA-dependent // inferred from mutant phenotype	
1425296_i	0.000250	-1.13	1.18	1.03	NM_001081650//NM	<i>Rgs3</i>		regulator of G-protein signaling 3	0007165 // signal transduction // not recorded//0007186 // G-protein coupled receptor signaling pathway // traceable author statement//0009968 // negative regulation of signal	
1452374_i	0.009388	-1.04	1.18	-1.10	NM_001111107//NM	<i>Zfp322a</i>		zinc finger protein 322A	0006351 // transcription, DNA-dependent // inferred from electronic annotation//0006355 // regulation of transcription, DNA-dependent // inferred from electronic	
1455553_i	0.009379	-1.39	1.18	-1.21	NM_001142647//NM	<i>Tmem194b</i>		transmembrane protein 194B		
1428947_i	0.001797	-1.83	1.18	-1.52	NM_027222	<i>Mzb1</i>		marginal zone B and B1 cell-specific protein 1	0002642 // positive regulation of immunoglobulin biosynthetic process // inferred from mutant phenotype//0008284 // positive regulation of cell proliferation // inferred from direct	
1435901_i	0.007335	1.01	1.19	1.04	NM_001033291//NM	<i>Usp40</i>		ubiquitin specific peptidase 40	0005068 // proteolysis // inferred from electronic annotation//0006511 // ubiquitin-dependent protein catabolic process // inferred from electronic annotation	
1426713_i	0.003599	1.33	1.19	1.14	NM_029735	<i>Eprs</i>		glutamyl-prolyl-RNA synthetase	0006412 // translation // inferred from electronic annotation//0006417 // regulation of translation // inferred from electronic annotation//0006418 // tRNA aminoacylation for	
1434300_i	0.002481	1.02	1.20	1.09	NM_00114977//NM	<i>U2surp</i>		U2 snRNP-associated SURP domain containing	0006396 // RNA processing // inferred from electronic annotation	
1471932_i	0.002278	-1.45	1.20	-1.31	NM_008960	<i>Il18</i>		interleukin 18	0001065 // MAPK cascade // not recorded//0001525 // angiogenesis // not recorded//0001525 // angiogenesis // inferred from sequence or structural similarity//0001649 //	
1435376_i	0.006683	-1.05	1.20	-1.01	NM_028102	<i>Dohd2</i>		DHHD domain containing 2	0006629 // lipid metabolic process // inferred from electronic annotation//0016042 // lipid catabolic process // inferred from electronic annotation	
1418578_i	0.002174	-1.14	1.20	-1.06	NM_016811	<i>Dgka</i>		diacylglycerol kinase, alpha	0007205 // protein kinase C-activating G-protein coupled receptor signaling pathway // inferred from electronic annotation//0008152 // metabolic process // inferred from electronic	
1425396_i	0.009538	-1.20	1.21	-1.07	NM_001162432//NM	<i>Lck</i>		lymphocyte protein tyrosine kinase	0006468 // protein phosphorylation // inferred from direct assay//0006468 // protein phosphorylation // inferred from electronic annotation//0006468 // protein phosphorylation //	
1428637_i	0.000264	-1.04	1.22	-1.05	NM_001014390	<i>Dyrk2</i>		dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 2	0006468 // protein phosphorylation // inferred from electronic annotation//0006468 // protein phosphorylation // not recorded//0006915 // apoptotic process // inferred from	
1426787_i	0.000443	-1.02	1.22	-1.10	NM_030207	<i>Sfi1</i>		SFI1 homolog, spindle assembly associated (yeast)	0010923 // negative regulation of phosphatase activity // not recorded	
1424029_i	0.000439	1.02	1.22	-1.10	NM_030203	<i>Tsyp14</i>		TSYP-like 4	0006334 // nucleosome assembly // inferred from electronic annotation	
1437557_i	0.002174	1.02	1.22	-1.05	NM_001101478	<i>D3Ertd254e</i>		DNA segment, Chr 3, ERATO D01 254, expressed	0006355 // regulation of transcription, DNA-dependent // inferred from electronic annotation	
1419768_i	0.000262	-1.52	1.22	-1.32	NM_001043317//NM	<i>Cd22</i>		CD22 antigen	0007155 // cell adhesion // inferred from electronic annotation//0007166 // cell surface receptor signaling pathway // traceable author statement	
1422411_i	0.001391	-1.40	1.23	-1.18	NM_001012766//NM	<i>Eor1//Eor12//Eor</i>		eosinophil-associated, ribonuclease A family, member 1//eosinophil-associated,	0009395 // chemotaxis // inferred from direct assay//0093035 // nucleic acid phosphodiester bond hydrolysis // inferred from electronic annotation	
1423003_i	0.006171	1.08	1.23	-1.05	NM_080793	<i>Setd7</i>		SET domain containing (lysine methyltransferase) 7	0006351 // transcription, DNA-dependent // inferred from electronic annotation//0006355 // regulation of transcription, DNA-dependent // inferred from electronic	
1419206_i	0.000250	-1.62	1.23	-1.33	NM_007645	<i>Cd37</i>		CD37 antigen	0002639 // positive regulation of immunoglobulin production // inferred from mutant phenotype//0002920 // regulation of humoral immune response // inferred from mutant	
1425367_i	0.004378	-1.07	1.24	-1.18	NM_001253872//NM	<i>Intsp1</i>		integrin alpha L	0002291 // T cell activation via T cell receptor contact with antigen bound to MHC molecule on antigen presenting cell // not recorded//0007155 // cell adhesion // inferred from	
1432415_i	0.000384	-1.03	1.24	-1.62	NM_023852	<i>Rab3c</i>		RAB3C, member RAS oncogene family	0007165 // signal transduction // inferred from electronic annotation//0007264 // small GTPase mediated signal transduction // inferred from electronic annotation//00015033 // protein	
1434620_i	0.007544	1.06	1.24	1.04	NM_146084	<i>Fam13b</i>		family with sequence similarity 13, member B	0006810 // transport // inferred from electronic annotation//00043547 // positive regulation of GTPase activity // inferred from electronic annotation	
1417230_i	0.001411	-1.22	1.24	-1.17	NM_001159965//NM	<i>Ralgs2p</i>		Raf GEF with PH domain and SH3 binding motif 2	0007264 // small GTPase mediated signal transduction // inferred from electronic annotation	
1435642_i	0.008996	1.10	1.24	-1.23	NM_178774//NR_028	<i>Prr18</i>		proline rich region 18		
1421107_i	0.007722	1.06	1.24	1.08	NM_021420	<i>Sk4</i>		serine/threonine kinase 4	0009092 // cell morphogenesis // not recorded//0001569 // patterning of blood vessels // inferred from genetic interaction//0001841 // neural tube formation // inferred from	
1449347_i	0.003785	-1.40	1.24	1.00	NM_001081642//NM	<i>Xlr4a//Xlr4b//Xlr</i>		X-linked lymphocyte-regulated 4A//X-linked lymphocyte-regulated 4B//X-linked		
1448194_i	0.001704	1.68	1.25	2.19	NR_001592	<i>H19</i>		H19 fetal liver mRNA	0002825 // negative regulation of cell proliferation // inferred from genetic interaction//0010468 // regulation of gene expression // inferred from direct assay	
1422411_i	0.001673	-1.37	1.25	-1.15	NM_001012766//NM	<i>Eor1//Eor12//Eor</i>		eosinophil-associated, ribonuclease A family, member 1//eosinophil-associated,	0009395 // chemotaxis // inferred from direct assay//0093035 // nucleic acid phosphodiester bond hydrolysis // inferred from electronic annotation	
1421298_i	0.007881	1.04	1.25	1.08	NM_010432	<i>Hipk1</i>		homeodomain interacting protein kinase 1	0001122 // negative regulation of transcription from RNA polymerase II promoter // inferred from sequence or structural similarity//0006351 // transcription, DNA-dependent //	
1435236_i	0.005102	-1.								

0030162 // regulation of proteolysis // not recorded//0034205 // beta-amyloid formation // inferred from direct assay//0034205 // beta-amyloid formation // not recorded

Table S3

Gene ID	p (Corr) (Treatment-Strain)	FD (Vehicle)	FD (1 day)	FD (5 day)	RefSeq Transcript ID	Gene Symbol	Gene Title	Gene Ontology Biological Process
1425822_z	0.001704	-1.32	1.27	-1.21	NM_008052	<i>Dxt1</i>	deltex 1 homolog (Drosophila)	0007219 // Notch signaling pathway // inferred from direct assay//0007219 // Notch signaling pathway // inferred from mutant phenotype//0008593 // regulation of Notch
1419406_z	0.002009	-1.28	1.28	-1.09	NM_001159289//NM	<i>Bcl11a</i>	B cell CLL/lymphoma 11A (zinc finger protein)	0006351 // transcription, DNA-dependent // inferred from electronic annotation//0006355 // regulation of transcription, DNA-dependent // inferred from electronic
1422201_z	0.000736	-1.48	1.28	-1.37	NM_010389	<i>H2-Qb</i>	histocompatibility 2, O region beta locus	0002504 // antigen processing and presentation of peptide or polysaccharide antigen via MHC class II // inferred from electronic annotation//0006955 // immune response // inferred
1436649_z	0.000264	-1.35	1.28	-1.15	NM_011771	<i>IKZF3</i>	IKAROS family zinc finger 3	0006351 // transcription, DNA-dependent // inferred from electronic annotation//0006355 // regulation of transcription, DNA-dependent // inferred from electronic
1418394_z	0.002917	1.03	1.29	1.10	NM_001163029//NM	<i>Cd97</i>	CD97 antigen	0007155 // cell adhesion // inferred from electronic annotation//0007165 // signal transduction // traceable author statement//0007166 // cell surface receptor signaling pathway
1450992_z	0.007181	-1.01	1.29	-1.03	NM_001193271//NM	<i>Meis1</i>	Meis homeobox 1	0001525 // angiogenesis // inferred from mutant phenotype//0002089 // lens morphogenesis in camera-type eye // inferred from mutant phenotype//0006351 // transcription,
1416799_z	0.000821	1.08	1.29	1.07	NM_001164325//NM	<i>Tpm7</i>	transient receptor potential cation channel, subfamily M, member 7	0006468 // protein phosphorylation // inferred from direct assay//0006468 // protein phosphorylation // inferred from electronic annotation//0006810 // transport // inferred from
1419394_z	0.000280	-1.09	1.29	1.69	NM_013650	<i>S100a8</i>	S100 calcium binding protein A8 (calgranulin A)	0005253 // leukocyte migration involved in inflammatory response // not recorded//0002526 // acute inflammatory response // inferred from electronic annotation//0002544 //
1434480_z	0.000254	1.11	1.30	1.10	NM_198308	<i>Pdpr</i>	pyruvate dehydrogenase phosphatase regulatory subunit	0006546 // glycine catabolic process // inferred from electronic annotation//005114 // oxidation-reduction process // inferred from electronic annotation
1419756_z	0.009091	-1.14	1.30	-1.02	NM_138650	<i>Dgkq</i>	diacylglycerol kinase, gamma	0007205 // protein kinase C-activating G-protein coupled receptor signaling pathway // inferred from electronic annotation//0008152 // metabolic process // inferred from electronic
1422124_z	0.000952	-1.05	1.30	1.12	NM_001111316//NM	<i>Ptpcr</i>	protein tyrosine phosphatase, receptor type, C	0000187 // activation of MAPK activity // inferred from mutant phenotype//0001915 // negative regulation of T cell mediated cytotoxicity // inferred from mutant
1421182_z	0.007329	-1.21	1.30	1.02	NM_001204239//NM	<i>Clec1b</i>	C-type lectin domain family 1, member b	0007165 // signal transduction // not recorded//0007166 // cell surface receptor signaling pathway // traceable author statement
1422644_z	0.000124	-1.17	1.30	-1.25	NM_026514	<i>Cdc42ep3</i>	CDC42 effector protein (Rho GTPase binding) 3	0008360 // regulation of cell shape // inferred from electronic annotation
1451793_z	0.003197	1.09	1.31	1.06	NM_029436	<i>Klhl24</i>	kelch-like 24	
1460245_z	0.001047	-1.48	1.31	1.00	NM_010654	<i>Klrd1</i>	killer cell lectin-like receptor, subfamily D, member 1	
1425062_z	0.000024	-1.63	1.31	-1.47	NM_001136236//NM	<i>Fcrl1</i>	Fc receptor-like 1	
1419297_z	0.008967	-1.32	1.31	-1.18	NM_008206	<i>H2-Oa</i>	histocompatibility 2, O region alpha locus	0002504 // antigen processing and presentation of peptide or polysaccharide antigen via MHC class II // inferred from electronic annotation//0006955 // immune response // inferred
1434301_z	0.005304	1.04	1.31	1.09	NM_001162926//NM	<i>Fam84b</i>	family with sequence similarity 84, member B	
1429316_z	0.001349	-1.06	1.32	-1.04	NM_027526	<i>Rasgef1a</i>	RasGEF domain family, member 1A	0007264 // small GTPase mediated signal transduction // inferred from electronic annotation//0016477 // cell migration // not recorded//0050790 // regulation of catalytic activity
1433997_z	0.001019	-1.34	1.32	-1.11	NM_174998	<i>Hippoc4l</i>	Hippocalin-like 4	
1430597_z	0.001432	-1.14	1.32	-1.09	NM_178394	<i>Jakmip1</i>	janus kinase and microtubule interacting protein 1	0006810 // transport // inferred from electronic annotation//0015031 // protein transport // inferred from electronic annotation
1427562_z	0.003580	1.06	1.34	1.03	NM_0011101	<i>Prkca</i>	protein kinase C, alpha	0000188 // inactivation of MAPK activity // inferred from mutant phenotype//0000302 // response to reactive oxygen species // not recorded//0001525 // angiogenesis // inferred
1456328_z	0.001072	-1.85	1.35	-1.63	NM_001033350	<i>Bank1</i>	B cell scaffold protein with ankyrin repeats 1	0006874 // cellular calcium ion homeostasis // not recorded//0042113 // B cell activation // inferred from electronic annotation
1450570_z	0.000209	-1.78	1.35	-1.58	NM_098844	<i>Cd19</i>	CD19 antigen	0050853 // B cell receptor signaling pathway // inferred from direct assay
1425014_z	0.000321	1.21	1.35	1.19	NM_0011630	<i>Nr2c2</i>	nuclear receptor subfamily 2, group C, member 2	0006351 // transcription, DNA-dependent // inferred from electronic annotation//0006355 // regulation of transcription, DNA-dependent // inferred from electronic
1421802_z	0.000325	-1.40	1.36	-1.07	NM_007894//XM_001	<i>Eor1//LOC101056</i>	eosinophil-associated, ribonuclease A family, member 1 // eosinophil cationic	0093035 // nucleic acid phosphodiester bond hydrolysis // inferred from electronic annotation//0006935 // chemotaxis // inferred from direct assay
1419907_z	0.001278	-1.37	1.36	-1.20	NM_001160215//NM	<i>Fcrla</i>	Fc receptor-like A	0030154 // cell differentiation // inferred from electronic annotation
1452249_z	0.003761	-1.08	1.37	-1.03	NM_001033217	<i>Prickle1</i>	prickle homolog 1 (Drosophila)	0001843 // neural tube closure // not recorded//0006606 // protein import into nucleus // not recorded//0031398 // positive regulation of protein ubiquitination // not
1455750_z	0.000166	1.09	1.37	-1.09	NM_001033348	<i>Ralgap2</i>	Ral GTPase activating protein, alpha subunit 2 (catalytic)	0032484 // Ral protein signal transduction // inferred from mutant phenotype//0032859 // activation of Ral GTPase activity // not recorded//0032859 // activation of Ral GTPase
1429139_z	0.001186	1.12	1.37	1.06	NM_001025613//NM	<i>Oudub7</i>	OTU domain containing 7B	0002385 // mucosal immune response // inferred from mutant phenotype//0006508 // proteolysis // inferred from electronic annotation//0016579 // protein deubiquitination
1423130_z	0.001357	1.05	1.37	1.32	NM_001079694//NM	<i>Srsf5</i>	serine/arginine-rich splicing factor 5	0006351 // transcription, DNA-dependent // inferred from electronic annotation//0006355 // regulation of transcription, DNA-dependent // inferred from electronic
1426514_z	0.000911	1.15	1.37	1.23	NM_001252584//NM	<i>Zmynd8</i>	zinc finger, MYND-type containing 8	
1456480_z	0.004410	-1.12	1.38	-1.08	NM_172887//NM_17	<i>Fxy</i>	furry homolog (Drosophila)	0016310 // phosphorylation // inferred from electronic annotation
1435955_z	0.002070	-1.25	1.38	-1.07	NM_172900	<i>Slc16c9</i>	sialic acid binding lg-like lectin G	
1430534_z	0.000286	-1.41	1.38	-1.03	NM_030098	<i>Rnase6</i>	ribonuclease, RNase A family, 6	0093035 // nucleic acid phosphodiester bond hydrolysis // inferred from electronic annotation
1417379_z	0.006032	1.30	1.38	1.20	NM_016721	<i>Iqgap1</i>	IQ motif containing GTPase activating protein 1	0001817 // regulation of cytokine production // inferred from mutant phenotype//0007165 // signal transduction // inferred from electronic annotation//0007264 // small GTPase
1423478_z	0.001330	-1.17	1.38	1.01	NM_008855	<i>Prkcb</i>	protein kinase C, beta	0006351 // transcription, DNA-dependent // inferred from electronic annotation//0006355 // regulation of transcription, DNA-dependent // inferred from electronic
1419135_z	0.001130	-1.23	1.39	-1.16	NM_008518	<i>Ltb</i>	lymphotoxin B	0006955 // immune response // inferred from electronic annotation//0010467 // gene expression // inferred from mutant phenotype//0043588 // skin development // inferred from
1436491_z	0.000250	-1.45	1.40	-1.69	NR_024599	<i>Gm11346</i>	X-linked lymphocyte-regulated 5 pseudogene	
1429144_z	0.000077	-1.16	1.40	-1.02	NM_001042671//NM	<i>Gpcpd1</i>	glycerophosphocholine phosphodiesterase GDE1 homolog (S. cerevisiae)	0006071 // glycerol metabolic process // inferred from electronic annotation//0006629 // lipid metabolic process // inferred from electronic annotation
1423100_z	0.009865	3.02	1.41	3.99	NM_010234	<i>Fos</i>	FB1 osteosarcoma oncogene	0001661 // conditioned taste aversion // inferred from electronic annotation//0006355 // regulation of transcription, DNA-dependent // inferred from direct assay//0006355 //
1417885_z	0.007288	1.16	1.42	1.22	NM_001038609//NM	<i>Maot</i>	microtubule-associated protein tau	0000226 // microtubule cytoskeleton organization // inferred from mutant phenotype//0000226 // microtubule cytoskeleton organization // not recorded//0001764 // neuron
1425436_z	0.000935	-1.29	1.42	1.21	NM_010648//NM_01	<i>Klra9//Klra9//LO</i>	killer cell lectin-like receptor, subfamily A, member 3 // killer cell lectin-like receptor	0007155 // cell adhesion // inferred from electronic annotation
1419874_z	0.001640	-1.63	1.43	-1.11	NM_001033324	<i>Zbtb16</i>	zinc finger and BTB domain containing 16	0001501 // skeletal system development // inferred from mutant phenotype//0001823 // mesonephros development // inferred from direct assay//0006355 // regulation of
1426619_z	0.007981	-1.38	1.43	1.04	NM_001033379	<i>Aim2</i>	absent in melanoma 2	0002218 // activation of innate immune response // inferred from direct assay//0002218 // activation of innate immune response // not recorded//0002230 // positive regulation of
1439176_z	0.008563	-1.26	1.44	-1.10	NM_001038651	<i>Zfp953</i>	zinc finger protein 953	0006355 // regulation of transcription, DNA-dependent // inferred from electronic annotation
1435116_z	0.005827	-1.02	1.45	-1.10	NM_028908	<i>Map10</i>	microtubule-associated protein 10	0007049 // cell cycle // inferred from electronic annotation//0031122 // cytoplasmic microtubule organization // not recorded//0032467 // positive regulation of cytokinesis // not
1435278_z	0.009813	1.05	1.45	-1.04	NM_026006	<i>Sfrd23</i>	SFT2 domain containing 3	0006810 // transport // inferred from electronic annotation//0015031 // protein transport // inferred from electronic annotation//0016192 // vesicle-mediated transport // inferred
1437202_z	0.009319	1.03	1.45	1.20	NM_177239	<i>Myms1</i>	myb-like, SWIRM and MPN domains 1	0006351 // transcription, DNA-dependent // inferred from electronic annotation//0006355 // regulation of transcription, DNA-dependent // inferred from electronic
1424609_z	0.000736	1.10	1.46	1.05	NM_0011723//NM_031	<i>Cuc22//Gm4354/</i>	CWC22 spliceosome-associated protein homolog (S. cerevisiae)//predicted gene	0001933 // negative regulation of protein phosphorylation // not recorded//0001937 // negative regulation of endothelial cell proliferation // not recorded//0006397 // mRNA
1418830_z	0.006371	-1.22	1.47	-1.21	NM_007655	<i>Cd79a</i>	CD79A antigen (immunoglobulin-associated alpha)	0007166 // cell surface receptor signaling pathway // inferred from electronic annotation//0030183 // B cell differentiation // inferred from mutant phenotype//0042100 // B cell
1417522_z	0.008319	-1.11	1.47	-1.11	NM_026346	<i>Fbxo32</i>	F-box protein 32	0014889 // muscle atrophy // not recorded//0014894 // response to denervation involved in regulation of muscle adaptation // inferred from direct assay//0016567 // protein
1421251_z	0.009093	1.06	1.48	1.07	NM_009555	<i>Zfp40</i>	zinc finger protein 40	0006355 // regulation of transcription, DNA-dependent // inferred from electronic annotation
1422166_z	0.003991	-1.43	1.48	-1.06	NM_020257	<i>Clec2i</i>	C-type lectin domain family 2, member i	0001765 // membrane raft assembly // non-traceable author statement//0007165 // signal transduction // inferred from sequence or structural similarity//0030833 // regulation of
1445862_z	0.002488	1.41	1.49	1.13	NM_001081154	<i>Marf1</i>	meiosis arrest female 1	0006302 // double-strand break repair // inferred from mutant phenotype//0007126 // meiosis // inferred from electronic annotation//0007143 // female meiosis // inferred from
1423835_z	0.004081	1.04	1.50	1.08	NM_145459	<i>Zfp503</i>	zinc finger protein 503	0006355 // transcription, DNA-dependent // inferred from electronic annotation//0006355 // regulation of transcription, DNA-dependent // inferred from electronic
1455656_z	0.000051	-1.63	1.51	-1.56	NM_001037719//NM	<i>Bilo</i>	B and T lymphocyte associated	0002768 // immune response-regulating cell surface receptor signaling pathway // inferred from mutant phenotype//0007166 // cell surface receptor signaling pathway // inferred
1432784_z	0.003236	1.36	1.52	1.25	NM_172458	<i>Zfp871</i>	zinc finger protein 871	0006355 // regulation of transcription, DNA-dependent // inferred from electronic annotation
1447918_z	0.001264	-1.40	1.53	-1.35		<i>Igfc2</i>	immunoglobulin lambda3 constant 2	
1429889_z	0.000369	-1.71	1.53	-1.55	NM_026976	<i>Faim3</i>	Fas apoptotic inhibitory molecule 3	
1427455_z	0.000139	-1.26	1.54	-1.12		<i>Igk-V28//Igkc//I</i>	immunoglobulin kappa chain variable 28 (V28) // immunoglobulin kappa	0030183 // B cell differentiation // inferred from mutant phenotype//0032496 // response to lipopolysaccharide // inferred from direct assay//0042493 // response to drug //
1416957_z	0.000319	-1.47	1.55	-1.38	NM_011136	<i>Pou2f1</i>	POU domain, class 2, associating factor 1	0006351 // transcription, DNA-dependent // inferred from electronic annotation//0006355 // regulation of transcription, DNA-dependent // inferred from electronic annotation
1429041_z	0.008517	1.21	1.56	1.37	NM_001024708//NM	<i>261000S107RIK//</i>	cadherin 11 pseudogene//uncharacterized LOC101056086	0007156 // homophilic cell adhesion // inferred from electronic annotation
1428057_z	0.000572	1.33	1.56	1.25	NM_001039959//NM	<i>Ahnak</i>	AHNAK nucleoprotein (desmoyokin)	
1450357_z	0.000113	-1.24	1.59	-1.28	NM_001190333//NM	<i>Cor6</i>	chemokine (C-C motif) receptor 6	
1417640_z	0.000200	-1.56	1.60	-1.47	NM_008339	<i>Cd79b</i>	CD79B antigen	
1444214_z	0.000781	-1.05	1.61	1.23	NM_001080971	<i>Tubb1</i>	tubulin, beta class I	0007166 // cell surface receptor signaling pathway // inferred from electronic annotation//0050853 // B cell receptor signaling pathway // inferred from direct assay//0006355 //
1438465_z	0.000994	1.18	1.61	1.05	NM_001001737//XR	<i>SX80A2H23RIK</i>	RIKEN cDNA 583042H23 gene	0006184 // GTP catalytic process // inferred from electronic annotation//0007017 // microtubule-based process // inferred from direct assay//0051225 // spindle assembly //
1456282_z	0.000296	1.02	1.61	1.19	NM_001162911//NM	<i>Zfp934</i>	zinc finger protein 934	0001570 // vasculogenesis // inferred from mutant phenotype//0001822 // kidney development // inferred from mutant phenotype//0006355 // regulation of transcription, DNA-
1425288_z	0.000036	-2.15	1.62	-1.77	NM_000758	<i>C2</i>	complement receptor 2	0006355 // regulation of transcription, DNA-dependent // inferred from electronic annotation
1427758_z	0.000114	-1.70	1.65	-1.77	XM_003689273	<i>Igh-V558//Ighg3/</i>	immunoglobulin heavy chain (V558 family) // immunoglobulin heavy constant	0000187 // activation of MAPK activity // inferred from direct assay//0001788 // antibody-dependent cellular cytotoxicity // inferred from direct assay//0001798 // positive
1456062_z	0.001426	1.19	1.67	-32.39	NM_008725	<i>Nappa</i>	natratrietic peptide type A	0006182 // cGMP biosynthetic process // not recorded//0007168 // receptor guanylyl cyclase signaling pathway // not recorded//0007565 // female pregnancy // inferred from
1460407_z	0.000070	-1.05	1.67	-1.03	NM_019866	<i>Spib</i>	Sp1-B transcription factor (Spi-1/PU.1 related)	0006351 // transcription, DNA-dependent // inferred from electronic annotation//0006355 // regulation of transcription, DNA-dependent // inferred from direct assay//0030225 //
1420609_z	0.000012	1.21	1.72	1.37	NM_020575	<i>7-Mar</i>	membrane-associated ring finger (3HC4) 7	0015657 // protein ubiquitination // inferred from electronic annotation
1436033_z	0.000084	1.00	1.73	1.17	NM_001113283//NM	<i>Fam214a</i>	family with sequence similarity 214, member A	
1418480_z	0.003226	-1.09	1.75	1.45	NM_023785	<i>Ppbp</i>	pro-platelet basic protein	0006955 // immune response // inferred from electronic annotation//0030593 // neutrophil chemotaxis // inferred from electronic annotation//0043312 // neutrophil degranulation
1437127_z	0.000100	1.02	1.75	1.23	NM_001110254//NM	<i>Zfp945</i>	zinc finger protein 945	0006355 // regulation of transcription, DNA-dependent // inferred from electronic annotation
1419562_z	0.004805	1.73	1.76	1.37	NM_007566	<i>Birc6</i>	baculoviral IAP repeat-containing 6	0001890 // placenta development // inferred from mutant phenotype//0006464 // cellular protein modification process // inferred from electronic annotation//0006915 //
1435050_z	0.009851	1.72	1.79	1.34	NM_001033258	<i>D108bwg1379e</i>	DNA segment, Chr 10, Brigham & Women's Genetics 1379 expressed	0010923 // negative regulation of phosphatase activity // not recorded//0016192 // vesicle-mediated transport // not recorded//0032012 // regulation of ARF protein signal
1421140_z	0.000994	1.54	1.89	1.56	NM_001197321//NM	<i>Foxp1</i>	forkhead box P1	0000122 // negative regulation of transcription from RNA polymerase II promoter // not recorded//0000122 // negative regulation of transcription from RNA polymerase II promoter
1423226_z	0.000007	-1.22	2.03	-1.22	NM_007641	<i>Meis4</i>	Meis homeobox 4	0042113 // B cell activation // inferred from electronic annotation
1430672_z	0.003461	1.17	2.04	1.51		<i>S033418A1RIK</i>	RIKEN cDNA 5033418A18 gene	
144115_z	0.001330	1.02	2.05	0.98		<i>D18Erd1232e</i>	DNA segment, Chr 18, ERATO D0 232, expressed	
1457579_z	0.009935	1.47	2.07	1.48		<i>D11Erd1717e</i>	DNA segment, Chr 11, ERATO D0 717, expressed	
1430185_z	0.002833	1.84	2.10	1.57	NM_029332	<i>Akap13</i>	A kinase (PRKA) anchor protein 13	0010611 // regulation of cardiac muscle hypertrophy // not recorded//0016310 // phosphorylation // inferred from electronic annotation//0035023 // regulation of rho protein
1427537_z	0.003322	1.75	2.28	1.58	NM_144848	<i>Eppk1</i>	epiplakin 1	

Table S4. Lung genes basally varied between C3H/HeOu (Ou) and C3H/HeJ (He) mice (> 2-fold, p<0.01).

Moderated t-test [p < 0.01]. Blue(-): fold lower in Vehicle-HeJ vs vehicle-Ou. Red : fold higher in Vehicle-HeJ vs vehicle-Ou.

Gene_ID	p (Corr)	FD (Vehicle HeJ vs Ou)	RefSeq Transcript ID	Gene Symbol	Gene Title	Gene Ontology Biological Process
1418455_a	0.000017	-5.70	NM_019877	Copa2	coatamer protein complex, subunit zeta 2	0006810 // transport // inferred from electronic annotation//0015031 // protein transport // inferred from electronic annotation//0016192 // vesicle-mediated transport // inferred from electronic annotation
1421653_a	0.000026	-4.42	NM_0010624700	Igh-vJ558//Igha	immunoglobulin heavy chain (J558)	0002385 // mucosal immune response // inferred from direct assay//0002455 // humoral immune response mediated by circulating immunoglobulin // inferred from direct assay//0016064 // immunoglobulin
1421653_a	0.000026	-4.22	NM_001024700//NM_1_1	Igh-vJ558//Igha	immunoglobulin heavy chain (J558)	0002385 // mucosal immune response // inferred from direct assay//0002455 // humoral immune response mediated by circulating immunoglobulin // inferred from direct assay//0016064 // immunoglobulin
1456391_a	0.000020	-2.91	NM_001134741//NM_1_1	Tdrd5	tudor domain containing 5	0007275 // multicellular organismal development // inferred from electronic annotation//0007283 // spermatogenesis // inferred from electronic annotation//0007286 // spermatid development // inferred from
1423624_a	0.000019	-2.87	NM_001277273//NM_1_1	Fancd1	Fanconi anemia, complementation group L	0006281 // DNA repair // not recorded//0006513 // protein monoubiquitination // not recorded//0006974 // response to DNA damage stimulus // not recorded//0007276 // gamete generation // inferred from
1444350_a	0.000040	-2.75	NM_181543//NR_0735	Sfn10-ps	schlafen 10, pseudogene	
1420764_a	0.000326	-2.57	NM_009136	Scrg1	scrapie responsive gene 1	
1425247_a	0.000079	-2.36	NM_009853	Ighj1	immunoglobulin heavy constant gamma 1 (G1m marker)	
1449164_a	0.000140	-2.34	NM_009853	Cd68	CD68 antigen	0071310 // cellular response to organic substance // inferred from direct assay
1425450_a	0.000344	-2.33	NM_145126//NM_0091	Chi3l4//Chi3l3	chitinase 3-like 4//chitinase 3-like 3	0005975 // carbohydrate metabolic process // inferred from electronic annotation//0006032 // chitin catabolic process // inferred from electronic annotation//0006954 // inflammatory response // inferred from
1451962_a	0.006116	-2.28		Igkv6-20	immunoglobulin kappa variable 6-20	0006959 // humoral immune response // inferred from sequence or structural similarity
1424305_a	0.0002250	-2.26	NM_152839	IgJ	immunoglobulin joining chain	
1418797_a	0.000288	-2.18	NM_022430	Ms4a8a	membrane-spanning 4-domains, subfamily A, member 8A	
1425289_a	0.000113	-2.14	NM_007758	Cr2	complement receptor 2	0002430 // complement receptor mediated signaling pathway // inferred from mutant phenotype//0006958 // complement activation, classical pathway // inferred from electronic annotation//0042113 // B cell
1433526_a	0.000090	-2.09	NM_178741	Klhl8	kelch-like 8	0016567 // protein ubiquitination // inferred from sequence or structural similarity//0042787 // protein ubiquitination involved in ubiquitin-dependent protein catabolic process // inferred from sequence or
1436131_a	0.000693	-2.09	NM_178706	Siglech	sialic acid binding Ig-like lectin H	
1419729_a	0.001743	-2.07	NM_001167997//NM_1_1	Tex11	testis expressed gene 11	0000712 // resolution of meiotic recombination intermediates // inferred from mutant phenotype//0006311 // meiotic gene conversion // inferred from mutant phenotype//0007060 // male meiosis chromosome
1417556_a	0.000156	-2.05	NM_017399	Fabp1	fatty acid binding protein 1, liver	0006810 // transport // inferred from electronic annotation//0008284 // positive regulation of cell proliferation // inferred from electronic annotation//0015909 // long-chain fatty acid transport // not
1460463_a	0.000226	-2.03	NM_01204916	H60c	histocompatibility 60c	0006955 // immune response // inferred from electronic annotation//0019882 // antigen processing and presentation // inferred from electronic annotation//0030101 // natural killer cell activation // inferred
1440900_a	0.000378	-2.01	NM_001033251//NM_1_1	Gpr174	G protein-coupled receptor 174	0007165 // signal transduction // inferred from electronic annotation//0007186 // G-protein coupled receptor signaling pathway // inferred from electronic annotation
1449153_a	0.005002	-2.01	NM_008605	Mmp12	matrix metalloproteinase 12	0006508 // proteolysis // inferred from electronic annotation//0008152 // metabolic process // inferred from electronic annotation//0035313 // wound healing, spreading of epidermal cells // not
1420464_s	0.000687	-2.01	NM_001166672//NM_1_1	Gm10693//Gm14548//Ll	predicted pseudogene 10693//predicted gene	0001782 // B cell homeostasis // inferred from mutant phenotype//0019221 // cytokine-mediated signaling pathway // inferred from mutant phenotype//0019724 // B cell mediated immunity // inferred from
1420464_s	0.000687	-2.01	NM_001166672//NM_1_1	Gm10693//Gm14548//Ll	predicted pseudogene 10693//predicted gene	0001782 // B cell homeostasis // inferred from mutant phenotype//0019221 // cytokine-mediated signaling pathway // inferred from mutant phenotype//0019724 // B cell mediated immunity // inferred from
1420464_s	0.000687	-2.01	NM_001166672//NM_1_1	Gm10693//Gm14548//Ll	predicted pseudogene 10693//predicted gene	0001782 // B cell homeostasis // inferred from mutant phenotype//0019221 // cytokine-mediated signaling pathway // inferred from mutant phenotype//0019724 // B cell mediated immunity // inferred from
1420464_s	0.000687	-2.01	NM_001166672//NM_1_1	Gm10693//Gm14548//Ll	predicted pseudogene 10693//predicted gene	0001782 // B cell homeostasis // inferred from mutant phenotype//0019221 // cytokine-mediated signaling pathway // inferred from mutant phenotype//0019724 // B cell mediated immunity // inferred from
1420464_s	0.000687	-2.01	NM_001166672//NM_1_1	Gm10693//Gm14548//Ll	predicted pseudogene 10693//predicted gene	0001782 // B cell homeostasis // inferred from mutant phenotype//0019221 // cytokine-mediated signaling pathway // inferred from mutant phenotype//0019724 // B cell mediated immunity // inferred from
1426538_a	0.000102	-2.00	NM_001127233//NM_1_1	Trp53	transformation related protein 53	0000060 // protein import into nucleus, translocation // inferred from direct assay//0000122 // negative regulation of transcription from RNA polymerase II promoter // inferred from direct assay//0000122 //
1417446_a	0.000015	11.89	NM_001253804//NM_1_1	Slc12a4	solute carrier family 12, member 4	0006810 // transport // inferred from electronic annotation//0006811 // ion transport // inferred from electronic annotation//0006813 // potassium ion transport // inferred from electronic annotation//00055085
1428240_a	0.000002	8.76	NM_020252//NM_177	Nrxn1	neurexin 1	0001525 // angiogenesis // inferred from electronic annotation//0007155 // cell adhesion // inferred from electronic annotation//0007157 // heterophilic cell-cell adhesion // inferred from direct assay//0007158
1441115_a	0.000017	4.47		D18Erd232e	DNA segment, Chr 18, ERATO Doi 232, expressed	
1418217_a	0.000017	4.31	NM_138314//NM_178	Nme7	NME/NUM23 family member 7	0003351 // epithelial cilium movement // inferred from mutant phenotype//0006165 // nucleoside diphosphate phosphorylation // inferred from electronic annotation//0006183 // GTP biosynthetic process //
1450297_a	0.000728	4.26	NM_031168	Il6	interleukin 6	0001781 // neutrophil apoptotic process // inferred from direct assay//0001781 // neutrophil apoptotic process // inferred from mutant phenotype//0001781 // neutrophil apoptotic process // not
1427878_a	0.000017	4.06	NM_001081365	Cystm1	cysteine-rich transmembrane module containing 1	
1418156_a	0.000050	3.48	NM_021342	Kcne4	potassium voltage-gated channel, Isk-related subfamily, F1	0006810 // transport // inferred from electronic annotation//0006811 // ion transport // inferred from electronic annotation//0006813 // potassium ion transport // inferred from electronic annotation//00034765
1423100_a	0.000023	3.40	NM_010234	Fos	FB1 osteosarcoma oncogene	0001661 // conditioned taste aversion // inferred from electronic annotation//0006355 // regulation of transcription, DNA-dependent // inferred from direct assay//0006355 // regulation of transcription, DNA-
1430622_a	0.000059	3.40	XR_105767//XR_10701	4833423F13Rik	RIKEN cDNA 4833423F13Rik gene	
1452519_a	0.000034	3.19	NM_011756	Zfp36	zinc finger protein 36	0000122 // negative regulation of transcription from RNA polymerase II promoter // inferred from mutant phenotype//0000122 // negative regulation of transcription from RNA polymerase II promoter // not
1416505_a	0.000046	3.12	NM_010444	Nr4a1	nuclear receptor subfamily 4, group A, member 1	0001938 // positive regulation of endothelial cell proliferation // not recorded//0002042 // cell migration involved in sprouting angiogenesis // not recorded//0006351 // transcription, DNA-dependent // inferred
1436788_a	0.000085	3.09	NM_001094152	JunB	DNA segment, Chr 5, Wayne State University 152, Jun-B oncogene	
1415899_a	0.000613	3.05	NM_008416	Fosb	FB1 osteosarcoma oncogene B	0001570 // vasculogenesis // inferred from mutant phenotype//0001649 // osteoblast differentiation // inferred from mutant phenotype//0001701 // in utero embryonic development // inferred from mutant
1422134_a	0.000298	3.03	NM_008036	Fosb	FB1 osteosarcoma oncogene B	0006355 // regulation of transcription, DNA-dependent // inferred from electronic annotation//0006366 // transcription from RNA polymerase II promoter // not recorded//001277 // cellular response to calcium
1417065_a	0.000086	3.02	NM_007913	Egr1	early growth response 1	0000122 // negative regulation of transcription from RNA polymerase II promoter // inferred from direct assay//0001975 // response to amphetamine // inferred from electronic annotation//0006351 //
1459326_a	0.000039	2.99		D9Erd256e	DNA segment, Chr 9, ERATO Doi 256, expressed	
1460417_a	0.000017	2.96	NM_144555//XR_0351	AB041803	cDNA sequence AB041803	
1441588_a	0.000017	2.95	NR_001461	Kcnq1ot1	KCNQ1 overlapping transcript 1	0006349 // regulation of gene expression by genetic imprinting // inferred from direct assay//0006349 // regulation of gene expression by genetic imprinting // inferred from mutant phenotype//0010216 //
1420747_a	0.000261	2.82	NM_012022//XR_0357	Ppnr	per-pentamer repeat gene	
1422272_a	0.000049	2.76	NM_008835//NR_0282	Phx4	per-hexamer repeat gene 4	
1442489_a	0.000117	2.75		D1Erd564e	DNA segment, Chr 1, ERATO Doi 564, expressed	
1418932_a	0.000830	2.74	NM_017373	Nfil3	nuclear factor, interleukin 3, regulated	0000122 // negative regulation of transcription from RNA polymerase II promoter // not recorded//0006351 // transcription, DNA-dependent // inferred from electronic annotation//0006355 // regulation of
1428655_a	0.000018	2.70	NM_028658	Ppp1r21	protein phosphatase 1, regulatory subunit 21	0055114 // oxidation-reduction process // inferred from electronic annotation
1443242_a	0.000733	2.66		D5Erd121e	DNA segment, Chr 5, ERATO Doi 121, expressed	
1441228_a	0.000692	2.55	NM_001109914	Apol1	apolipoprotein L domain containing 1	0001525 // angiogenesis // inferred from electronic annotation//0001666 // response to hypoxia // inferred from electronic annotation//0006869 // lipid transport // inferred from electronic
1434353_a	0.000120	2.55	NM_001198808//NM_1_1	Sfmbt2	Scm-like with four mbt domains 2	0006355 // regulation of transcription, DNA-dependent // inferred from electronic annotation//0010629 // negative regulation of gene expression // inferred from sequence or structural similarity
1456671_a	0.000138	2.54	NR_027799	Tbrg3	transforming growth factor beta regulated gene 3	
1427602_a	0.000708	2.53		D6p1	diabetic embryopathy 1	
1442409_a	0.000034	2.50		D9Wsu90e	DNA segment, Chr 9, Wayne State University 90, DNA segment, Chr 9, ERATO Doi 258, expressed	
1459190_a	0.000070	2.47		D3Erd258e	DNA segment, Chr 3, ERATO Doi 258, expressed	
1450749_a	0.000386	2.40	NM_001139509//NM_1_1	Nr4a2	nuclear receptor subfamily 4, group A, member 2	0001666 // response to hypoxia // inferred from mutant phenotype//0001764 // neuron migration // inferred from mutant phenotype//0001975 // response to amphetamine // inferred from mutant
1418349_a	0.000224	2.40	NM_010415	Hbegf	heparin-binding EGF-like growth factor	0001525 // angiogenesis // non-traceable author statement//0001832 // blastocyst growth // traceable author statement//0007173 // epidermal growth factor receptor signaling pathway // inferred from direct
1451173_a	0.000226	2.39	NM_001146046//NM_1_1	Lrrc49	leucine rich repeat containing 49	
1442484_a	0.000814	2.38		D9Erd306e	DNA segment, Chr 9, ERATO Doi 306, expressed	
1417601_a	0.000367	2.37	NM_015811	Rgs1	regulator of G-protein signaling 1	0007186 // G-protein coupled receptor signaling pathway // traceable author statement//0009968 // negative regulation of signal transduction // inferred from electronic annotation//0038032 // termination of G-
1444872_a	0.000063	2.34		D3Erd740e	DNA segment, Chr 3, ERATO Doi 740, expressed	
1457539_a	0.000106	2.33		D10Erd709e	DNA segment, Chr 10, ERATO Doi 709, expressed	
1433000_a	0.000288	2.33	NM_153287	Csrnp1	cysteine-serine-rich nuclear protein 1	0006351 // transcription, DNA-dependent // inferred from electronic annotation//0006355 // regulation of transcription, DNA-dependent // inferred from mutant phenotype//0006915 // apoptotic process //
1421514_a	0.000036	2.30	NM_133194	Scml2	sex comb on midleg-like 2 (Drosophila)	0006355 // regulation of transcription, DNA-dependent // inferred from electronic annotation
1430386_a	0.000142	2.29	NR_033228	E030024N20Rik	peptidylprolyl isomerase A pseudogene 8	
1416442_a	0.000810	2.28	NM_010499	Ier2	immediate early response 2	
1422064_a	0.000022	2.28	NM_019778//NM_181	Zbtb20	zinc finger and BTB domain containing 20	0000122 // negative regulation of transcription from RNA polymerase II promoter // inferred from mutant phenotype//0006351 // transcription, DNA-dependent // inferred from electronic annotation//0006355
1457901_a	0.000181	2.28		D4Erd76e	DNA segment, Chr 4, ERATO Doi 76, expressed	
1438222_a	0.000885	2.21		D2Erd612e	DNA segment, Chr 2, ERATO Doi 612, expressed	
1426438_a	0.000032	2.20	NM_012008	Ddx3	DEAD (Asp-Glu-Ala-Gln) box polypeptide 3, Y-linked	
1417262_a	0.000575	2.19	NM_011198	Ptg2	prostaglandin-endoperoxide synthase 2	0001516 // prostaglandin biosynthetic process // inferred from direct assay//0001516 // prostaglandin biosynthetic process // not recorded//0001525 // angiogenesis // not recorded//0006629 // lipid metabolic
1420097_a	0.000119	2.19		D13Erd787e	DNA segment, Chr 13, ERATO Doi 787, expressed	
1419766_a	0.000131	2.18	NM_010831	Sik1	salt inducible kinase 1	0000122 // negative regulation of transcription from RNA polymerase II promoter // not recorded//0002028 // regulation of sodium ion transport // not recorded//0006468 // protein phosphorylation // inferred
1422247_a	0.000045	2.15	NM_009484	Uty	ubiquitously transcribed tetratricopeptide repeat gene, Y	0001701 // in utero embryonic development // inferred from mutant phenotype//0007507 // heart development // inferred from mutant phenotype//0016568 // chromatin modification // inferred from
1449530_a	0.000022	2.15	NM_032000	Trps1	trichorhinalphalangeal syndrome 1 (human)	0000122 // negative regulation of transcription from RNA polymerase II promoter // not recorded//0002062 // chondrocyte differentiation // inferred from genetic interaction//0006351 // transcription, DNA-
1425229_a	0.000037	2.14	NM_001142918//NM_1_1	Tcf7l2	transcription factor 7 like 2, T cell specific, HMG box	0000122 // negative regulation of transcription from RNA polymerase II promoter // not recorded//0001568 // blood vessel development // not recorded//0006351 // transcription, DNA-dependent // inferred
1438130_a	0.000378	2.13	NM_027427	Taf15	TAFl5 RNA polymerase II, TATA box binding protein (TBP)-	
1416039_x	0.000111	2.10	NM_010516	Cyr61	cysteine rich protein 61	0001558 // regulation of cell growth // inferred from electronic annotation//0001649 // osteoblast differentiation // inferred from genetic interaction//0001934 // positive regulation of protein phosphorylation //
1429432_a	0.000172	2.09	NM_001081290	Prrc2c	proline-rich coiled-coil 2C	
1437595_a	0.000282	2.08	NM_183160	Tmem252	transmembrane protein 252	
1420649_a	0.000034	2.07	NM_007496	Zfx3	zinc finger homeobox 3	0000122 // negative regulation of transcription from RNA polymerase II promoter // not recorded//0006351 // transcription, DNA-dependent // inferred from electronic annotation//0006355 // regulation of
1445999_a	0.000051	2.06		D19Erd132e	DNA segment, Chr 19, ERATO Doi 132, expressed	

Table S4

Gene_ID	p (Corr)	FD (Vehicle Hej vs Ouj)	RefSeq Transcript ID	Gene Symbol	Gene Title	Gene Ontology Biological Process
1460063_a	0.000038	2.05		D5Ertd798e	DNA segment, Chr 5, ERATO Doi 798, expressed	
1422473_a	0.000086	2.04	NM_001177980//NM_i	Pde4b	phosphodiesterase 4B, cAMP specific	0001780 // neutrophil homeostasis // inferred from mutant phenotype//0006198 // cAMP catabolic process // not recorded//0006939 // smooth muscle contraction // inferred from mutant phenotype//0007165
1450716_a	0.000739	2.02	NM_009621	Adams1	a disintegrin-like and metallopeptidase (reprolysin type)	0001542 // ovulation from ovarian follicle // inferred from mutant phenotype//0001822 // kidney development // inferred from mutant phenotype//0006508 // proteolysis // inferred from electronic
1459749_s	0.000209	2.02	NM_183221	Fat4	FAT tumor suppressor homolog 4 (Drosophila)	0007155 // cell adhesion // inferred from electronic annotation//0007156 // homophilic cell adhesion // inferred from electronic annotation
1431659_a	0.000248	2.01	NM_023440	Tmem86b	transmembrane protein 86B	0008152 // metabolic process // inferred from electronic annotation//0046485 // ether lipid metabolic process // not recorded
1418936_a	0.000138	2.00	NM_010755	Maff	v-maf musculoaponeurotic fibrosarcoma oncogene	0001701 // in utero embryonic development // inferred from genetic interaction//0006351 // transcription, DNA-dependent // inferred from electronic annotation//0006355 // regulation of transcription, DNA-
1427555_a	0.000226	2.00	NM_001033276//NM_i	Kmt2d	lysine (K)-specific methyltransferase 2D	0001555 // oocyte growth // inferred from mutant phenotype//0001701 // in utero embryonic development // inferred from mutant phenotype//0006342 // chromatin silencing // inferred from mutant

Table S5. Comparative pathway analysis of respiratory syncytial virus-responses lung genes in *Tlr4* normal inbred strains of mice.

Strain	Ingenuity Canonical Pathways	-LogP	Ingenuity Networks	Score	Upstream Regulators	P (overlap)
C57BL/6J	Role of Macrophages, Fibroblasts and Endothelial Cells in Rheumatoid Arthritis	14.0	Cardiovascular System Development & Function, Cell-To-Cell Signaling & Interaction, Cellular Growth	32	lipopolysaccharide	8.68E-59
	IL-10 Signaling	12.8			IFNG	3.04E-43
	Dendritic Cell Maturation	11.8	Developmental Disorder, Hereditary Disorder, Ophthalmic Disease	32	TNF	1.22E-42
	Hepatic Fibrosis / Hepatic Stellate Cell Activation	11.2			TGFB1	2.85E-33
	NF- κ B Signaling	10.9	Cancer, Organismal Injury & Abnormalities, Cellular Assembly & Organization	32	poly rI:rC-RNA	2.88E-28
	Granulocyte Adhesion and Diapedesis	10.5			TLR4	6.06E-28
	Atherosclerosis Signaling	9.33			IL1B	3.59E-27
	Acute Phase Response Signaling	9.25			IFNA	5.35E-26
	IL-6 Signaling	8.80			IRF7	1.10E-25
	Activation of IRF by Cytosolic Pattern Recognition Receptors	8.47			NFkB (complex)	1.77E-25
	Role of Pattern Recognition Receptors in Recognition of Bacteria and Viruses	8.14				
	IL-8 Signaling	7.69				
BALB/cJ	Dendritic Cell Maturation	15.9	Embryonic Development, Organismal Development, Tissue Development	38	lipopolysaccharide	8.07E-78
	Granulocyte Adhesion and Diapedesis	13.3			IFNG	7.96E-65
	Agranulocyte Adhesion and Diapedesis	11.6	Cellular Assembly & Organization, Cellular Function & Maintenance, Cellular Movement	38	TNF	3.79E-52
	Role of Pattern Recognition Receptors in Recognition of Bacteria and Viruses	11.2			STAT1	1.76E-46
	Role of Macrophages, Fibroblasts and Endothelial Cells in Rheumatoid Arthritis	11.1	Connective Tissue Disorders, Developmental Disorder, Hereditary Disorder	36	IL1B	6.54E-45
	IL-10 Signaling	10.1			STAT3	6.52E-43
	Hepatic Fibrosis / Hepatic Stellate Cell Activation	9.10	Cell-To-Cell Signaling & Interaction, Cellular Movement, Hematological System Development & Function	36	IFNA	6.31E-41
	Activation of IRF by Cytosolic Pattern Recognition Receptors	8.65			IRF7	6.91E-41
	Communication between Innate and Adaptive Immune Cells	8.57			TGFB1	3.57E-40
	Acute Phase Response Signaling	7.61				
	Altered T Cell and B Cell Signaling in Rheumatoid Arthritis	7.35				
	LXR/RXR Activation	7.09				
C3H/HeOuJ	Granulocyte Adhesion and Diapedesis	14.9	Cell Death & Survival, Skeletal & Muscular Disorders, etc.	48	lipopolysaccharide	1.58E-47
	Agranulocyte Adhesion and Diapedesis	10.5			TNF	1.51E-41
	Communication between Innate and Adaptive Immune Cells	10.2	Cellular Movement, Hematological System Development & Function, Immune Cell Trafficking	45	IFNG	3.62E-34
	Role of Hypercytokinemia/hyperchemokine in the Pathogenesis of Influenza	9.80			IL1B	1.44E-33
	Altered T Cell and B Cell Signaling in Rheumatoid Arthritis	9.64	Reproductive System Development & Function, Dermatological Diseases	43	MYD88	1.33E-32
	IL-10 Signaling	9.57			IL10	5.95E-31
	Systemic Lupus Erythematosus Signaling	7.94	Hereditary Disorder, Neurological Disease, Organismal Injury, etc.	40		
	Cholecystokinin/Gastrin-mediated Signaling	7.51				
	Toll-like Receptor Signaling	7.44	RNA Post-Transcriptional Modification, Hereditary Disorder, etc. DNA Replication, Recombination, & Repair, Cell Morphology, Cellular Compromise	38		
	Differential Regulation of Cytokine Production in Intestinal Epithelial Cells by IL-17A and IL-17F	6.89				
				36		
A/J	Granulocyte Adhesion and Diapedesis	9.85	Developmental Disorder, Hereditary Disorder, Metabolic Disease	38	IFNAR1	6.05E-19
	Agranulocyte Adhesion and Diapedesis	8.54			TLR3	2.60E-18
	Role of Hypercytokinemia/hyperchemokine in the Pathogenesis of Influenza	4.55	Antimicrobial Response, Inflammatory Response, Infectious Diseases	33	TLR9	4.07E-15
	Differential Regulation of Cytokine Production in Intestinal Epithelial Cells by IL-17A and IL-17F	4.27			MYD88	5.97E-15
AKR/J	IL-17A Signaling in Fibroblasts	3.55	RNA Post-Transcriptional Modification, Protein Synthesis, Gene Expression	28	dalfampridine	5.23E-13
	Corticotropin Releasing Hormone Signaling	3.10			bicuculline	2.38E-12
DBA/2J	Cell Cycle: G2/M DNA Damage Checkpoint Regulation	4.95	Cell Cycle, Cellular Movement, Cancer	48	dextran sulfate	1.24E-14
	Mitotic Roles of Polo-Like Kinase	3.15			CDKN1A	1.71E-13
					CSF2	1.65E-12

Table S6. Lung genes significantly altered by respiratory syncytial virus (RSV) in BALB/c (BALBc) mice (One-Way ANOVA at p<0.01).

Blue(-): fold decrease by RSV vs vehicle. Red : fold increase by RSV vs vehicle.

Gene ID	p (Corr)	FC-RSV 1 d	FC-RSV 5 d	RefSeq Transcript ID	Gene Symbol	Gene Title	Gene Ontology Biological Process
AFFX-DapX-3_at	0.005097	221.21	19.96	NM_203320	Cxcl3	chemokine (C-X-C motif) ligand 3	0006935 // chemotaxis // inferred from electronic annotation//0006954 // inflammatory response // not recorded//0006955 //
AFFX-Lyx-3_at	0.007104	216.68	34.13	NM_021274	Cxcl10	chemokine (C-X-C motif) ligand 10	0002690 // positive regulation of leukocyte chemotaxis // not recorded//0006935 // chemotaxis // not recorded//0006954 //
AFFX-r2-Bs-dap-3	0.005614	196.43	2.19	NM_009140	Cxcl2	chemokine (C-X-C motif) ligand 2	0001975 // response to amphetamine // inferred from electronic annotation//0002237 // response to molecule of bacterial origin //
AFFX-MURINE_b	0.003874	161.55	3.02	NM_011337	Ccl3	chemokine (C-C motif) ligand 3	0000165 // MAPK cascade // inferred from sequence or structural similarity//0001649 // osteoblast differentiation // inferred from
1415683_at,1414f	0.005114	146.78	20.33	NM_019494//NR_038116	Cxcl11	chemokine (C-X-C motif) ligand 11	0002690 // positive regulation of leukocyte chemotaxis // inferred from electronic annotation//0006935 // chemotaxis // inferred from
1415686_at,1415f	0.009010	146.46	26.91	NM_011315	Saa3	serum amyloid A 3	0006953 // acute-phase response // inferred from electronic annotation//00035634 // response to stilbenoid // inferred from expression
1415694_at,1425f	0.000738	133.39	6.02	NM_008392//XM_006518582	Irg1	immunoresponsive gene 1	0002376 // immune system process // inferred from electronic annotation//0002760 // positive regulation of antimicrobial humoral
1415695_at,143f	0.002521	101.39	1.43	NM_009117//XM_006540724	Saa1	serum amyloid A 1	0006953 // acute-phase response // inferred from electronic annotation//0008203 // cholesterol metabolic process // inferred from
1415703_at,1424f	0.007025	98.97	5.95	NM_011410//XM_006532659	Sifn4//Sifn3	schlafen 4//schlafen 3	0008285 // negative regulation of cell proliferation // inferred from direct assay
1415710_at,231f	0.004006	86.18	53.34	NM_008599	Cxcl9	chemokine (C-X-C motif) ligand 9	0006935 // chemotaxis // inferred from electronic annotation//0006935 // chemotaxis // inferred from sequence or structural
1415716_a_at,14f	0.003438	82.18	1.79	NM_011409//XM_006532656	Sifn3//Sifn4	schlafen 3//schlafen 4	0008285 // negative regulation of cell proliferation // inferred from direct assay
1415716_a_at,15f	0.002258	77.47	3.87	NM_019948	Clec4e	C-type lectin domain family 4, member e	0002376 // immune system process // inferred from electronic annotation//0006955 // immune response // inferred from mutant
1415743_at,151f	0.008196	71.22	4.49	NM_011333	Ccl2	chemokine (C-C motif) ligand 2	0000165 // MAPK cascade // inferred from electronic annotation//0001525 // angiogenesis // traceable author statement//0001666 //
1415764_at,142f	0.004098	71.06	1.96	NM_031168	Il6	interleukin 6	0001781 // neutrophil apoptotic process // inferred from direct assay//0001781 // neutrophil apoptotic process // inferred from mutant
1415764_at,142f	0.003821	70.05	3.30	NM_010846//NR_003520	Mx1	myxovirus (influenza virus) resistance 1	0002376 // immune system process // inferred from electronic annotation//0006184 // GTP cascade process // traceable author
1415770_at,145f	0.002196	65.15	11.53	NM_008327//NM_011940//X	Ifi202b//LOC100044068	interferon-activated gene 202b//interferon-activable protein 202-like	0002376 // immune system process // inferred from electronic annotation//0006954 // inflammatory response // inferred from
1415806_at,145f	0.000837	54.15	9.18	NM_031367	Ifi44l	interferon-induced protein 44 like	0006955 // immune response // inferred from direct assay
1415827_a_at,14f	0.002818	52.76	3.63	NM_001044384//NM_001294	Timp1	tissue inhibitor of metalloproteinase 1	0001775 // cell activation // not recorded//0007568 // aging // inferred from electronic annotation//0008284 // positive regulation of
1415837_at,144f	0.006015	52.27	3.16	NM_015783//XR_168557//X	Gm9706//Isg15	predicted gene 9706//I5G15 ubiquitin-like modifier	0019941 // modification-dependent protein catabolic process // inferred from direct assay//0031397 // negative regulation of protein
1415849_a_at,14f	0.009022	51.70	8.09	NM_026835	Ms4a6d	membrane-spanning 4-domains, subfamily A, member 6D	
1415860_at,166f	0.006813	51.63	-2.19	NM_008768	Orm1	orosomucoid 1	0002682 // regulation of immune system process // inferred from electronic annotation//0006810 // transport // inferred from
1415871_at,143f	0.004799	49.20	2.01	NM_001039701//NM_001159	Il1rn	interleukin 1 receptor antagonist	0001660 // fever generation // not recorded//0001960 // negative regulation of cytokine-mediated signaling pathway // not
1415876_a_at,12f	0.006419	47.32	8.07	NM_001004174//XM_006499	AA467197	expressed sequence AA467197	
1415877_at,143f	0.000893	45.59	3.54	NM_029499//XM_006527250	Ms4a4c	membrane-spanning 4-domains, subfamily A, member 4C	
1415881_at,141f	0.004257	44.46	12.46	NM_011331	Ccl12	chemokine (C-C motif) ligand 12	0000165 // MAPK cascade // not recorded//0001525 // angiogenesis // inferred from direct assay//0002548 // monocyte chemotaxis //
1415886_at,273f	0.004522	42.31	3.74	NM_001252600//NM_001252	Ifi7	interferon regulatory factor 7	0002376 // immune system process // inferred from electronic annotation//0002819 // regulation of adaptive immune response // not
1415890_at,239f	0.007406	41.74	1.51	NM_001101605//NM_001110	Mx1446	predicted gene 14446	0009615 // response to virus // inferred from electronic annotation//0005688 // regulation of defense response to virus // inferred from
1415912_a_at,14f	0.006413	41.71	7.32	NM_009141	Cxcl5	chemokine (C-X-C motif) ligand 5	0001776 // leukocyte homeostasis // inferred from mutant phenotype//0001816 // cytokine production // not recorded//0006935 //
1415912_a_at,14f	0.006413	40.22	2.00	NM_145209//XM_006530294	Oas1	2'-5' oligoadenylate synthetase-like 1	0002376 // immune system process // inferred from electronic annotation//0006955 // immune response // inferred from electronic
1415912_a_at,14f	0.006413	39.78	2.73	NM_015783//XR_168557//X	Gm9706//Isg15	predicted gene 9706//I5G15 ubiquitin-like modifier	0019941 // modification-dependent protein catabolic process // inferred from direct assay//0031397 // negative regulation of protein
1415922_s_at,14f	0.006675	39.63	4.94	NM_011407	Sifn1	schlafen 1	0000122 // negative regulation of transcription from RNA polymerase II promoter // inferred from direct assay//0001933 // negative
1415927_at,114f	0.000240	37.44	2.82	NM_013654	Ccl7	chemokine (C-C motif) ligand 7	0006935 // chemotaxis // inferred from electronic annotation//0006954 // inflammatory response // inferred from electronic
1415945_at,143f	0.008675	36.63	3.11	NM_175026	Pyhin1	pyrin and HIN domain family, member 1	0035458 // cellular response to interferon-beta // inferred from direct assay
1415949_at,143f	0.000412	36.49	2.07	NM_013652	Ccl4	chemokine (C-C motif) ligand 4	0006935 // chemotaxis // inferred from electronic annotation//0006954 // inflammatory response // not recorded//0006955 //
1415950_a_at,14f	0.001213	34.51	6.79	NM_001139519//NM_021394	Zbp1	Z-DNA binding protein 1	0002376 // immune system process // inferred from electronic annotation//0008152 // metabolic process // inferred from electronic
1415958_at,141f	0.005661	34.11	1.81	NM_009252	Serpina3n	serine (or cysteine) peptidase inhibitor, clade A, member 3N	0006953 // acute-phase response // inferred from electronic annotation//0006954 // inflammatory response // inferred from electronic
1415975_at,141f	0.006015	34.01	5.52	NM_133871//XM_006502485	Ifi44	interferon-induced protein 44	
1415984_at,113f	0.002242	33.71	5.14	NM_020498//XM_006521212	Ly6i	lymphocyte antigen 6 complex, locus I	0002639 // positive regulation of immunoglobulin production // inferred from mutant phenotype//0002925 // positive regulation of
1415989_at,144f	0.004493	33.41	1.16	NM_017371	Hpx	hemopexin	0006810 // transport // inferred from electronic annotation//0006811 // ion transport // inferred from electronic annotation
1415994_at,131f	0.007782	32.90	2.60	NM_008331	Ifi1	interferon-induced protein with tetratricopeptide repeats 1	0002376 // immune system process // inferred from electronic annotation//0006164 // purine nucleotide biosynthetic process //
1416006_at,172f	0.009117	30.67	21.71	NM_175449	Fam26f	family with sequence similarity 26, member F	0001788 // antibody-dependent cellular cytotoxicity // inferred from mutant phenotype//0001798 // positive regulation of type Ila
1416010_a_at,14f	0.006230	29.56	1.76	NM_145226	Oas3	2'-5' oligoadenylate synthetase 3	0006351 // transcription, DNA-templated // inferred from sequence or structural similarity//0006810 // transport // inferred from
1416016_at,144f	0.000573	29.40	5.68	NM_010186	Fcgr1	Fc receptor, IgG, high affinity 1	0000122 // negative regulation of transcription from RNA polymerase II promoter // not recorded//0000165 // MAPK cascade // not
1416018_at,141f	0.003213	28.89	2.11	NM_001171024//NM_010215	Il4i1//Nup62-il4i1	interleukin 4 induced 1//Nup62-il4i1 protein	0001503 // ossification // not recorded//0002376 // immune system process // inferred from electronic annotation//0008152 //
1416021_a_at,14f	0.003018	28.68	4.16	NM_008361//XM_006498795	Il1b	interleukin 1 beta	0002518 // lymphocyte chemotaxis across high endothelial venule // inferred from mutant phenotype//0006935 // chemotaxis //
1416023_at,144f	0.001559	28.68	1.63	NM_021384//XM_006515160	Rsd2	radical S-adenosyl methionine domain containing 2	0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 // regulation of transcription, DNA-templated
1416034_at,143f	0.004684	26.57	2.71	NM_018866	Cxcl13	chemokine (C-X-C motif) ligand 13	0006508 // proteolysis // inferred from mutant phenotype//0006511 // ubiquitin-dependent protein catabolic process // inferred from
1416041_at,203f	0.006543	26.19	2.42	NM_001167828//NM_199146	Trim30d//Trim30a	tripartite motif-containing 30D//tripartite motif-containing 30A	0035690 // cellular response to drug // inferred from expression pattern
1416049_at,104f	0.006127	25.85	2.16	NM_011909	Usp18	ubiquitin specific peptidase 18	0002376 // immune system process // inferred from electronic annotation//0006915 // apoptotic process // inferred from electronic
1416051_at,144f	0.000380	25.48	4.51	NM_001033122//XM_006505	Cd69	CD69 antigen	0002376 // immune system process // inferred from electronic annotation//0006164 // purine nucleotide biosynthetic process //
1416056_a_at,14f	0.006230	25.42	2.34	NM_008332//XM_006526705	Ifi2	interferon-induced protein with tetratricopeptide repeats 2	0008152 // metabolic process // inferred from electronic annotation//0009615 // response to virus // not recorded//0051607 //
1416059_at,270f	0.002591	25.34	3.59	NM_011854//XM_006530314	Oas2	2'-5' oligoadenylate synthetase-like 2	0002237 // response to molecule of bacterial origin // not recorded//0002526 // acute inflammatory response // not
1416060_at,141f	0.001384	25.00	1.70	NM_001081215//NM_001293	Ddx60	DEAD (Asp-Glu-Ala-Asp) box polypeptide 60	0002376 // immune system process // inferred from electronic annotation//0006508 // proteolysis // inferred from electronic
1416067_at,159f	0.006069	24.22	2.93	NM_008176	Cxcl1	chemokine (C-X-C motif) ligand 1	0019221 // cytokine-mediated signaling pathway // inferred from electronic annotation
1416069_at,143f	0.009006	23.93	3.27	NM_001142706//NM_008198	Cfb	complement factor B	0006955 // immune response // not recorded//0007165 // signal transduction // not recorded//0007166 // cell surface receptor
1416072_at,124f	0.005005	23.66	1.82	NM_010555//XM_006495724	Il1r2	interleukin 1 receptor, type II	0006165 // nucleoside diphosphate phosphorylation // not recorded//000221 // pyrimidine nucleotide biosynthetic process // inferred
1416076_at,141f	0.002012	23.46	9.26	NM_021893//XM_006527249	Cd274	CD274 antigen	0006508 // proteolysis // not recorded//0030574 // collagen catabolic process // inferred from electronic annotation
1416076_at,141f	0.002295	22.58	2.06	NM_020557//XR_381188	Cmpk2	cytidine diphosphate (UMP-CMP) kinase 2, mitochondrial	0002376 // immune system process // inferred from electronic annotation//0006164 // purine nucleotide biosynthetic process //
1416077_at,144f	0.000099	22.51	2.02	NM_008611	Mmp8	matrix metalloproteinase 8	0006629 // lipid metabolic process // inferred from electronic annotation//0006633 // fatty acid biosynthetic process // inferred from
1416083_at,141f	0.004786	22.28	3.39	NM_145211//XM_006530330	Oas1a	2'-5' oligoadenylate synthetase 1A	0002376 // immune system process // inferred from electronic annotation
1416091_at,141f	0.006150	21.83	9.48	NM_009890	Ch25h	cholesterol 25-hydroxylase	0006351 // transcription, DNA-templated // inferred from sequence or structural similarity//0006810 // transport // inferred from
1416105_at,145f	0.007025	20.98	4.84	NM_001291892//NM_001291	Gp49a//Lilrb4	glycoprotein 49 A//leukocyte immunoglobulin-like receptor, subfamily B,	0001913 // T cell mediated cytotoxicity // inferred from mutant phenotype//0006508 // proteolysis // not recorded//0006915 //
1416121_at,143f	0.000233	20.90	1.78	NM_001171024//NM_010215	Il4i1//Nup62-il4i1	interleukin 4 induced 1//Nup62-il4i1 protein	0006810 // transport // inferred from electronic annotation//0006820 // anion transport // inferred from sequence or structural
1416125_at,144f	0.000333	20.87	12.79	NM_013542	Gzmb	granzyme B	0010466 // negative regulation of peptidase activity // inferred from electronic annotation
1416128_at,144f	0.004247	20.66	9.36	NM_011867//XM_006515091	Slc26a4	solute carrier family 26, member 4	0002376 // immune system process // inferred from electronic annotation//0045087 // innate immune response // inferred from
1416128_at,143f	0.003327	19.94	3.38	NM_001081957	Wfcd17	WAP four-disulfide core domain 17	0032496 // response to lipopolysaccharide // inferred from electronic annotation//0042088 // T-helper 1 type immune response // not
1416129_at,141f	0.000807	19.76	2.30	NM_001163161//NM_010819	Clec4d	C-type lectin domain family 4, member d	0006629 // lipid metabolic process // inferred from electronic annotation//0016042 // lipid catabolic process // inferred from electronic
1416141_a_at,14f	0.006702	19.75	4.69	NM_010531//XM_006507380	Il18bp	interleukin 18 binding protein	
1416158_at,141f	0.000614	19.42	1.92	NM_134102//XM_006522771	Plat1a	phospholipase A1 member A	
1416164_at,144f	0.008806	19.21	3.37	NM_001166376//NM_028595	Ms4a6c	membrane-spanning 4-domains, subfamily A, member 6C	
1416168_at,145f	0.004794	18.42	14.26	NM_001033767//XM_006525	Gm4951	predicted gene 4951	
1416183_a_at,14f	0.003312	18.08	2.27	NM_025992//NM_028861	Herc6	hect domain and RLD 6	
1416213_x_at,14f	0.005866	17.84	1.60	NM_008630	Mt2	metallothionein 2	
1416217_a_at,14f	0.004189	17.65	2.31	NM_001162883//NM_001168	Apol9a//Apol9b	apolipoprotein L 9a//apolipoprotein L 9b	
1416234_a_at,141f	0.002104	17.27	2.29	NM_001166672//NM_001289	Gm10693//Gm14548//Lilra6f	predicted pseudogene 10693//predicted gene 14548//leukocyte	
1416260_a_at,15f	0.003291	17.08	2.31	NM_198095	Bst2	bone marrow stromal cell antigen 2	

Table S6

Gene_ID	p (Corr)	FC-RSV 1 d	FC-RSV 5 d	RefSeq Transcript ID	Gene Symbol	Gene Title	Gene Ontology Biological Process
1416269_at 143	0.002826	17.07	2.33	NM_001012236///NM_011637	<i>Atrip///Trex1</i>	ATR interacting protein///three prime repair exonuclease 1	0000738 // DNA catabolic process, exonucleolytic // inferred from direct assay///0006259 // DNA metabolic process // inferred from
1416270_at 677	0.005199	17.02	1.19	NM_009899///XM_006500965	<i>Clacl1//Clea2</i>	chloride channel calcium activated 1///chloride channel calcium activated 2	0006821 // chloride transport // inferred from direct assay///1902476 // chloride transmembrane transport // inferred from direct
1416271_at 640	0.002314	16.95	3.19	NM_001039559///NR_029457	<i>G530011006Rik</i>	RIKEN cDNA G530011006 gene	0007026 // negative regulation of microtubule depolymerization // inferred from genetic interaction///0008152 // metabolic process //
1416273_at 143	0.004362	16.58	1.74	NM_009627	<i>Adm</i>	adrenomedullin	0001570 // vasculogenesis // not recorded///0001666 // response to hypoxia // inferred from electronic annotation///0001843 // neural
1416293_at 142	0.001965	16.39	3.01	NM_008329///XM_006496675	<i>Ifi204//Ifi205//Mnda//Mndal</i>	interferon activated gene 204///interferon activated gene 205///myeloid cell	0006351 // transcription, DNA-templated // inferred from electronic annotation///0006355 // regulation of transcription, DNA-templated
1416298_at 144	0.004257	16.37	2.31	NM_001085518///NM_172980	<i>Gm14085//Sic28a2</i>	predicted gene 14085///solute carrier family 28 (sodium-coupled nucleoside	0001895 // retina homeostasis // not recorded///0006810 // transport // inferred from electronic annotation///0015860 // purine
1416303_at 141	0.002801	16.23	4.77	NM_001281852///NM_009114	<i>S100a9</i>	S100 calcium binding protein A9 (calgranulin B)	0002376 // immune system process // inferred from electronic annotation///0002523 // leukocyte migration involved in inflammatory
1416309_at 141	0.001385	16.22	2.28	NM_001033632	<i>Ifitm6</i>	interferon induced transmembrane protein 6	0009607 // response to biotic stimulus // inferred from electronic annotation
1416336_s_at 2	0.004362	16.21	3.65	NM_139198	<i>Plac8</i>	placenta-specific 8	0008284 // positive regulation of cell proliferation // inferred from direct assay///0009409 // response to cold // inferred from mutant
1416336_s_at 1	0.004362	16.16	1.43	NM_153511	<i>Il1f9</i>	interleukin 1 family, member 9	0001819 // positive regulation of cytokine production // inferred from direct assay///0006954 // inflammatory response // inferred from
1416351_at 263	0.000337	15.90	2.14	NM_013737///XM_006524365	<i>Pla2g7</i>	phospholipase A2, group VII (platelet-activating factor acetylhydrolase,	0006508 // proteolysis // inferred from electronic annotation///0006629 // lipid metabolic process // inferred from electronic
1416362_a_at 14	0.008668	15.77	2.94	NM_023380	<i>Samsn1</i>	SAM domain, SH3 domain and nuclear localization signals, 1	0002820 // negative regulation of adaptive immune response // inferred from mutant phenotype///0050732 // negative regulation of
1416371_at 144	0.000099	15.57	1.30	NM_013606///NR_003508	<i>Mx2</i>	myxovirus (influenza virus) resistance 2	0002376 // immune system process // inferred from electronic annotation///0006184 // GTP catalytic process // traceable author
1416374_at 141	0.009652	15.34	2.73	NM_009705	<i>Arg2</i>	arginase type II	0000050 // urea cycle // inferred from electronic annotation///0001657 // ureteric bud development // inferred from expression
1416378_at 590	0.004189	14.93	1.06	NM_030601///XM_006502345	<i>Clacl2//Clea1</i>	chloride channel calcium activated 2///chloride channel calcium activated 1	0006821 // chloride transport // not recorded///0043276 // anoikis // inferred from direct assay///0097192 // extrinsic apoptotic
1416382_at 143	0.000103	14.76	1.53	NM_001172588///NM_153101	<i>Mrgpra2a//Mrgpra2b</i>	MAS-related GPR, member A2A///MAS-related GPR, member A2B	0007165 // signal transduction // inferred from electronic annotation///0007186 // G-protein coupled receptor signaling pathway //
1416404_s_at 14	0.000099	14.47	4.29	NM_001039676///XM_006518	<i>Sic39a2</i>	solute carrier family 39 (zinc transporter), member 2	0006829 // zinc ion transport // inferred from direct assay///0030001 // metal ion transport // inferred from electronic
1416404_s_at 14	0.000834	14.34	2.56	NM_030701	<i>Hcar2</i>	hydroxycarboxylic acid receptor 2	0001781 // neutrophil apoptotic process // not recorded///0006915 // apoptotic process // inferred from electronic
1416404_s_at 14	0.000834	14.00	-1.33	NM_007470///XM_006521716	<i>Apod</i>	apolipoprotein D	0003002 // response to reactive oxygen species // inferred from mutant phenotype///0000302 // response to reactive oxygen species //
1416414_at 143	0.004199	13.83	3.11	NM_001113326///NM_031195	<i>Msr1</i>	macrophage scavenger receptor 1	0006897 // endocytosis // inferred from electronic annotation///0006898 // receptor-mediated endocytosis // inferred from electronic
1416415_a_at 14	0.001404	13.72	4.62	NM_008039	<i>Fpr2</i>	formyl peptide receptor 2	0006935 // chemotaxis // inferred from electronic annotation///0007165 // signal transduction // inferred from electronic
1416431_at 144	0.001965	13.60	2.86	NM_001164323///NM_199015	<i>Phf11d</i>	PHD finger protein 11D	0006351 // transcription, DNA-templated // inferred from electronic annotation///0006355 // regulation of transcription, DNA-templated
1416432_at 145	0.003972	13.59	4.06	NM_019467///NM_006523502	<i>Ajl1</i>	allograft inflammatory factor 1	0001774 // microglial cell activation // non-traceable author statement///0001934 // positive regulation of protein phosphorylation //
1416453_x_at 14	0.001785	13.33	2.89	NM_023044	<i>Sic15a3</i>	solute carrier family 15, member 3	0006810 // transport // inferred from electronic annotation///0006857 // oligopeptide transport // inferred from electronic
1416453_x_at 14	0.001785	13.29	1.91	NM_010501	<i>Ifit3</i>	interferon-induced protein with tetratricopeptide repeats 3	0002376 // immune system process // inferred from electronic annotation///0008285 // negative regulation of cell proliferation //
1416453_x_at 14	0.001785	13.26	2.76	NM_030691///XM_006508351	<i>Igfb6</i>	immunoglobulin superfamily, member 6	
1416453_x_at 14	0.001785	13.25	1.89	NM_030150	<i>Dhx58</i>	DEXH (Asp-Glu-X-His) box polypeptide 58	0002376 // immune system process // inferred from electronic annotation///0008152 // metabolic process // inferred from electronic
1416453_x_at 14	0.001785	13.19	2.00	NM_001012236///NM_011637	<i>Atrip///Trex1</i>	ATR interacting protein///three prime repair exonuclease 1	0000738 // DNA catabolic process, exonucleolytic // inferred from direct assay///0006259 // DNA metabolic process // inferred from
1416453_x_at 14	0.001785	13.18	4.18	NM_008491	<i>Lcn2</i>	lipocalin 2	0002376 // immune system process // inferred from electronic annotation///0006810 // transport // inferred from electronic
1416453_x_at 14	0.001785	13.11	2.47	NM_001033450///NM_001170	<i>Ifi204//Ifi205//Mnda//Mndal</i>	interferon activated gene 204///interferon activated gene 205///myeloid cell	0006351 // transcription, DNA-templated // inferred from electronic annotation///0006355 // regulation of transcription, DNA-templated
1416453_x_at 14	0.001785	13.08	2.90	NM_001038604///NM_021364	<i>Clec5a</i>	C-type lectin domain family 5, member a	0002076 // osteoblast development // inferred from direct assay///0002376 // immune system process // inferred from electronic
1416453_x_at 14	0.001785	13.02	2.07	NM_001167743///NM_181545	<i>Slf1n8</i>	schlafen 8	
1416454_s_at 14	0.004684	12.80	1.46	NM_011087///NM_011088//	<i>Pira1//Pira11//Pira2//Pira5//</i>	paired-Ig-like receptor A11///paired-Ig-like receptor A11///paired-Ig-like	0001782 // B cell homeostasis // inferred from mutant phenotype///0002376 // immune system process // inferred from electronic
1416482_at 141	0.001848	12.91	2.44	NM_010554///XM_006498792	<i>Il1a</i>	interleukin 1 alpha	0001660 // fever generation // inferred from electronic annotation///0006954 // inflammatory response // inferred from electronic
1416489_at 142	0.006701	12.75	1.02	NM_009971///XM_006532128	<i>Csf3</i>	colony stimulating factor 3 (granulocyte)	0006955 // immune response // inferred from electronic annotation///0008284 // positive regulation of cell proliferation // not
1416492_at 144	0.007498	12.73	1.32	NM_009253///XM_006515637	<i>Serpina3m</i>	serine (or cysteine) peptidase inhibitor, clade A, member 3M	0010466 // negative regulation of peptidase activity // inferred from electronic annotation///0010951 // negative regulation of
1416507_at 143	0.009700	12.72	2.50	NM_001033130///XM_006517	<i>D13Ertd608e//LOC102631530</i>	DNA segment, Chr 13, ERATO Doi 608, expressed///uncharacterized	
1416519_at 141	0.009319	12.63	6.20	NM_001289492///NM_001289	<i>Gbp3</i>	guanylate binding protein 3	0006184 // GTP catalytic process // inferred from sequence or structural similarity///00035458 // cellular response to interferon-beta //
1416527_at 678	0.003821	12.51	15.79	NM_194336///XM_006534687	<i>Gbp6</i>	guanylate binding protein 6	0006184 // GTP catalytic process // inferred from electronic annotation///0006955 // immune response // inferred from mutant
1416530_s_at 14	0.001490	12.36	3.93	NM_013650	<i>S100a8</i>	S100 calcium binding protein A8 (calgranulin A)	0002376 // immune system process // inferred from electronic annotation///0002523 // leukocyte migration involved in inflammatory
1416531_at 145	0.008437	12.30	1.84	NM_001082960///NM_008401	<i>Igcam</i>	integrin alpha M	0002523 // leukocyte migration involved in inflammatory response // inferred from mutant phenotype///0006412 // translation //
1416544_at 140	0.004031	12.24	3.01	NM_011905///XM_006501460	<i>Tlr2</i>	Toll-like receptor 2	0001666 // response to hypoxia // inferred from electronic annotation///0001774 // microglial cell activation // not recorded///0002224
1416547_at 664	0.003846	12.06	4.27	NM_008152	<i>Gpr65</i>	G-protein coupled receptor 65	0006915 // apoptotic process // traceable author statement///0007165 // signal transduction // inferred from electronic
1416551_at 142	0.000834	12.05	6.12	NM_144559	<i>Fcgr4</i>	Fc receptor, IgG, low affinity IV	0001866 // NK T cell proliferation // not recorded///00051930 // regulation of sensory perception of pain // not recorded///0071222 //
1416554_at 143	0.002835	11.99	3.21	NM_001002898///NM_001173	<i>LOC10038947//Sirpb1a//Sirpb</i>	signal-regulatory protein beta 1-like///signal-regulatory protein beta	0035556 // intracellular signal transduction // inferred from direct assay///00050766 // positive regulation of phagocytosis // inferred
1416576_at 145	0.001979	11.99	3.95	NM_009912	<i>Ccr1</i>	chemokine (C-C motif) receptor 1	0006816 // calcium ion transport // not recorded///0006874 // cellular calcium ion homeostasis // not recorded///0006887 // exocytosis
1416589_at 144	0.008775	11.98	4.43	NM_009917	<i>Ccr5</i>	chemokine (C-C motif) receptor 5	0001974 // blood vessel remodeling // inferred from electronic annotation///0006816 // calcium ion transport // not
1416592_at 141	0.001564	11.97	15.12	NM_001146275///NM_021792	<i>Ilgp1</i>	interferon inducible GTPase 1	0002376 // immune system process // inferred from electronic annotation///0006184 // GTP catalytic process // inferred from sequence
1416595_at 646	0.003974	11.96	14.04	NM_001145164///NM_011579	<i>Tgtp11//Tgtp2</i>	T cell specific GTPase 11//T cell specific GTPase 2	0006184 // GTP catalytic process // inferred from direct assay///0006955 // immune response // non-traceable author
1416607_at 145	0.009261	11.96	2.81	NM_010185///XM_006496656	<i>Fcer1g</i>	Fc receptor, IgE, high affinity I, gamma polypeptide	0001798 // positive regulation of type IIa hypersensitivity // inferred from mutant phenotype///0001805 // positive regulation of type III
1416612_at 141	0.001987	11.93	3.88	NM_001169153///NM_154634	<i>Cd300f</i>	CD300 antigen like family member F	0002376 // immune system process // inferred from electronic annotation///00030316 // osteoclast differentiation // inferred from direct
1416614_at 144	0.006692	11.71	8.47	NM_010260///XM_006501000	<i>Gbp2</i>	guanylate binding protein 2	0006184 // GTP catalytic process // inferred from sequence or structural similarity///00035458 // cellular response to interferon-beta //
1416617_at 143	0.000897	11.54	10.27	NM_010259///XM_006500999	<i>Gbp2b</i>	guanylate binding protein 2b	0002376 // immune system process // inferred from electronic annotation///0006184 // GTP catalytic process // inferred from
1416623_at 218	0.004017	11.47	2.28	NM_011087///NM_011088//	<i>Pira1//Pira11//Pira2//Pira5//</i>	paired-Ig-like receptor A11///paired-Ig-like receptor A11///paired-Ig-like	0001782 // B cell homeostasis // inferred from mutant phenotype///0002376 // immune system process // inferred from electronic
1416624_a_at 14	0.000749	11.36	2.75	NM_013653	<i>Ccl5</i>	chemokine (C-C motif) ligand 5	0000165 // MAPK cascade // not recorded///0002230 // positive regulation of defense response to virus by host // inferred by
1416625_at 122	0.005114	11.30	12.60	NM_001033207///XM_006531	<i>Nlr-c5</i>	NLR family, CARD domain containing 5	0002376 // immune system process // inferred from electronic annotation///0006952 // defense response // inferred from electronic
1416629_at 144	0.007010	11.26	7.27	NM_008326///XM_006532305	<i>Irgm1</i>	immunity-related GTPase family M member 1	0002376 // immune system process // inferred from electronic annotation///0006914 // autophagy // inferred from electronic
1416631_at 142	0.005305	11.23	1.07	NM_001159738///NM_016960	<i>Ccl20</i>	chemokine (C-C motif) ligand 20	0006935 // chemotaxis // not recorded///0006954 // inflammatory response // inferred from electronic annotation///0006955 //
1416642_a_at 2	0.002358	11.22	1.29	NM_007482	<i>Arg3</i>	arginase, liver	0000050 // urea cycle // not recorded///0001889 // liver development // inferred from electronic annotation///0001938 // positive
1416654_at 145	0.003281	11.16	11.18	NM_009251///XM_00654030	<i>Serpina3g</i>	serine (or cysteine) peptidase inhibitor, clade A, member 3G	0002376 // immune system process // inferred from electronic annotation///0006915 // apoptotic process // inferred from electronic
1416664_at 143	0.000905	11.14	2.92	NM_029005///XM_006531441	<i>Mkl1</i>	mixed lineage kinase domain-like	0006468 // protein phosphorylation // inferred from electronic annotation///00012501 // programmed cell death // inferred from
1416673_at 143	0.006848	10.95	1.51	NM_024495	<i>Car13</i>	carbonic anhydrase 13	0006730 // one-carbon metabolic process // inferred from electronic annotation
1416686_at 141	0.002306	10.81	-1.04	NM_011016	<i>Orm2</i>	orosomucoid 2	0002682 // regulation of immune system process // inferred from electronic annotation///0006810 // transport // inferred from
1416690_at 141	0.001615	10.81	2.80	NM_001291058///NM_009853	<i>Cd68</i>	CD68 antigen	0071310 // cellular response to organic substance // inferred from direct assay
1416695_at 143	0.000296	10.72	2.76	NM_001204241///NM_153197	<i>Clec4a3</i>	C-type lectin domain family 4, member a3	0006508 // proteolysis // inferred from electronic annotation
1416697_at 144	0.003312	10.71	2.45	NM_019963///XM_006513433	<i>Stat2</i>	signal transducer and activator of transcription 2	0006351 // transcription, DNA-templated // inferred from electronic annotation///0006355 // regulation of transcription, DNA-templated
1416698_s_at 14	0.001588	10.68	2.34	NM_145227///XM_006530324	<i>Oas2</i>	2'-5' oligoadenylate synthetase 2	0002376 // immune system process // inferred from electronic annotation///0006164 // purine nucleotide biosynthetic process // not
1416705_at 141	0.000533	10.66	2.45	NM_009099///XM_006507471	<i>Trim30a//Trim30d</i>	tripartite motif-containing 30A///tripartite motif-containing 30D	0006351 // transcription, DNA-templated // inferred from electronic annotation///0006355 // regulation of transcription, DNA-templated
1416710_at 679	0.002573	10.64	2.22	NM_001081746///NM_033616	<i>Cspsr//Gm15433//Gm2666//</i>	component of Sp100-rs//predicted pseudogene 15433//predicted gene	0007186 // G-protein coupled receptor signaling pathway // inferred from electronic annotation
1416713_at 679	0.000939	10.58	12.83	NM_018738	<i>Igtp</i>	interferon gamma induced GTPase	0006184 // GTP catalytic process // inferred from direct assay///0008152 // metabolic process // inferred from electronic
1416735_at 118	0.006665	10.56	2.30	NM_020509	<i>Retnla</i>	resistin like alpha	
1416740_at 141	0.000787	10.49	2.80	NM_001002898///NM_001173	<i>LOC10038947//Sirpb1a//Sirpb</i>	signal-regulatory protein beta 1-like///signal-regulatory protein beta	0035556 // intracellular signal transduction // inferred from direct assay///00050766 // positive regulation of phagocytosis // inferred
1416742_at 238	0.006480	10.46	11.70	NM_011704///XM_006512718	<i>Vnn1</i>	vanin 1	0002526 // acute inflammatory response // inferred from direct assay///0002544 // chronic inflammatory response // inferred from
1416746_at 152	0.005057	10.42	3.38	NM_027209	<i>Ms4a6b</i>	membrane-spanning 4-domains, subfamily A, member 6B	
1416752_at 143	0.000239	10.37	2.46	NM_011408	<i>Sfnf2</i>	schlafen 2	0008285 // negative regulation of cell proliferation // inferred from direct assay
1416755_at 141	0.009896	10.08	1.58	NM_011150///XM_006532506	<i>Lgals3bp</i>	lectin, galactoside-binding, soluble, 3 binding protein	0006898 // receptor-mediated endocytosis // inferred from sequence or structural similarity///0007155 // cell adhesion // inferred from
1416761_at 154	0.001588	10.03	2.56	NM_001083322///NM_001286	<i>Klrk1</i>	killer cell lectin-like receptor subfamily K, member 1	0002223 // stimulatory C-type lectin receptor signaling pathway // inferred from mutant phenotype///0002376 // immune system
1416767_a_at 14	0.005684	9.99	2.07	NM_001081746///NM_033616	<i>Cspsr//Gm2666//Gm7609//</i>	component of Sp100-rs//predicted gene 2666//predicted pseudogene	0007186 // G-protein coupled receptor signaling pathway // inferred from electronic annotation

Table S6

Gene_ID	p (Corr)	FC-RSV 1 d	FC-RSV 5 d	RefSeq Transcript ID	Gene Symbol	Gene Title	Gene Ontology Biological Process
1416821_at,1414f	0.006440	9.90	2.28	NM_011087//NM_011088//	<i>Pira1</i> // <i>Pira11</i> // <i>Pira2</i> // <i>Pira5</i> //	paired-Ig-like receptor A11//paired-Ig-like receptor A11//paired-Ig-like	0001782 // B cell homeostasis // inferred from mutant phenotype//0002376 // immune system process // inferred from electronic
1416827_at,1213f	0.007202	9.81	2.43	NM_007825//NM_006535383	<i>Cyp7b1</i>	cytochrome P450, family 7, subfamily b, polypeptide 1	0006629 // lipid metabolic process // inferred from electronic annotation//0006699 // bile acid biosynthetic process // inferred from
1416832_at,1444f	0.006586	9.76	1.87	NM_001159301//NM_010708	<i>Lgals9</i>	lectin, galactose binding, soluble 9	0007157 // heterophilic cell-cell adhesion // not recorded
1416835_s_at,14	0.006927	9.75	1.60	NM_001166402//NM_009397	<i>Tnfrsf3</i>	tumor necrosis factor, alpha-induced protein 3	0001922 // B-1 B cell homeostasis // inferred from mutant phenotype//0002237 // response to molecule of bacterial origin // inferred
1416840_at,1680f	0.001693	9.69	3.65	NM_001170851//NM_008462	<i>Klra2</i>	killer cell lectin-like receptor, subfamily A, member 2	0007155 // cell adhesion // inferred from electronic annotation
1416845_at,1981f	0.006996	9.56	3.07	NM_009779	<i>C3or1</i>	complement component 3a receptor 1	0002430 // complement receptor mediated signaling pathway // not recorded//0002462 // tolerance induction to nonself antigen // not
1416849_at,1414f	0.001306	9.50	2.77	NM_054098	<i>Steap4</i>	STEAP family member 4	0006810 // transport // inferred from electronic annotation//0006811 // ion transport // inferred from electronic annotation//0015677
1416860_s_at,14	0.009586	9.45	2.75	NM_008690//NM_006523789	<i>Nfkfi</i>	nuclear factor of kappa light polypeptide gene enhancer in B cells inhibitor,	0042942 // D-serine transport // not recorded//0045892 // negative regulation of transcription, DNA-templated // inferred from
1416875_at,1414f	0.009843	9.45	1.15	NM_011227	<i>Rab20</i>	RAB20, member RAS oncogene family	0006184 // GTP catalytic process // inferred from electronic annotation//0006810 // transport // inferred from electronic
1416885_at,117f	0.009682	9.42	1.54	NM_030720//NM_006521554	<i>Gpr84</i>	G protein-coupled receptor 84	0007165 // signal transduction // inferred from electronic annotation//0007186 // G-protein coupled receptor signaling pathway //
1416897_at,1802f	0.000291	9.32	1.33	NM_001113527//NM_001291	<i>Isg20</i>	interferon-stimulated protein	0000738 // DNA catabolic process, exonucleolytic // not recorded//0002376 // immune system process // inferred from electronic
1416901_at,1444f	0.002300	9.32	1.51	NM_011338	<i>Ccl9</i>	chemokine (C-C motif) ligand 9	0006935 // chemotaxis // inferred from electronic annotation//0006955 // immune response // inferred from electronic
1416906_at,1433f	0.001533	9.22	2.94	NM_009763//NM_006503706	<i>Bst1</i>	bone marrow stromal cell antigen 1	0008152 // metabolic process // inferred from electronic annotation
1416933_at,189f	0.005038	9.06	6.83	NM_001271676//NM_001271	<i>Ifi47</i>	interferon gamma inducible protein 47	0006952 // defense response // inferred from mutant phenotype//0007165 // signal transduction // inferred from electronic
1416939_at,1678f	0.005334	8.79	1.74	NM_007746//NM_006525943	<i>Map3k8</i>	mitogen-activated protein kinase kinase kinase 8	0001165 // MAPK cascade // not recorded//0000186 // activation of MAPK activity // not recorded//0002376 // immune system
1416942_at,1433f	0.005356	8.74	1.76	NM_029495//NM_178825//X	<i>Eps11</i>	epithelial stromal interaction 1 (breast)	
1416945_at,1433f	0.008597	8.73	4.38	NM_007534//NM_007536//	<i>Bcl2a1a</i> // <i>Bcl2a1b</i> // <i>Bcl2a1d</i>	B cell leukemia/lymphoma 2 related protein A1a//B cell leukemia/lymphoma	0001782 // B cell homeostasis // inferred from direct assay//0002903 // negative regulation of B cell apoptotic process // inferred from
1416961_at,1444f	0.002971	8.71	2.84	NM_205820//NM_006528078	<i>Tlr13</i>	toll-like receptor 13	0002237 // response to molecule of bacterial origin // inferred from electronic annotation//0002376 // immune system process //
1416968_s_at,11f	0.009324	8.64	1.15	NM_010220	<i>Fkbp5</i>	FK506 binding protein 5	0000413 // protein peptidyl-prolyl isomerization // not recorded//0006457 // protein folding // inferred from electronic
1416974_at,1414f	0.002923	8.63	1.68	NM_001033922//NM_001163	<i>Trem4</i>	triggering receptor expressed on myeloid cells-like 4	
1416981_at,1414f	0.004513	8.62	1.83	NM_001037713//NM_001291	<i>Xaf1</i>	XAP associated factor 1	0006915 // apoptotic process // inferred from electronic annotation//0001333 // negative regulation of protein complex assembly //
1416990_at,201f	0.002691	8.57	3.49	NM_027988//NM_006524949	<i>Nox1</i>	NADPH oxidase organizer 1	0006801 // superoxide metabolic process // inferred from direct assay//0007154 // cell communication // inferred from electronic
1416997_s_at,11f	0.002620	8.48	9.60	NM_019440	<i>Irgm2</i>	immunity-related GTPase family M member 2	0006184 // GTP catalytic process // inferred from sequence or structural similarity//0008152 // metabolic process // inferred from
1417006_at,1661f	0.007603	8.47	1.87	NM_001164477//NM_027835	<i>Ifih1</i>	interferon induced with helicase C domain 1	0002376 // immune system process // inferred from electronic annotation//0008152 // metabolic process // inferred from electronic
1417009_at,1454f	0.001995	8.47	2.10	NM_001164059//NM_011346	<i>Sell</i>	selectin, lymphocyte	0007155 // cell adhesion // inferred from electronic annotation//0033198 // response to ATP // inferred from direct assay//0042981 //
1417015_at,1444f	0.008787	8.47	1.46	NM_022430	<i>Ms4a8a</i>	membrane-spanning 4-domains, subfamily A, member 8A	
1417023_s_at,14f	0.001958	8.45	1.52	NM_001161790//NM_001161	<i>Mefv</i>	Mediterranean fever	0002376 // immune system process // inferred from electronic annotation//0006954 // inflammatory response // not
1417025_at,149f	0.001858	8.41	3.25	NM_009807	<i>Casp1</i>	caspase 1	0001666 // response to hypoxia // inferred from mutant phenotype//0001666 // response to hypoxia // not recorded//0001774 //
1417027_at,1414f	0.009586	8.41	6.95	NM_001205313//NM_001205	<i>Str1</i>	signal transducer and activator of transcription 1	0000122 // negative regulation of transcription from RNA polymerase II promoter // inferred from sequence or structural
1417039_s_at,16f	0.004538	8.36	1.15	NM_139138	<i>Emr4</i>	EGF-like module containing, mucin-like, hormone receptor-like sequence 4	0007165 // signal transduction // inferred from electronic annotation//0007166 // cell surface receptor signaling pathway // inferred
1417040_s_at,15f	0.001889	8.22	2.83	NM_023386//NM_006522490	<i>Rtp4</i>	receptor transporter protein 4	0001580 // detection of chemical stimulus involved in sensory perception of bitter taste // not recorded//0006612 // protein targeting
1417045_at,1444f	0.008786	8.18	1.98	NM_007609//NM_006509837	<i>Casp4</i>	caspase 4, apoptosis-related cysteine peptidase	0006508 // proteolysis // not recorded//0006508 // proteolysis // inferred from reviewed computational analysis//0006915 //
1417052_at,146f	0.005618	8.16	5.64	NM_001161730//NM_013683	<i>Tap1</i>	transporter 1, ATP-binding cassette, sub-family B (MDR/TAP)	0001916 // positive regulation of T cell mediated cytotoxicity // --//0002376 // immune system process // inferred from electronic
1417056_at,191f	0.001588	8.04	2.37	NM_173398	<i>Gpr171</i>	G protein-coupled receptor 171	0007165 // signal transduction // inferred from electronic annotation//0007186 // G-protein coupled receptor signaling pathway //
1417063_at,1434f	0.001164	8.03	2.34	NM_173869	<i>Stfa2l1</i>	stefin A2 like 1	0010951 // negative regulation of endopeptidase activity // inferred from electronic annotation
1417087_at,1444f	0.002226	8.03	1.26	NM_008289	<i>Hsd11b2</i>	hydroxysteroid 11-beta dehydrogenase 2	0001666 // response to hypoxia // inferred from electronic annotation//0002017 // regulation of blood volume by renal aldosterone //
1417088_at,1444f	0.000738	7.93	1.35	NM_001081249//NM_001134	<i>Vcan</i>	versican	0001649 // osteoblast differentiation // not recorded//0001657 // ureteric bud development // inferred from expression
1417095_s_at,14f	0.003462	7.87	2.70	NM_001276445//NM_030682	<i>Tlr1</i>	toll-like receptor 1	0001774 // microglial cell activation // not recorded//0002224 // toll-like receptor signaling pathway // not recorded//0002376 //
1417101_at,155f	0.007490	7.81	1.76	NM_033075	<i>D17H6556E-5</i>	DNA segment, Chr 17, human D6S566-5	0019058 // viral life cycle // inferred from electronic annotation
1417102_s_at,14f	0.009843	7.80	2.18	NM_001252651//NM_007782	<i>Csf3r</i>	colony stimulating factor 3 receptor (granulocyte)	0007155 // cell adhesion // inferred from electronic annotation//0019221 // cytokine-mediated signaling pathway // inferred from
1417109_at,1942f	0.003013	7.79	4.06	NM_015811	<i>Rgs1</i>	regulator of G-protein signaling 1	0001886 // G-protein coupled receptor signaling pathway // traceable author statement//0009968 // negative regulation of signal
1417124_at,1564f	0.007770	7.78	1.13	NM_017466//NM_006512185	<i>Ccr1</i>	chemokine (C-C motif) receptor-like 2	0006935 // chemotaxis // inferred from electronic annotation//0006954 // inflammatory response // inferred from direct
1417130_s_at,14f	0.000147	7.75	1.57	NM_010807	<i>Marcks1</i>	MARCKS-like 1	0008284 // positive regulation of cell proliferation // inferred from direct assay
1417141_at,161f	0.000160	7.71	1.49	NM_017373//NM_006516875	<i>Nfil3</i>	nuclear factor, interleukin 3, regulated	0000122 // negative regulation of transcription from RNA polymerase II promoter // not recorded//0006351 // transcription, DNA-
1417143_at,1424f	0.003814	7.66	2.35	NM_013521	<i>Fpr1</i>	formyl peptide receptor 1	0006935 // chemotaxis // traceable author statement//0007165 // signal transduction // inferred from electronic annotation//0007186
1417160_s_at,14f	0.004362	7.61	1.96	NM_001281830//NM_029803	<i>Ifi272a</i>	interferon, alpha-inducible protein 27 like 2A	0007568 // aging // inferred from direct assay//0006915 // response to virus // inferred from direct assay
1417165_at,1421f	0.009716	7.49	1.54	NM_009699//NM_006532127	<i>Csf2</i>	colony stimulating factor 2 (granulocyte-macrophage)	0001892 // embryonic placenta development // inferred from mutant phenotype//0006955 // immune response // inferred from
1417172_at,1567f	0.001511	7.44	2.40	NM_001077189//NM_010187	<i>Fcgr2b</i>	Fc receptor, IgG, low affinity IIB	0001811 // negative regulation of type I hypersensitivity // inferred from mutant phenotype//0002638 // negative regulation of
1417181_s_at,14f	0.000268	7.42	2.79	NM_001126182//NM_010872	<i>Naiip2</i>	NLR family, apoptosis inhibitory protein 2	0002376 // immune system process // inferred from electronic annotation//0006915 // apoptotic process // inferred from electronic
1417185_at,1110f	0.002826	7.42	3.02	NM_008677//NM_006520564	<i>Ncf4</i>	neutrophil cytosolic factor 4	0007154 // cell communication // inferred from electronic annotation//0043085 // positive regulation of catalytic activity // not
1417189_at,191f	0.001359	7.35	2.31	NM_007832	<i>Dck</i>	deoxycytidine kinase	0006139 // nucleobase-containing compound metabolic process // inferred from electronic annotation//0006220 // pyrimidine
1417189_at,1621f	0.001359	7.32	1.46	NM_021407//NM_006524731	<i>Trem3</i>	triggering receptor expressed on myeloid cells 3	0002374 // cytokine secretion involved in immune response // inferred from genetic interaction//0016477 // cell migration // inferred
1417190_at,1444f	0.000285	7.31	1.17	NM_001030294//NM_006519	<i>Olfm4</i>	olfactomedin 4	0007155 // cell adhesion // inferred from electronic annotation//0043124 // negative regulation of I-kappaB kinase/NF-kappaB signaling
1417193_at,1414f	0.001807	7.30	2.18	NM_001242368//NM_007972	<i>F10</i>	coagulation factor X	0006508 // proteolysis // not recorded//0007596 // blood coagulation // not recorded//0007599 // hemostasis // inferred from
1417213_s_at,14f	0.005924	7.17	3.35	NM_001113474//NM_178611	<i>Lair1</i>	leukocyte-associated Ig-like receptor 1	
1417230_at,1424f	0.004646	7.13	2.42	NM_001104529//NM_001271	<i>Gpr35</i>	G protein-coupled receptor 35	0007165 // signal transduction // inferred from electronic annotation//0007186 // G-protein coupled receptor signaling pathway // not
1417231_at,1414f	0.003408	7.13	1.69	NM_001081746//NM_033616	<i>Csprs</i> // <i>Gm2666</i> // <i>Gm7609</i> // <i>LC</i>	component of Sp100-rs//predicted gene 2666//predicted pseudogene	0007186 // G-protein coupled receptor signaling pathway // inferred from electronic annotation//0000723 // telomere maintenance //
1417237_at,1454f	0.007041	7.10	2.60	NM_001170853//NM_006496	<i>Mnda</i> // <i>Ifi204</i> // <i>Ifi205</i> // <i>Mnda</i>	myeloid nuclear differentiation antigen like//interferon activated gene	0030308 // negative regulation of cell growth // inferred from mutant phenotype//0035458 // cellular response to interferon-beta //
1417240_at,1433f	0.002826	7.01	2.84	NM_010696	<i>Lcp2</i>	lymphocyte cytosolic protein 2	0045576 // mast cell activation // inferred from mutant phenotype//0006663 // cytokine secretion // inferred from mutant phenotype
1417244_s_at,15f	0.000126	6.97	1.95	NM_153510	<i>Pilra</i>	paired immunoglobulin-like type 2 receptor alpha	0007165 // signal transduction // not recorded
1417255_at,1106f	0.003455	6.89	3.09	NM_134152//NM_006526576	<i>Lpxn</i>	leupaxin	0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 // regulation of transcription, DNA-templated
1417266_at,1424f	0.001384	6.83	2.47	NM_026405	<i>Rab32</i>	RAB32, member RAS oncogene family	0006184 // GTP catalytic process // inferred from electronic annotation//0006886 // intracellular protein transport // inferred from
1417268_at,1124f	0.003576	6.83	1.13	NM_001135151//NM_001135	<i>Slc39a14</i>	solute carrier family 39 (zinc transporter), member 14	0006810 // transport // inferred from electronic annotation//0006811 // ion transport // inferred from electronic annotation//0006826
1417273_at,1272f	0.001953	6.82	1.18	NM_011314//NM_006540727	<i>Sao2</i>	serum amyloid A 2	0006953 // acute-phase response // inferred from electronic annotation//0035634 // response to stilbenoid // inferred from expression
1417279_at,146f	0.002571	6.80	4.71	NM_009396//NM_006515792	<i>Tnfrsf2</i> // <i>AK080484</i>	tumor necrosis factor, alpha-induced protein 2//Mus musculus 7 days	0001525 // angiogenesis // inferred from electronic annotation//0006887 // exocytosis // inferred from electronic
1417283_at,1444f	0.007548	6.77	1.63	NM_009841	<i>Cd14</i>	CD14 antigen	0002237 // response to molecule of bacterial origin // inferred from direct assay//0002376 // immune system process // inferred from
1417292_at,159f	0.000905	6.66	5.09	NM_001039160//NM_001243	<i>Gm4070</i> // <i>Gvin1</i>	predicted gene 4070//GTPase, very large interferon inducible 1	
1417300_at,100f	0.005827	6.65	-1.38	NM_183201//NM_006533574	<i>Sifn5</i>	schlafen 5	0030154 // cell differentiation // inferred from electronic annotation
1417314_at,1469f	0.000296	6.52	2.50	NM_007498	<i>Atf3</i>	activating transcription factor 3	0000122 // negative regulation of transcription from RNA polymerase II promoter // inferred from direct assay//0006094 //
1417316_at,1668f	0.003312	6.52	1.78	NM_024444//NM_006509748	<i>Cyp4f18</i>	cytochrome P450, family 4, subfamily f, polypeptide 18	0000038 // very long-chain fatty acid metabolic process // not recorded//0001676 // long-chain fatty acid metabolic process // not
1417328_at,1433f	0.001995	6.46	2.73	NM_030253//NM_006522755	<i>Parp9</i>	poly (ADP-ribose) polymerase family, member 9	0006281 // DNA repair // inferred from electronic annotation//0006302 // double-strand break repair // not recorded//0006974 //
1417329_at,1414f	0.009075	6.46	1.39	NM_010751//NM_006505670	<i>Mxd1</i>	MAX dimerization protein 1	0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 // regulation of transcription, DNA-templated
1417334_at,1544f	0.007516	6.44	3.58	NM_007649//NM_006496636	<i>Cd48</i>	CD48 antigen	0007165 // signal transduction // inferred from direct assay//0042110 // T cell activation // inferred from direct assay//0045576 //
1417344_at,1414f	0.002502	6.42	1.43	NM_023141	<i>Tor3a</i>	torsin family 3, member A	0006200 // ATP catalytic process // not recorded//0051085 // chaperone mediated protein folding requiring cofactor // inferred from
1417346_at,1414f	0.001347	6.34	1.39	NM_001081746//NM_033616	<i>Csprs</i> // <i>Gm15433</i> // <i>Gm2666</i> // <i>LC</i>	component of Sp100-rs//predicted pseudogene 15433//predicted gene	0007186 // G-protein coupled receptor signaling pathway // inferred from electronic annotation
1417349_at,1414f	0.003324	6.32	3.81	NM_001198560//NM_001198	<i>H2-Q7</i> // <i>H2-Q9</i>	histocompatibility 2, Q region locus 7//histocompatibility 2, Q region locus 9	0001916 // positive regulation of T cell mediated cytotoxicity // inferred from electronic annotation//0001916 // positive regulation of T
1417364_at,1454f	0.009319	6.30	1.75	NM_001077508//NM_001077	<i>Tnfrsf9</i>	tumor necrosis factor receptor superfamily, member 9	0042127 // regulation of cell proliferation // inferred from direct assay//0070207 // protein homotrimerization // inferred from direct
1417373_s_at,14f	0.007171	6.29	1.41	NM_019777//NM_006529761	<i>Ikbke</i>	inhibitor of kappaB kinase epsilon	0006468 // protein phosphorylation // not recorded//0006974 // cellular response to DNA damage stimulus // inferred from electronic

Table S6

Gene ID	p (Corr)	FC-RSV 1 d	FC-RSV 5 d	RefSeq Transcript ID	Gene Symbol	Gene Title	Gene Ontology Biological Process
1417376_a_at14	0.001468	6.29	1.69	NM_009909//XM_006495638	Cxcr2	chemokine (C-X-C motif) receptor 2	0002438 // acute inflammatory response to antigenic stimulus // not recorded//0002690 // positive regulation of leukocyte chemotaxis
1417379_at1411	0.006111	6.24	1.14	NM_001252374//NM_026004	Nt5c3	5'-nucleotidase, cytosolic III	0008152 // metabolic process // inferred from electronic annotation//0009117 // nucleotide metabolic process // inferred from
1417392_a_at14	0.002211	6.24	6.19	NM_001040201//NM_145357	BC023105	cDNA sequence BC023105	0008152 // metabolic process // inferred from electronic annotation
1417408_at140	0.002211	6.19	1.66	NM_007494//NR_002687	Ass1//Gm5424	argininosuccinate synthetase 1//argininosuccinate synthase pseudogene	0000050 // urea cycle // not recorded//0000053 // argininosuccinate metabolic process // not recorded//0006526 // arginine
1417419_at1411	0.004386	6.14	1.40	NM_197944	Hsh2d	hematopoietic SH2 domain containing	0002903 // negative regulation of B cell apoptotic process // inferred from direct assay//0009967 // positive regulation of signal
1417423_at1436	0.002489	6.14	2.27	NM_001134391//NM_031159	Apobec1	apolipoprotein B mRNA editing enzyme, catalytic polypeptide 1	0006397 // mRNA processing // inferred from electronic annotation//0006970 // response to osmotic stress // not recorded//0009972
1417425_at1441	0.007253	6.14	2.33	NM_172893	Parp12	poly (ADP-ribose) polymerase family, member 12	0008152 // metabolic process // inferred from electronic annotation
1417427_at190	0.002566	6.13	1.63	NM_011817	Gadd45g	growth arrest and DNA-damage-inducible 45 gamma	0000185 // activation of MAPKKK activity // not recorded//0000186 // activation of MAPKK activity // inferred from direct
1417427_at1435	0.009182	6.13	1.99	NM_028808	P2ry13	purinergic receptor P2Y, G-protein coupled 13	0007165 // signal transduction // inferred from electronic annotation//0007186 // G-protein coupled receptor signaling pathway //
1417445_at1670	0.004366	6.12	3.91	NM_010724//XM_006536549	Psmb8	proteasome (prosome, macropain) subunit, beta type 8 (large multifunctional	0002376 // immune system process // inferred from electronic annotation//0006508 // proteolysis // inferred from electronic
1417464_at219	0.006565	6.11	2.57	NM_001039530//XM_006522	Parp14	poly (ADP-ribose) polymerase family, member 14	0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 // regulation of transcription, DNA-templated
1417465_at1441	0.007794	6.11	1.87	NM_007707//XM_006532110	Socs3	suppressor of cytokine signaling 3	0011932 // regulation of protein phosphorylation // inferred from direct assay//0007165 // signal transduction // not
1417466_at142C	0.009716	6.10	1.41	NM_172845	Adamts4	a disintegrin-like and metalloproteinase (reprolysin type) with	0006508 // proteolysis // inferred from direct assay//0006508 // proteolysis // not recorded//0042742 // defense response to
1417468_at1411	0.007975	6.08	1.26	NM_001038664//NM_001284	Gngt2	guanine nucleotide binding protein (G protein), gamma transducing activity	0006184 // GTP catabolic process // not recorded//0007165 // signal transduction // inferred from electronic annotation//0007186 // G-
1417470_at1802	0.006015	6.03	1.54	NM_001199733//NM_007829	Daxx	Fas death domain-associated protein	0000281 // mitotic cytokinesis // inferred from mutant phenotype//0006334 // nucleosome assembly // not recorded//0006338 //
1417474_at1765	0.001511	5.99	1.61	NM_001278601//NM_013693	Tnf	tumor necrosis factor	0000060 // protein import into nucleus, translocation // not recorded//0000122 // negative regulation of transcription from RNA
1417478_a_at14	0.003787	5.98	1.82	NM_013612//XM_006495773	Slc11a1	solute carrier family 11 (proton-coupled divalent metal ion transporters),	0000060 // protein import into nucleus, translocation // inferred from mutant phenotype//0000165 // MAPK cascade // not
1417481_at1431	0.004938	5.97	1.17	NM_011163//XM_006523863	Ezf2ak2	eukaryotic translation initiation factor 2-alpha kinase 2	0000186 // activation of MAPKK activity // not recorded//0001819 // positive regulation of cytokine production // inferred from mutant
1417487_at1411	0.000568	5.95	1.58	NM_013673//XM_006529280	Sp100	nuclear antigen Sp100	0000723 // telomere maintenance // inferred from sequence or structural similarity//0006351 // transcription, DNA-templated //
1417490_at1411	0.003143	5.94	1.27	NM_021406//XM_006524726	Trem1	triggering receptor expressed on myeloid cells 1	0002374 // cytokine secretion involved in immune response // inferred from genetic interaction//0016477 // cell migration // inferred
1417494_a_at14	0.001570	5.91	1.16	NM_001102404//NM_001102	Acp5	acid phosphatase 5, tartrate resistant	0008152 // metabolic process // inferred from electronic annotation//0016311 // dephosphorylation // inferred from direct
1417500_a_at14	0.009967	5.90	-1.29	NM_010442	Hmxo1	heme oxygenase (decycling) 1	0001525 // angiogenesis // not recorded//0001666 // response to hypoxia // inferred from electronic annotation//0002246 // wound
1417501_at1441	0.003281	5.89	1.33	NM_001033196//NM_001291	Znfx1	zinc finger, NFX1-type containing 1	0006355 // regulation of transcription, DNA-templated // inferred from electronic annotation
1417516_at1441	0.000583	5.79	-1.03	NM_020581	Angptl4	angiopoietin-like 4	0001525 // angiogenesis // inferred from electronic annotation//0001666 // response to hypoxia // inferred from electronic
1417523_at1441	0.003974	5.78	2.15	NM_001029841//NM_009192	Sla	src-like adaptor	
1417526_at1431	0.009767	5.75	1.16	NM_013463	Gla	galactosidase, alpha	0005975 // carbohydrate metabolic process // inferred from electronic annotation//0008152 // metabolic process // inferred from
1417552_at1401	0.007283	5.69	1.92	NM_019549	Plek	pleckstrin	0002244 // hematopoietic progenitor cell differentiation // inferred from electronic annotation//0002576 // platelet degranulation //
1417574_at1441	0.001877	5.64	1.52	NM_021788	Sap30	sin3 associated polypeptide	0000122 // negative regulation of transcription from RNA polymerase II promoter // inferred from direct assay//0006351 //
1417578_a_at14	0.008054	5.64	1.75	NM_001141948//NM_001141	Nmi	N-myc (and STAT) interactor	
1417583_a_at16	0.004189	5.62	-1.05	NM_001276301//NM_009667	Ampd3	adenosine monophosphate deaminase 3	0006188 // IMP biosynthetic process // inferred from direct assay//0006188 // IMP biosynthetic process // inferred from mutant
1417585_at1545	0.001225	5.62	1.60	NM_008102	Gch1	GTP cyclohydrolase 1	0006184 // GTP catabolic process // not recorded//0006461 // protein complex assembly // not recorded//0006729 //
1417586_at1411	0.003125	5.62	3.01	NM_011662	Tyrobp	TYRO protein tyrosine kinase binding protein	0002281 // macrophage activation involved in immune response // inferred from mutant phenotype//0002283 // neutrophil activation
1417590_at104	0.004199	5.61	1.26	NM_025658	Ms4a4d	membrane-spanning 4-domains, subfamily A, member 4D	
1417591_at1969	0.009131	5.60	2.59	NM_011723//XR_385314	Xdh	xanthine dehydrogenase	0001933 // negative regulation of protein phosphorylation // not recorded//0001937 // negative regulation of endothelial cell
1417598_a_at14	0.006185	5.60	1.56	NM_001111099//NM_007669	Cdkn1a	cyclin-dependent kinase inhibitor 1A (P21)	0000079 // regulation of cyclin-dependent protein serine/threonine kinase activity // inferred from mutant phenotype//0000082 // G1/S
1417601_at1507	0.003917	5.56	2.32	NM_031376//XM_006527472	Pik3ap1	phosphoinositide 3-kinase adaptor protein 1	0014068 // positive regulation of phosphatidylinositol 3-kinase signaling // inferred from mutant phenotype//0034122 // negative
1417607_at1451	0.000695	5.54	1.58	NM_007494//NR_002687	Ass1//Gm5424	argininosuccinate synthetase 1//argininosuccinate synthase pseudogene	0000050 // urea cycle // not recorded//0000053 // argininosuccinate metabolic process // not recorded//0006526 // arginine
1417608_a_at14	0.002680	5.50	1.33	NM_001254747//NM_008357	Il15	interleukin 15	0001779 // natural killer cell differentiation // inferred from genetic interaction//0001866 // NK T cell proliferation // inferred from
1417614_at1441	0.002578	5.47	1.08	NM_029796	Lrg1	leucine-rich alpha-2-glycoprotein 1	0001938 // positive regulation of endothelial cell proliferation // inferred from mutant phenotype//0030511 // positive regulation of
1417625_s_at11	0.008490	5.45	5.24	NM_028967//XM_006531851	Batf2	basic helix zipper transcription factor, ATF-like 2	0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 // regulation of transcription, DNA-templated
1417626_at146C	0.007260	5.43	1.22	NM_007679	Cebpd	CCAAT/enhancer binding protein (C/EBP), delta	0002244 // hematopoietic progenitor cell differentiation // inferred from genetic interaction//0006351 // transcription, DNA-templated
1417638_at1351	0.007666	5.40	2.24	NM_010401	Hal	histidine ammonia lyase	0006547 // histidine metabolic process // inferred from electronic annotation//0006548 // histidine catabolic process // inferred from
1417644_at1411	0.006034	5.40	1.01	NM_010809	Mmp3	matrix metalloproteinase 3	0006508 // proteolysis // inferred from electronic annotation//0030163 // protein catabolic process // inferred from mutant
1417666_at1456	0.008641	5.39	1.44	NM_053108//XM_006517477	Glxr	glutaredoxin	0006810 // transport // inferred from electronic annotation//0045454 // cell redox homeostasis // inferred from electronic
1417673_at1451	0.008115	5.38	1.79	NM_001172117//NM_010407	Hck	hemopoietic cell kinase	0002376 // immune system process // inferred from electronic annotation//0006468 // protein phosphorylation // inferred from
1417674_s_at14	0.008948	5.36	1.56	NM_009369	Tgfb1	transforming growth factor, beta induced	0001525 // angiogenesis // inferred from electronic annotation//0002062 // chondrocyte differentiation // inferred from electronic
1417680_at1641	0.002912	5.32	1.22	NM_001173550//NM_007577	Csrr1	complement component 5a receptor 1	0002430 // complement receptor mediated signaling pathway // not recorded//0006915 // apoptotic process // not
1417688_at1441	0.009378	5.32	2.09	NM_001005846//NM_026656	Mcoln2	mucoilin 2	0006810 // transport // inferred from electronic annotation//0006811 // ion transport // inferred from electronic annotation
1417689_a_at14	0.006439	5.30	1.39	NM_001161714//NM_001161	Tgm1	transglutaminase 1, K polypeptide	0009887 // organ morphogenesis // inferred from mutant phenotype//0018149 // peptide cross-linking // inferred from electronic
1417698_at1411	0.007237	5.25	-1.34	NM_013602//XM_006530752	Mt1	metallothionein 1	0006486 // protein glycosylation // inferred from electronic annotation//0006493 // protein O-linked glycosylation // inferred from
1417703_at1421	0.007933	5.25	2.71	NM_133888	Smpd3b	sphingomyelin phosphodiesterase, acid-like 3B	0006685 // sphingomyelin catabolic process // inferred from electronic annotation//0008152 // metabolic process // inferred from
1417707_at1451	0.004659	5.25	1.26	NM_053217	RIKEN cDNA 2010002M12Rik	RIKEN cDNA 2010002M12 gene	0009615 // response to virus // not recorded//0019060 // intracellular transport of viral protein in host cell // not recorded//0032091
1417719_at1604	0.001298	5.24	1.55	NM_001271476//NM_001271	Pglyrp2	peptidoglycan recognition protein 2	0002221 // pattern recognition receptor signaling pathway // not recorded//0002376 // immune system process // inferred from
1417723_at1441	0.005199	5.22	1.83	NM_139142	Slc6a20a	solute carrier family 6 (neurotransmitter transporter), member 20A	0003333 // amino acid transmembrane transport // inferred from direct assay//0003333 // amino acid transmembrane transport // not
1417732_at1421	0.005950	5.17	2.01	NM_183249	Wfdc21	WAP four-disulfide core domain 21	0010466 // negative regulation of peptidase activity // inferred from electronic annotation//0032496 // response to lipopolysaccharide
1417753_at1441	0.007870	5.16	2.01	NM_001033435//NM_001271	Milr1	mast cell immunoglobulin like receptor 1	0033004 // negative regulation of mast cell activation // inferred from mutant phenotype//0043303 // mast cell degranulation //
1417785_at1850	0.000240	5.15	-1.00	NM_001172472//NM_001172	Sphk1	sphingosine kinase 1	0001568 // blood vessel development // inferred from genetic interaction//0001934 // positive regulation of protein phosphorylation //
1417786_a_at14	0.005953	5.14	1.86	NM_001040005//XM_006534	Rnf213	ring finger protein 213	0000620 // ATP catabolic process // not recorded//0016567 // protein ubiquitination // not recorded//0051865 // protein
1417789_at1202	0.004764	5.11	2.16	NM_001286037//NM_010876	Ncf1	neutrophil cytosolic factor 1	0001878 // response to yeast // inferred from mutant phenotype//0001909 // leukocyte mediated cytotoxicity // inferred from mutant
1417790_at1431	0.008297	5.08	2.51	NM_023124//NM_207648//X	H2-Q6//H2-Q8//LOC68395//H	histocompatibility 2, Q region locus 6//histocompatibility 2, Q region locus	0000245 // spliceosomal complex assembly // inferred from electronic annotation//0000398 // mRNA splicing, via spliceosome //
1417815_a_at14	0.005121	5.07	12.18	NM_021443	Ccl8	chemokine (C-C motif) ligand 8	0006935 // chemotaxis // inferred from electronic annotation//0006954 // inflammatory response // inferred from electronic
1417821_at1411	0.000849	5.05	1.50	NM_153287//XM_006512035	Csrp1	cysteine-serine-rich nuclear protein 1	0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 // regulation of transcription, DNA-templated
1417825_at1431	0.005884	5.05	1.97	NM_010156//NM_177590//X	Samd9l	sterile alpha motif domain containing 9-like	0002244 // hematopoietic progenitor cell differentiation // inferred from mutant phenotype//0017145 // stem cell division // inferred
1417825_at1431	0.005884	5.05	1.82	NM_001290755//NM_001290	Tlr7	toll-like receptor 7	0001774 // microglial cell activation // not recorded//0002224 // toll-like receptor signaling pathway // not recorded//0002282 //
1417829_a_at11	0.009875	5.04	3.33	NM_010821//XM_006526734	Mpeg1	macrophage expressed gene 1	
1417848_at1411	0.001136	5.03	1.38	NM_028679//XM_006514227	Irak3	interleukin-1 receptor-associated kinase 3	0001960 // negative regulation of cytokine-mediated signaling pathway // inferred by curator//0006468 // protein phosphorylation //
1417851_at1441	0.000412	5.02	1.33	NM_199223//XM_006499592	Rtn4rl2	reticulon 4 receptor-like 2	0031103 // axon regeneration // traceable author statement
1417852_x_at14	0.000099	4.99	3.41	NM_001110320//NM_001110	Cd72	CD72 antigen	
1417865_at1411	0.006842	4.97	1.26	NM_001243916//NM_030684	Trim34a//Trim34b	tripartite motif-containing 34A//tripartite motif-containing 34B	
1417867_at1115	0.001914	4.97	1.62	NM_00114144	Slpi	serpin peptidase inhibitor	0006508 // proteolysis // inferred from electronic annotation//0010466 // negative regulation of peptidase activity // inferred from
1417868_a_at14	0.007918	4.93	1.49	NM_001177627//NM_172659	Scl26a	solute carrier family 2 (facilitated glucose transporter), member 6	0006810 // transport // inferred from electronic annotation//0008643 // carbohydrate transport // inferred from electronic
1417876_at1431	0.000858	4.92	3.22	NM_007780//XM_006520387	Csf2rb//Csf2rb2	colony stimulating factor 2 receptor, beta, low-affinity (granulocyte-	0019221 // cytokine-mediated signaling pathway // inferred from electronic annotation
1417885_at1421	0.005670	4.90	1.90	NM_001163540//NM_001163	Pf2b//Plec	poly (ADP-ribose) polymerase family, member 10//plectin	0006471 // protein ADP-ribosylation // not recorded//0007584 // response to nutrient // not recorded//0008152 // metabolic process
1417889_at1441	0.000257	4.90	2.64	NM_007651	Cd53	CD53 antigen	0016337 // single organismal cell-cell adhesion // inferred from direct assay//0045661 // regulation of myoblast differentiation //
1417896_at1273	0.001698	4.89	3.84	NM_001025610//NM_001276	Ms4a7	membrane-spanning 4-domains, subfamily A, member 7	
1417900_a_at14	0.007434	4.88	-1.17	NM_009994//XM_006523577	Cyp1b1	cytochrome P450, family 1, subfamily b, polypeptide 1	0001525 // angiogenesis // inferred from mutant phenotype//0002930 // trabecular meshwork development // inferred from mutant
1417910_at1411	0.001189	4.87	3.61	NM_010188//XM_006496658	Fcgr3	Fc receptor, IgG, low affinity III	0001788 // antibody-dependent cellular cytotoxicity // inferred from mutant phenotype//0001798 // positive regulation of type Ila
1417917_at1271	0.006710	4.83	2.81	NM_001127348//NM_001127	Snx10	sorting nexin 10	0006810 // transport // inferred from electronic annotation//0006886 // intracellular protein transport // not recorded//0007032 //

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Gene_ID	p (Corr)	FC-RSV 1 d	FC-RSV 5 d	RefSeq Transcript ID	Gene Symbol	Gene Title	Gene Ontology Biological Process
1417921_at[676]	0.005685	4.83	2.08	NM_001163470//NM_172275	<i>Traf1</i>	TRAF type zinc finger domain containing 1	0034097 // response to cytokine // inferred from electronic annotation//00045824 // negative regulation of innate immune response //
1417925_at[202]	0.006440	4.82	1.47	NM_029077//NM_00638323	<i>Trim14</i>	tripartite motif-containing 14	0032897 // negative regulation of viral transcription // not recorded//00054087 // innate immune response // not recorded//0051091 //
1417929_at[509]	0.007381	4.82	13.50	NM_001293690//NM_008324	<i>Idd1</i>	indoleamine 2,3-dioxygenase 1	0002534 // cytokine production involved in inflammatory response // inferred from mutant phenotype//0002666 // positive regulation
1417936_at[1444]	0.000573	4.78	4.31	NM_207244//NM_00652128	<i>Cd2004</i>	CD200 receptor 4	
1417956_at[126]	0.000383	4.77	1.01	NM_001286181//NM_001286	<i>Lox</i>	lysyl oxidase	0001568 // blood vessel development // inferred from mutant phenotype//0009725 // response to hormone // not recorded//0030199
1417961_a_at,14	0.001198	4.77	2.38	NM_001013371	<i>Dtx3l</i>	death 3-like (Drosophila)	0006281 // DNA repair // inferred from electronic annotation//0006302 // double-strand break repair // not recorded//0006974 //
1417963_at[1454]	0.009892	4.76	2.77	NM_001271005//NM_010398	<i>C920025E04Rik</i> // <i>H2-T23</i> // <i>LOC1</i>	RIKEN cDNA C920025E04 gene//histocompatibility 2, T region locus 23//h-2	0001916 // positive regulation of T cell mediated cytotoxicity // inferred from direct assay//0002376 // immune system process //
1418015_at[1411]	0.007888	4.76	2.93	NM_013706	<i>Cd52</i>	CD52 antigen	
1418021_at[625]	0.005223	4.74	1.82	NM_011610	<i>Tnfrsf1b</i>	tumor necrosis factor receptor superfamily, member 1b	0006954 // inflammatory response // inferred from mutant phenotype//0006955 // immune response // not recorded//0007166 // cell
1418026_at[1411]	0.001680	4.74	2.47	NM_001190320//NM_001190	<i>Clec4n</i>	C-type lectin domain family 4, member n	0002376 // immune system process // inferred from electronic annotation//00043123 // positive regulation of I-kappaB kinase/NF-
1418045_at[1444]	0.005618	4.67	4.78	NM_001083312//NM_145545	<i>Gbp7</i>	AT rich interactive domain 16340//interferon activated gene 203//floculation protein	0006184 // GTP catabolic process // inferred from electronic annotation//00042832 // defense response to protozoan // inferred from
1418049_at[1433]	0.002933	4.66	2.49	NR_051981//NM_001001892	<i>H2-Q5</i> // <i>H2-K1</i>	histocompatibility 2, Q region locus 5//histocompatibility 2, K1, K region	0001916 // positive regulation of T cell mediated cytotoxicity // inferred from electronic annotation//0002474 // antigen processing and
1418061_at[169]	0.006702	4.64	1.92	NM_144830//NM_006533036	<i>Tmem106a</i>	transmembrane protein 106A	
1418062_at[136]	0.001862	4.63	1.23	NM_001162921//NM_006510	<i>Zc3h12c</i>	zinc finger CCH type containing 12C	
1418068_at[1444]	0.003281	4.63	1.34	NM_010639	<i>Klk1</i>	kalikrein 1	0008152 // metabolic process // inferred from electronic annotation//0090305 // nucleic acid phosphodiester bond hydrolysis //
1418077_at[1444]	0.000583	4.63	2.49	NM_013484//NM_006523530	<i>C2</i>	complement component 2 (within H-2S)	0006508 // proteolysis // inferred from electronic annotation
1418099_at[1444]	0.009497	4.57	1.60	NM_026913	<i>Mitf1</i>	MIT, microtubule interacting and transport, domain containing 1	0002376 // immune system process // inferred from electronic annotation//0006508 // proteolysis // inferred from electronic
1418110_a_at,14	0.005058	4.56	3.39	NM_010745	<i>Ly86</i>	lymphocyte antigen 86	0000281 // mitotic cytokinesis // not recorded//0000920 // cytokinetic cell separation // not recorded//0006810 // transport //
1418115_a_at,14	0.001785	4.55	1.47	NM_133209//NM_006504554	<i>Pilrb1</i>	paired immunoglobulin-like type 2 receptor beta 1	0002376 // immune system process // inferred from electronic annotation//0006954 // inflammatory response // inferred from
1418122_at[1444]	0.002863	4.55	1.27	NM_172689	<i>Ddx58</i>	DEAD (Asp-Glu-Ala-Asp) box polypeptide 58	0001773 // myeloid dendritic cell activation // inferred from direct assay//00045671 // negative regulation of osteoclast differentiation //
1418123_at[222]	0.008611	4.47	1.85	NM_010553//NM_006495708	<i>Il18rap</i>	interleukin 18 receptor accessory protein	0002230 // positive regulation of defense response to virus by host // not recorded//0002376 // immune system process // inferred
1418124_at[1433]	0.006522	4.46	8.90	NM_029509//NM_006535281	<i>Gbp8</i> // <i>Gbp4</i>	guanylate-binding protein 8//guanylate binding protein 4	0007165 // signal transduction // inferred from electronic annotation//00019221 // cytokine-mediated signaling pathway // inferred from
1418126_at[203]	0.003290	4.46	1.60	NM_001172205//NM_001172	<i>Arid5a</i>	AT rich interactive domain 5A (MRF1-like)	0006184 // GTP catabolic process // inferred from electronic annotation//0071346 // cellular response to interferon-gamma // inferred
1418128_at[115]	0.007171	4.45	2.02	NM_001045481//NM_008328	<i>Gm16340</i> // <i>ffj203</i> // <i>LOC1008624</i>	predicted gene 16340//interferon activated gene 203//floculation protein	0002062 // chondrocyte differentiation // inferred from direct assay//0006351 // transcription, DNA-templated // inferred from
1418131_at[1420]	0.002211	4.44	1.62	NM_007464//NM_006509828	<i>Birc3</i>	baculoviral IAP repeat-containing 3	0030308 // negative regulation of cell growth // inferred from mutant phenotype//0035458 // cellular response to interferon-beta //
1418138_at[1444]	0.001335	4.42	1.24	NM_022415//NM_006498216	<i>Ptges</i>	prostaglandin H synthase	0006915 // apoptotic process // inferred from electronic annotation//0007283 // spermatogenesis // inferred from electronic
1418156_at[578]	0.001372	4.41	2.11	NM_008638//NM_006505697	<i>Mthfd2</i>	methylene tetrahydrofolate dehydrogenase (NAD+ dependent),	0005156 // prostaglandin biosynthetic process // not recorded//0002526 // acute inflammatory response // inferred from electronic
1418162_at[1411]	0.003281	4.40	2.16	NM_145133//NM_006501236	<i>Tjfa</i>	TRAF-interacting protein with forkhead-associated domain	0006730 // one-carbon metabolic process // not recorded//0008152 // metabolic process // inferred from electronic
1418174_at[1433]	0.000380	4.39	2.15	NM_001159417//NM_001159	<i>Irf9</i>	interferon regulatory factor 9	0007249 // I-kappaB kinase/NF-kappaB signaling // inferred from direct assay
1418188_a_at,14	0.002983	4.34	1.96	NM_001033135//NM_006496	<i>Rnf149</i>	ring finger protein 149	0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 // regulation of transcription, DNA-templated
1418190_at[189]	0.002902	4.33	2.22	NM_001033711//NM_001077	<i>Evi2a</i> // <i>Evi2a-Evi2b</i> // <i>Evi2b</i>	ecotropic viral integration site 2a//Evi2a-Evi2b readthrough//ecotropic viral	0016567 // protein ubiquitination // inferred from direct assay//0031647 // regulation of protein stability // inferred from direct
1418191_at[241]	0.000103	4.33	2.66	NM_001080944//NM_006499	<i>Atg8b4</i>	ATPase, class I, type 8B, member 4	0006812 // cation transport // inferred from electronic annotation//0008152 // metabolic process // inferred from electronic
1418204_s_at,1	0.006764	4.31	2.50	NM_023258	<i>Pycard</i>	PYD and CARD domain containing	0001773 // myeloid dendritic cell activation // not recorded//0002218 // activation of innate immune response // inferred from mutant
1418216_at[1454]	0.007888	4.30	1.60	NM_001271497//NM_001271	<i>Il15ra</i>	interleukin 15 receptor, alpha chain	0007259 // JAK-STAT cascade // not recorded//0010977 // negative regulation of neuron projection development // not
1418219_at[161]	0.004626	4.28	2.28	NM_010395//NM_010396//H2-T10//H2-T22//H2-T9	<i>H2-T10</i> // <i>H2-T22</i> // <i>H2-T9</i>	histocompatibility 2, T region locus 10//histocompatibility 2, T region locus	0001916 // positive regulation of T cell mediated cytotoxicity // inferred from electronic annotation//0002474 // antigen processing and
1418241_at[146]	0.004235	4.26	2.65	NM_008404//NM_006513271	<i>Igfb2</i>	insulin like growth factor 2	0005253 // leukocyte migration involved in inflammatory response // not recorded//0007155 // cell adhesion // inferred from genetic
1418244_at[678]	0.001570	4.26	1.91	NM_023738	<i>Uba7</i>	ubiquitin-like modifier activating enzyme 7	0006464 // cellular protein modification process // not recorded//0016567 // protein ubiquitination // --//0019941 // modification-
1418248_at[1444]	0.003561	4.24	1.84	NM_001081024	<i>Setdb2</i>	SET domain, bifurcated 2	0001947 // heart looping // inferred from sequence or structural similarity//0007049 // cell cycle // inferred from electronic
1418253_a_at,14	0.002754	4.23	2.46	NM_001164107//NM_001164	<i>Ripk3</i>	receptor-interacting serine-threonine kinase 3	0001914 // regulation of T cell mediated cytotoxicity // inferred from genetic interaction//0002819 // regulation of adaptive immune
1418254_at[563]	0.001807	4.23	2.31	NM_0010130//NM_006523601	<i>Erm1</i>	EGF-like module containing, mucin-like, hormone receptor-like sequence 1	0007165 // signal transduction // inferred from electronic annotation//0007166 // cell surface receptor signaling pathway // inferred
1418267_at[152]	0.006103	4.23	-1.93	NM_001033324//NM_006510	<i>Zbtb16</i>	zinc finger and BTB domain containing 16	0001501 // skeletal system development // inferred from mutant phenotype//0001823 // mesonephros development // inferred from
1418269_at[169]	0.002258	4.21	1.85	NM_172142//NM_006539951	<i>Nfkbid</i>	nuclear factor of kappa light polypeptide gene enhancer in B cells inhibitor,	0006954 // inflammatory response // inferred from electronic annotation//00032088 // negative regulation of NF-kappaB transcription
1418273_a_at,14	0.006854	4.20	1.97	NM_023158//NM_006533920	<i>Cxcl16</i>	chemokine (C-X-C motif) ligand 16	0006898 // receptor-mediated endocytosis // inferred from direct assay//0006935 // chemotaxis // inferred from electronic
1418273_a_at,14	0.005839	4.20	2.19	NM_001042534//NM_001271	<i>Capg</i>	capping protein (actin filament), gelsolin-like	0030031 // cell projection assembly // inferred from direct assay//0051693 // actin filament capping // inferred from electronic
1418273_a_at,14	0.006854	4.19	1.95	NM_001166372//NM_001166	<i>1-Mar</i>	membrane-associated ring finger (C3HC4) 1	0002029 // protein polyubiquitination // inferred from direct assay//0000209 // protein polyubiquitination // not recorded//0002376 //
1418273_a_at,14	0.006854	4.18	1.54	NM_183162//NM_006500599	<i>Helz2</i>	helicase with zinc finger 2, transcriptional coactivator	0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 // regulation of transcription, DNA-templated
1418273_a_at,14	0.006854	4.16	1.92	NM_001045481//NM_008328	<i>Gm16340</i> // <i>ffj203</i> // <i>LOC1008624</i>	predicted gene 16340//interferon activated gene 203//floculation protein	000308 // negative regulation of cell growth // inferred from mutant phenotype//0035458 // cellular response to interferon-beta //
1418281_at[193]	0.005199	4.16	2.16	NM_001082552//NM_009277	<i>Trim21</i>	tripartite motif-containing 21	0000209 // protein polyubiquitination // not recorded//0006513 // protein monoubiquitination // not recorded//0007049 // cell cycle
1418282_x_at,14	0.000939	4.16	3.91	NM_013585//NM_006523729	<i>Psmb9</i>	proteasome (prosome, macropain) subunit, beta type 9 [large multifunctional	0002376 // immune system process // inferred from electronic annotation//0006508 // proteolysis // inferred from electronic
1418293_at[159]	0.000208	4.15	2.07	NM_026438	<i>Ppa1</i>	pyrophosphatase (inorganic) 1	0006796 // phosphate-containing compound metabolic process // inferred by curator
1418294_at[1454]	0.006927	4.14	1.14	NM_019949	<i>Ube2l6</i>	ubiquitin-conjugating enzyme E2L 6	0016567 // protein ubiquitination // inferred from electronic annotation//0019941 // modification-dependent protein catabolic process
1418314_a_at,14	0.005879	4.14	1.26	NM_008207//NM_006523704	<i>H2-T24</i>	histocompatibility 2, T region locus 24	0001916 // positive regulation of T cell mediated cytotoxicity // inferred from electronic annotation//0002474 // antigen processing and
1418326_at[205]	0.006324	4.12	3.05	NM_177320//NM_006533548	<i>Pik3r5</i>	phosphoinositide-3-kinase, regulatory subunit 5, p101	0007186 // G-protein coupled receptor signaling pathway // inferred from sequence or structural similarity//0014065 //
1418340_at[141]	0.001819	4.05	1.70	NM_021524	<i>Nampt</i>	nicotinamide phosphoribosyltransferase	0007565 // female pregnancy // inferred from electronic annotation//0009435 // NAD biosynthetic process // inferred from direct
1418355_at[533]	0.007688	4.04	1.66	NM_016748//NM_006503225	<i>Ctps</i>	cytidine 5'-triphosphate synthase	0006221 // pyrimidine nucleotide biosynthetic process // inferred from electronic annotation//0006241 // CTP biosynthetic process //
1418365_at[1444]	0.007110	4.03	2.00	NM_001170332//NM_001170	<i>Clec4a2</i> // <i>Clec4b1</i>	C-type lectin domain family 4, member a2//C-type lectin domain family 4,	0002376 // immune system process // inferred from electronic annotation//00045087 // innate immune response // inferred from
1418372_at[115]	0.002434	4.01	2.77	NM_008842	<i>Pim1</i>	proliferation inducing myeloid cell protein 1	0006468 // protein phosphorylation // not recorded//0008283 // cell proliferation // not recorded//0009103 // lipopolysaccharide
1418373_at[560]	0.000959	4.00	-1.19	NM_144557//NM_006512125	<i>Myr1</i>	myosin VIIA and Rab interacting protein	0006886 // intracellular protein transport // inferred from electronic annotation//0030050 // vesicle transport along actin filament //
1418392_a_at[5]	0.000658	3.99	1.71	NM_001001892//NM_010380	<i>H2-D1</i> // <i>H2-K1</i> // <i>LOC101056305</i>	histocompatibility 2, D region locus 1//histocompatibility 2, K1, K region//h-	0001916 // positive regulation of T cell mediated cytotoxicity // inferred from direct assay//0002376 // immune system process //
1418393_a_at[10]	0.002871	3.99	1.29	NM_001159711//NM_016923	<i>Ly96</i>	lymphocyte antigen 96	0002221 // pattern recognition receptor signaling pathway // not recorded//0002376 // immune system process // inferred from
1418395_at[674]	0.000239	3.96	1.06	NM_001042611//NM_001276	<i>Cp</i>	ceruloplasmin	0006810 // transport // inferred from electronic annotation//0006811 // ion transport // inferred from electronic annotation//0006825
1418397_at[270]	0.008988	3.96	1.85	NM_001045481//NM_008328	<i>Gm16340</i> // <i>ffj203</i> // <i>LOC1008624</i>	predicted gene 16340//interferon activated gene 203//floculation protein	0030308 // negative regulation of cell growth // inferred from mutant phenotype//0035458 // cellular response to interferon-beta //
1418454_at[1444]	0.002271	3.94	1.90	NM_013831//NM_177831	<i>Pstpip2</i>	proline-serine-threonine phosphatase-interacting protein 2	0007010 // cytoskeleton organization // non-traceable author statement
1418460_at[1411]	0.006127	3.93	1.66	NM_010851	<i>Myd88</i>	myeloid differentiation primary response gene 88	0002238 // response to molecule of fungal origin // inferred from mutant phenotype//0002376 // immune system process // inferred
1418464_at[171]	0.002018	3.93	2.25	NM_015766//NM_006524599	<i>Ebi3</i>	Epstein-Barr virus induced gene 3	0019221 // cytokine-mediated signaling pathway // not recorded
1418465_at[179]	0.005060	3.93	1.28	NM_001243916//NM_030684	<i>Trim34a</i> // <i>Trim34b</i>	tripartite motif-containing 34A//tripartite motif-containing 34B	
1418471_at[186]	0.002966	3.92	1.10	NM_001159299//NM_001289	<i>Itih4</i>	inter alpha-trypsin inhibitor, heavy chain 4	
1418473_at[663]	0.004403	3.92	-1.17	NM_008046//NM_006517527	<i>Fst</i>	folliculin	
1418483_a_at,14	0.005243	3.91	1.46	NM_001024703//NM_006540	<i>Mctp2</i>	multiple C2 domains, transmembrane 2	
1418486_at[1444]	0.000129	3.90	2.48	NM_001077496//NM_146023	<i>Evi2a-evi2b</i> // <i>Evi2b</i> // <i>Evi2a</i>	Evi2a-Evi2b readthrough//ecotropic viral integration site 2b//ecotropic viral	
1418505_at[1444]	0.008675	3.88	2.15	NM_010877//NM_006529235	<i>Ncf2</i>	neutrophil cytosolic factor 2	0006742 // NADP catabolic process // not recorded//0006801 // superoxide metabolic process // not recorded//0007568 // aging //
1418511_at[564]	0.002150	3.87	2.24	NM_181402//NM_006505231	<i>Parp11</i>	poly (ADP-ribose) polymerase family, member 11	0008152 // metabolic process // inferred from electronic annotation
1418517_at[163]	0.005022	3.86	1.16	NM_016972//NM_006519249	<i>Sic7a8</i>	solute carrier family 7 (cationic amino acid transporter, y+ system), member 8	0003333 // amino acid transmembrane transport // not recorded//0006810 // transport // inferred from electronic
1418524_at[1411]	0.006133	3.86	1.06	NM_144544	<i>2210407C18Rik</i>	RIKEN cDNA 2210407C18 gene	
1418536_at[150]	0.000296	3.83	2.28	NM_013640//NM_006530769	<i>Psmb10</i>	proteasome (prosome, macropain) subunit, beta type 10	0000902 // cell morphogenesis // inferred from mutant phenotype//0006508 // proteolysis // inferred from electronic
1418536_at[110]	0.000296	3.82	1.66	NM_016767	<i>Batf</i>	basic leucine zipper transcription factor, ATF-like	0001816 // cytokine production // inferred from mutant phenotype//0002320 // lymphoid progenitor cell differentiation // inferred
1418579_at[1433]	0.008942	3.81	1.48	NM_001123371//NM_013632	<i>Pnp1</i> // <i>Pnp2</i>	purine-nucleoside phosphorylase//purine-nucleoside phosphorylase 2	0001916 // positive regulation of T cell mediated cytotoxicity // inferred from mutant phenotype//0006139 // nucleobase-containing
1418580_at[1444]	0.000239	3.78	-1.16	NM_053247	<i>Lyve1</i>	lymphatic vessel endothelial hyaluronan receptor 1	0006027 // glycosaminoglycan catabolic process // inferred from direct assay//0006810 // transport // inferred from electronic

Table S6

Gene_ID	p (Corr)	FC-RSV 1 d	FC-RSV 5 d	RefSeq Transcript ID	Gene Symbol	Gene Title	Gene Ontology Biological Process
1418586_at 141f	0.001995	3.78	1.39	NM_153159	<i>Zc3h12a</i>	zinc finger CCHH type containing 12A	0001525 // angiogenesis // inferred from electronic annotation//0006915 // apoptotic process // inferred from electronic
1418589_a_at 1	0.002102	3.75	1.66	NM_027320	<i>Ifi35</i>	interferon-induced protein 35	
1418591_at 141f	0.002198	3.74	2.00	NM_027450	<i>Glipr2</i>	GLI pathogenesis-related 2	0010634 // positive regulation of epithelial cell migration // not recorded//0010718 // positive regulation of epithelial to mesenchymal
1418596_at 142f	0.006078	3.74	2.19	NM_001287389//NM_007781	<i>Csf2rb2//Csf2rb</i>	cytokine stimulating factor 2 receptor, beta 2, low-affinity (granulocyte-colony stimulating factor 1 (macrophage)	0019221 // cytokine-mediated signaling pathway // inferred from electronic annotation
1418601_at 263f	0.008875	3.73	1.58	NM_001113529//NM_001113	<i>Csf1</i>	colony stimulating factor 1 (macrophage)	0001503 // ossification // not recorded//0001954 // positive regulation of cell-matrix adhesion // inferred from genetic
1418612_at 205f	0.000834	3.72	2.23	NM_031198//NM_006505035	<i>Tfec</i>	transcription factor EC	0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 // regulation of transcription, DNA-templated
1418641_at 141f	0.005296	3.70	1.47	NM_001136091//NM_001167	<i>Tcirg1</i>	T cell, immune regulator 1, ATPase, H+ transporting, lysosomal V0 protein A3	0015991 // ATP hydrolysis coupled proton transport // inferred from electronic annotation
1418643_at 146f	0.004366	3.67	1.61	NM_001008497//NM_001287	<i>P2ry14</i>	purinergic receptor P2Y, G-protein coupled, 14	0006955 // immune response // not recorded//0007165 // signal transduction // inferred from electronic annotation//0007186 // G-
1418652_at 145f	0.000759	3.66	1.55	NM_001290660//NM_025422	<i>Cd302</i>	CD302 antigen	0006909 // phagocytosis // not recorded
1418653_at 107f	0.008505	3.65	-1.59	NM_183187//NM_006518019	<i>Fam107a</i>	family with sequence similarity 107, member A	0001558 // regulation of cell growth // not recorded
1418666_at 145f	0.008235	3.59	1.31	NM_126166//NM_006509278	<i>Tlr3</i>	toll-like receptor 3	0001774 // microglial cell activation // not recorded//0001819 // positive regulation of cytokine production // inferred from electronic
1418669_at 141f	0.003247	3.59	1.42	NM_001190974//NM_001190	<i>Axl</i>	AXL receptor tyrosine kinase	0001764 // neuron migration // inferred from genetic interaction//0001764 // neuron migration // inferred from mutant
1418672_at 145f	0.000652	3.57	-1.11	NM_016693//NM_006539040	<i>Map3k6</i>	mitogen-activated protein kinase kinase kinase 6	0000165 // MAPK cascade // not recorded//0000186 // activation of MAPKK activity // not recorded//0006468 // protein
1418673_at 144f	0.002971	3.57	1.01	NM_001168333//NM_023476	<i>Tinag1</i>	tubulointerstitial nephritis antigen-like 1	0006508 // proteolysis // inferred from electronic annotation//0006898 // receptor-mediated endocytosis // inferred from electronic
1418674_at 141f	0.007369	3.56	-1.05	NM_008458	<i>Serpina3c</i>	serine (or cysteine) peptidase inhibitor, clade A, member 3C	0010466 // negative regulation of peptidase activity // inferred from electronic annotation//0010951 // negative regulation of
1418687_at 118f	0.007559	3.56	2.49	NM_029612//NM_006497067	<i>Slamf9</i>	SLAM family member 9	
1418693_at 146f	0.006808	3.52	1.23	NM_001164074//NM_001164	<i>Tgfr1</i>	TGFβ-induced factor homeobox 1	0000122 // negative regulation of transcription from RNA polymerase II promoter // inferred from genetic interaction//0000122 //
1418715_at 143f	0.001979	3.51	1.19	NM_008872//NM_006509027	<i>Plat</i>	plasminogen activator, tissue	0001666 // response to hypoxia // inferred from mutant phenotype//0006508 // proteolysis // inferred from direct assay//0006508 //
1418718_at 144f	0.000860	3.50	1.40	NM_172796//NM_006533235	<i>Sifn9</i>	schlafen 9	
1418743_a_at 14	0.007858	3.50	1.98	NM_145158//NM_006524285	<i>Emilin2</i>	elastin microfibril interfacer 2	0007155 // cell adhesion // inferred from electronic annotation
1418752_at 116f	0.000914	3.49	1.43	NM_008884//NM_178087//X	<i>Pml</i>	promyelocytic leukemia	0001666 // response to hypoxia // inferred from mutant phenotype//0001666 // response to hypoxia // not recorded//0001932 //
1418753_at 145f	0.000099	3.49	1.63	NM_026414	<i>Asprv1</i>	aspartic peptidase, retroviral-like 1	0006508 // proteolysis // inferred from direct assay//0016485 // protein processing // inferred from direct assay//0016485 // protein
1418797_at 643f	0.000204	3.48	1.78	NM_009663	<i>AloxSap</i>	arachidonate 5-lipoxygenase activating protein	0002540 // leukotriene production involved in inflammatory response // inferred from mutant phenotype//0002675 // positive
1418806_at 129f	0.001801	3.48	3.02	NM_001267695//NM_021281	<i>Ctss</i>	cathepsin 5	0002250 // adaptive immune response // inferred from electronic annotation//0006508 // proteolysis // inferred from direct
1418809_at 142f	0.001877	3.47	2.33	NM_009151//NM_006530229	<i>Selplg</i>	selectin, platelet (p-selectin) ligand	000165 // cell adhesion // inferred from electronic annotation//00050901 // leukocyte tethering or rolling // inferred from mutant
1418809_at 142f	0.001785	3.46	1.60	NM_001146007//NM_175677	<i>Trim12c</i>	tripartite motif-containing 12C	0002221 // pattern recognition receptor signaling pathway // not recorded//0016567 // protein ubiquitination // not recorded
1418809_at 142f	0.001877	3.44	1.54	NM_031373//NM_006500711	<i>Oagr</i>	opioid growth factor receptor	0040008 // regulation of growth // inferred from electronic annotation
1418809_at 142f	0.001785	3.43	1.63	NM_009778	<i>C3</i>	complement component 3	0001798 // positive regulation of type Ila hypersensitivity // inferred from mutant phenotype//0001934 // positive regulation of protein
1418809_at 142f	0.002161	3.42	1.29	NM_010510	<i>Ifnb1</i>	interferon beta 1, fibroblast	0002250 // adaptive immune response // inferred from direct assay//0002286 // T cell activation involved in immune response // not
1418815_at 144f	0.000645	3.40	1.87	NM_011193//NM_00651085	<i>Pstpip1</i>	proline-serine-threonine phosphatase-interacting protein 1	0000910 // cytokinesis // inferred by curator//0002376 // immune system process // inferred from electronic annotation//0006897 //
1418825_at 159f	0.000383	3.40	2.36	NM_001077705//NM_013545	<i>Ptnc6</i>	protein tyrosine phosphatase, non-receptor type 6	0002244 // hematopoietic progenitor cell differentiation // inferred from mutant phenotype//0002924 // negative regulation of
1418826_at 143f	0.003039	3.39	1.96	NM_011888//NM_001472168	<i>Ccl19//Gm12407//Gm13309//</i>	chemokine (C-C motif) ligand 19//predicted gene 12407//predicted gene	0001768 // establishment of T cell polarity // not recorded//0001771 // immunological synapse formation // inferred from direct
1418888_a_at 2f	0.006335	3.37	1.19	NM_030218//NM_006514328	<i>Misp</i>	mitotic spindle positioning	0007049 // cell cycle // inferred from electronic annotation//0007067 // mitotic nuclear division // inferred from electronic
1418899_at 141f	0.006672	3.36	4.88	NM_145126//NM_009892//X	<i>Chil4//Chil3</i>	chitinase-like 4//chitinase-like 3	0005975 // carbohydrate metabolic process // inferred from electronic annotation//0006032 // chitin catabolic process // inferred from
1418907_at 144f	0.003042	3.35	1.82	NM_001001892//NM_010380	<i>H2-D1//H2-K1//LOC101056305</i>	histocompatibility 2, D region locus 1//histocompatibility 2, K1, K region//h-	0001916 // positive regulation of T cell mediated cytotoxicity // inferred from direct assay//0002376 // immune system process //
1418912_at 144f	0.001640	3.34	1.53	NM_001146708//NM_007987	<i>Fos</i>	fos (TNF receptor superfamily member 6)	0002377 // immunoglobulin production // inferred from mutant phenotype//0003014 // renal system process // inferred from mutant
1418919_at 143f	0.007072	3.31	1.60	NM_026960//NM_006521342	<i>Gsdmd</i>	gasdermin D	001668 // cellular response to extracellular stimulus // inferred from direct assay
1418930_at 159f	0.000103	3.30	1.14	NM_013671	<i>Sod2</i>	superoxide dismutase 2, mitochondrial	0000302 // response to reactive oxygen species // inferred from mutant phenotype//0000303 // response to superoxide // inferred
1418932_at 180f	0.001115	3.29	2.05	NM_001252382//NM_012057	<i>Irf5</i>	interferon regulatory factor 5	0002376 // immune system process // inferred from electronic annotation//0006351 // transcription, DNA-templated // inferred from
1418936_at 171f	0.000834	3.29	2.31	NM_001289591//NM_001289	<i>Tmem173</i>	transmembrane protein 173	0002218 // activation of innate immune response // inferred from mutant phenotype//0002218 // activation of innate immune
1418939_at 152f	0.007227	3.28	-1.42	NM_133670//NM_006507538	<i>Sult1a1</i>	sulfotransferase family 1A, phenol-preferring, member 1	0006584 // catecholamine metabolic process // not recorded//0006629 // lipid metabolic process // inferred from electronic
1418943_at 142f	0.002300	3.28	2.40	NM_026985//NM_006508871	<i>Mcomp1</i>	mast cell expressed membrane protein 1	
1418946_at 144f	0.006498	3.28	1.25	NM_001111267//NM_172495	<i>Snx20</i>	naucel receptor coactivator 7	0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 // regulation of transcription, DNA-templated
1418949_at 238f	0.005093	3.28	1.51	NM_013632//NM_001123371	<i>Pnpf//Pnp2</i>	purine-nucleoside phosphorylase//purine-nucleoside phosphorylase 2	0001916 // positive regulation of T cell mediated cytotoxicity // inferred from mutant phenotype//0006139 // nucleobase-containing
1418951_at 141f	0.005683	3.27	2.06	NM_013599//NM_006498861	<i>Mmp9</i>	matrix metalloproteinase 9	0001501 // skeletal system development // inferred from genetic interaction//0001501 // skeletal system development // inferred from
1418957_at 208f	0.007104	3.27	1.37	NM_009775//NM_006520358	<i>Tspo</i>	translocator protein	0006694 // steroid biosynthetic process // not recorded//0006811 // ion transport // not recorded//0006821 // chloride transport //
1418963_at 143f	0.000533	3.27	1.59	NM_027840//NM_006531371	<i>Snx20</i>	sorting nexin 20	0006810 // transport // inferred from electronic annotation//0007154 // cell communication // inferred from electronic
1418970_a_at 14	0.002826	3.27	2.30	NM_001029929//NM_006533	<i>Zmynd15</i>	zinc finger, MYND-type containing 15	0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 // regulation of transcription, DNA-templated
1418973_at 141f	0.008582	3.27	1.24	NM_001271411//NM_001271	<i>Nfam1</i>	Nfat activating molecule with ITAM motif 1	0007165 // signal transduction // not recorded//0007165 // signal transduction // inferred from sequence or structural
1418981_at 144f	0.006180	3.27	1.28	NM_001083925//NR_003507	<i>Oas1b</i>	2'-5' oligoadenylate synthetase 1B	0002376 // immune system process // inferred from electronic annotation//0006955 // immune response // inferred from electronic
1418982_at 126f	0.004366	3.26	1.04	NM_001271705//NM_008827	<i>Pgf</i>	placental growth factor	0001525 // angiogenesis // inferred from electronic annotation//0001658 // branching involved in uterine bud morphogenesis //
1418992_at 141f	0.004938	3.24	1.35	NM_001038587//NM_001146	<i>Ador</i>	adenosine deaminase, RNA-specific	0001701 // in utero embryonic development // inferred from mutant phenotype//0002376 // immune system process // inferred from
1419000_at 146f	0.003158	3.24	1.29	NM_010234	<i>Fos</i>	FBI osteosarcoma oncogene	0001661 // conditioned taste aversion // inferred from electronic annotation//0006355 // regulation of transcription, DNA-templated //
1419004_s_at 14	0.000749	3.23	1.06	NM_133990	<i>Il13ra1</i>	interleukin 13 receptor, alpha 1	0002639 // positive regulation of immunoglobulin production // inferred from electronic annotation//0019221 // cytokine-mediated
1419004_s_at 14	0.000749	3.23	1.58	NM_023731	<i>Ccdc86</i>	coiled-coil domain containing 86	
1419004_s_at 14	0.000749	3.23	-1.09	NM_029083	<i>Ddit4</i>	DNA-damage-inducible transcript 4	0001666 // response to hypoxia // inferred from mutant phenotype//0001666 // response to hypoxia // not recorded//0001764 //
1419005_at 129f	0.008667	3.21	1.65	NM_173014//NM_006531051	<i>Lpcat2</i>	lysophosphatidylcholine acyltransferase 2	0006629 // lipid metabolic process // inferred from electronic annotation//0006644 // phospholipid metabolic process // inferred from
1419026_at 131f	0.001752	3.19	1.19	NM_172409//NM_006498330	<i>Fnnl2</i>	formin-like 2	0007010 // cytoskeleton organization // not recorded//0016043 // cellular component organization // inferred from electronic
1419042_at 141f	0.000240	3.19	1.37	NM_001177352//NM_001177	<i>Myc</i>	myelocytomatosis oncogene	0000122 // negative regulation of transcription from RNA polymerase II promoter // inferred from direct assay//0000122 // negative
1419045_at 669f	0.004430	3.19	-1.13	NM_007986//NM_006498746	<i>Fap</i>	fibroblast activation protein	0006508 // proteolysis // not recorded//0010716 // negative regulation of extracellular matrix disassembly // not recorded//00043542
1419050_at 661f	0.003832	3.15	1.35	NM_011113//NM_006539638	<i>Plaur</i>	plasminogen activator, urokinase receptor	0001628 // positive regulation of gene expression // not recorded//0016310 // phosphorylation // inferred from electronic
1419060_at 149f	0.005114	3.14	1.10	NM_011352//NM_006510888	<i>Sema7a</i>	sema domain, immunoglobulin domain (lg), and GPI membrane anchor,	0001649 // osteoblast differentiation // not recorded//0001934 // positive regulation of protein phosphorylation // inferred from direct
1419100_at 207f	0.000196	3.13	1.73	NM_023220//NM_006500006	<i>Spp1a2</i>	signal peptide peptidase like 2A	0006508 // proteolysis // inferred from electronic annotation//0006509 // membrane protein ectodomain proteolysis // not
1419109_at 154f	0.003991	3.13	1.73	NM_001025313//NM_009318	<i>Tapbp</i>	TAP binding protein	0002397 // MHC class I protein complex assembly // inferred from electronic annotation//0002479 // antigen processing and
1419122_at 143f	0.005546	3.10	1.35	NM_019980//NM_006522427	<i>Ltalf//Gm9861</i>	LPS-induced TNF factor//predicted gene 9861	0001817 // regulation of cytokine production // inferred from mutant phenotype//0006351 // transcription, DNA-templated // inferred
1419128_at 164f	0.003004	3.09	1.12	NM_001290475//NM_146142	<i>Tdrd7</i>	tdrd domain containing 7	0002089 // lens morphogenesis in camera-type eye // inferred from mutant phenotype//0002089 // lens morphogenesis in camera-type
1419132_at 240f	0.002149	3.08	1.51	NM_001290518//NM_025286	<i>Slc31a2</i>	solute carrier family 31, member 2	0006810 // transport // inferred from electronic annotation//0006811 // ion transport // inferred from electronic annotation//0006825
1419137_at 582f	0.001680	3.08	1.67	NM_023143//NM_001113356	<i>C1ra//C1rb</i>	complement component 1, r subcomponent A//complement component 1, r	0002376 // immune system process // inferred from electronic annotation//0006508 // proteolysis // not recorded//0006956 //
1419152_at 141f	0.000437	3.07	-4.10	NM_026862//NM_006540336	<i>Cd177</i>	CD177 antigen	
1419154_at 144f	0.002826	3.06	1.16	NM_010404//NM_177981//X	<i>Hap1</i>	huntingtin-associated protein 1	0008104 // protein localization // not recorded//0010976 // positive regulation of neuron projection development // not
1419155_a_at 14	0.000137	3.05	1.26	NM_029415//NM_006535278	<i>Slc10a6</i>	solute carrier family 10 (sodium/bile acid cotransporter family), member 6	0006810 // transport // inferred from electronic annotation//0006811 // ion transport // inferred from electronic annotation//0006814
1419186_a_at 14	0.001489	3.03	2.06	NM_001033468//NM_001145	<i>Gpr114</i>	G protein-coupled receptor 114	0007165 // signal transduction // inferred from electronic annotation//0007166 // cell surface receptor signaling pathway // inferred
1419192_at 143f	0.000931	3.02	1.80	NM_001113356//NM_023143	<i>C1ra//C1rb</i>	complement component 1, r subcomponent A//complement component 1, r	0002376 // immune system process // inferred from electronic annotation//0006508 // proteolysis // not recorded//0006956 //
1419196_at 141f	0.003594	3.00	1.42	NM_022325	<i>Ctsz</i>	cathepsin Z	0006508 // proteolysis // inferred from electronic annotation//0006441 // epithelial tube branching involved in lung morphogenesis //
1419208_at 264f	0.003729	2.98	1.84	NM_021325	<i>Cd200r1</i>	CD200 receptor 1	
1419209_at 144f	0.000255	2.97	1.19	NM_001177752//NM_001177	<i>Pfkfb3</i>	6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase 3	0006000 // fructose metabolic process // inferred from electronic annotation//0006003 // fructose 2,6-bisphosphate metabolic process
1419214_at 143f	0.006440	2.97	1.94	NM_183390	<i>Klhl6</i>	kelch-like 6	0002467 // germinal center formation // inferred from mutant phenotype//0005853 // B cell receptor signaling pathway // inferred
1419219_at 143f	0.002138	2.97	1.78	NM_144846//NM_006520760	<i>Fam49b</i>	family with sequence similarity 49, member B	

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Gene_ID	p (Corr)	FC-RSV 1 d	FC-RSV 5 d	RefSeq Transcript ID	Gene Symbol	Gene Title	Gene Ontology Biological Process
1419253_at 1411	0.001755	2.95	1.56	NM_007793	Cstb	cystatin B	0008344 // adult locomotory behavior // inferred from mutant phenotype//0010466 // negative regulation of peptidase activity // not
1419255_at 1411	0.007031	2.95	2.33	NM_001139520//NM_018851	Samhd1	SAM domain and HD domain, 1	0002376 // immune system process // inferred from electronic annotation//0006203 // dGTP catabolic process // not
1419272_at 178	0.002022	2.95	1.24	NM_007544//XM_006505408	bid	BH3 interacting domain death agonist	0001836 // release of cytochrome c from mitochondria // inferred from direct assay//0001836 // release of cytochrome c from
1419282_at 202	0.000160	2.94	2.07	NM_001267808//NM_010380	H2-D1//H2-L//H2-Q2//LOC576	histocompatibility 2, D region locus 1//histocompatibility 2, D region locus	0001916 // positive regulation of T cell mediated cytotoxicity // inferred from direct assay//0001916 // positive regulation of T cell
1419292_at 142	0.005210	2.92	1.80	NM_011189	Psmc1	proteasome (prosome, macropain) activator subunit 1 (PA28 alpha)	0010950 // positive regulation of endopeptidase activity // inferred from physical interaction//0019884 // antigen processing and
1419295_at 264	0.004034	2.89	1.01	NM_001199043//NM_001291	Lga8	lectin, galactose binding, soluble 8	0002317 // plasma cell differentiation // inferred from direct assay//0031295 // T cell costimulation // inferred from direct
1419314_at 269	0.005310	2.89	1.71	NM_030743//XM_006500439	Rnf114	ring finger protein 114	0007275 // multicellular organismal development // inferred from electronic annotation//0007283 // spermatogenesis // inferred from
1419315_at 983	0.001412	2.88	1.54	NM_009728//XM_006540579	Atp10a	ATPase, class V, type 10A	0006810 // transport // inferred from electronic annotation//0006812 // cation transport // inferred from electronic
1419318_at 1415	0.002274	2.88	1.36	NM_053110	Gpnmb	glycoprotein (transmembrane) nmb	0001649 // osteoblast differentiation // inferred from electronic annotation//0007155 // cell adhesion // inferred from direct
1419321_at 140	0.002274	2.87	1.37	NM_001083918	Gm13139	predicted gene 13139	0002244 // hematopoietic progenitor cell differentiation // inferred from mutant phenotype//0006355 // regulation of transcription,
1419328_at 1435	0.000658	2.87	1.60	NM_197986//XM_006506540	Tmem140	transmembrane protein 140	
1419351_a_at 14	0.007215	2.87	1.17	NM_011452	Serpinc9b	serine (or cysteine) peptidase inhibitor, clade B, member 9b	0010951 // negative regulation of endopeptidase activity // not recorded//0019835 // cytolysis // inferred from direct assay//0030162
1419353_at 142	0.005375	2.87	2.25	NM_009982//XM_006507319	Ctsc	cathepsin C	0001913 // T cell mediated cytotoxicity // inferred from genetic interaction//0006508 // proteolysis // inferred from mutant
1419358_at 818	0.000285	2.86	1.42	NM_009404//XM_006524033	Tnfrsf9	tumor necrosis factor (ligand) superfamily, member 9	0006955 // immune response // inferred from electronic annotation//0032729 // positive regulation of interferon-gamma production //
1419360_a_at 14	0.006103	2.86	-1.52	NM_010720//XM_006525692	Lipg	lipase, endothelial	0006629 // lipid metabolic process // inferred from electronic annotation//0007584 // response to nutrient // inferred from electronic
1419380_at 941	0.003900	2.86	1.55	NM_011316	Saa4	serum amyloid A 4	0006953 // acute-phase response // inferred from electronic annotation
1419385_a_at 14	0.004749	2.85	2.25	NM_001029855//NM_001281	Psmc2//Psmc2b	proteasome (prosome, macropain) activator subunit 2 (PA28	0010950 // positive regulation of endopeptidase activity // inferred from physical interaction//0019884 // antigen processing and
1419401_at 1445	0.000196	2.84	1.61	NM_001252472//NM_001289	Cd84	CD84 antigen	0007155 // cell adhesion // inferred from electronic annotation
1419403_at 170	0.005767	2.84	-1.12	NM_020047	Tacstd2	tumor-associated calcium signal transducer 2	0010633 // negative regulation of epithelial cell migration // inferred from direct assay//0050678 // regulation of epithelial cell
1419407_at 151	0.002933	2.84	1.45	NM_028341//XM_006526284	Ttc39c	tetratricopeptide repeat domain 39C	
1419410_at 533	0.003054	2.82	3.27	NM_009777	C1qb	complement component 1, q subcomponent, beta polypeptide	0002376 // immune system process // inferred from electronic annotation//0006958 // complement activation, classical pathway //
1419426_s_at 11	0.002923	2.82	-1.14	NM_008987	Ptx3	pentraxin related gene	0001878 // response to yeast // inferred from mutant phenotype//0008228 // opsonization // inferred from mutant
1419426_s_at 6	0.002923	2.82	2.17	NM_009921	Camp	cathelicidin antimicrobial peptide	0001934 // positive regulation of protein phosphorylation // not recorded//0002227 // innate immune response in mucosa // not
1419426_s_at 11	0.002923	2.81	1.38	NM_001164036//NM_001164	Ly6e	lymphocyte antigen 6 complex, locus E	0001701 // in utero embryonic development // inferred from mutant phenotype//0030325 // adrenal gland development // inferred
1419426_s_at 11	0.002923	2.81	1.23	NM_001243048//NM_007489	Arlnt	aryl hydrocarbon receptor nuclear translocator-like	0000600 // protein import into nucleus, translocation // inferred from direct assay//0006351 // transcription, DNA-templated // inferred
1419426_s_at 11	0.002923	2.81	-1.14	NM_172612	Rnd1	Rho family GTPase 1	0006184 // GTP catabolic process // inferred from electronic annotation//0007015 // actin filament organization // not
1419426_s_at 11	0.002923	2.79	1.90	NM_145391//XM_006505862	Taphb1	TAP binding protein-like	0019885 // antigen processing and presentation of endogenous peptide antigen via MHC class I // inferred from electronic annotation
1419426_s_at 11	0.002923	2.79	1.56	NM_145626//NM_181732	Aida	axon interactor, dorsalization associated	0007275 // multicellular organismal development // inferred from electronic annotation//0009953 // dorsal/ventral pattern formation
1419426_s_at 11	0.002923	2.79	1.37	NM_011019//XM_006519973	Osmr	oncostatin M receptor	0007166 // cell surface receptor signaling pathway // traceable author statement//0008284 // positive regulation of cell proliferation //
1419426_s_at 11	0.002923	2.75	2.06	NM_001044740//NM_007514	Sclt2a	solute carrier family 7 (cationic amino acid transporter, y+ system), member 2	0002537 // nitric oxide production involved in inflammatory response // inferred from mutant phenotype//0003333 // amino acid
1419427_at 129	0.002908	2.75	1.29	NM_001025261//NM_001025	Tpd52	tumor protein D52	0008284 // positive regulation of cell proliferation // inferred from direct assay//0030183 // B cell differentiation // inferred from
1419440_at 585	0.004425	2.75	-1.06	NM_145523	Gca	grancalcin	0006508 // proteolysis // not recorded//0006810 // transport // inferred from electronic annotation//0006811 // ion transport //
1419442_at 145	0.005253	2.74	1.70	NM_001190310//NM_027218	Clec4b1//Clec4a2	C-type lectin domain family 4, member b1//C-type lectin domain family 4,	0051281 // positive regulation of release of sequestered calcium ion into cytosol // inferred from direct assay//0002376 // immune
1419457_at 1415	0.003362	2.74	1.76	NM_008359//XM_006505618	Il17ra	interleukin 17 receptor A	0032747 // positive regulation of interleukin-23 production // not recorded//0071345 // cellular response to cytokine stimulus // not
1419463_at 146	0.000103	2.74	1.39	NM_010908//XM_006539613	Nfkbb	nuclear factor of kappa light polypeptide gene enhancer in B cells inhibitor,	0007165 // signal transduction // not recorded//0007253 // cytoplasmic sequestering of NF-kappaB // not recorded
1419469_at 1415	0.006144	2.73	-1.03	NM_001042725//NM_007588	Calcr	calcitonin receptor	0007165 // signal transduction // inferred from electronic annotation//0003556 // cell surface receptor signaling pathway // inferred
1419482_at 1415	0.001947	2.72	1.35	NM_011979	Vnn3	vanin 3	0006807 // nitrogen compound metabolic process // inferred from electronic annotation//0015939 // pantothenate metabolic process
1419484_a_at 14	0.005412	2.71	1.15	NM_001111058//NM_021293	Cd33	CD33 antigen	0007155 // cell adhesion // inferred from electronic annotation
1419485_at 1415	0.001160	2.69	-1.01	NM_020049	Sclt6a14	solute carrier family 6 (neurotransmitter transporter), member 14	0006810 // transport // inferred from electronic annotation//0006836 // neurotransmitter transport // inferred from electronic
1419493_a_at 14	0.003742	2.69	1.05	NM_011756	Zfp36	zinc finger protein 36	0000122 // negative regulation of transcription from RNA polymerase II promoter // inferred from mutant phenotype//0000122 //
1419508_at 1445	0.004646	2.68	1.67	NM_001159631//NM_021606	Nek6	NIMA (never in mitosis gene a)-related expressed kinase 6	0006468 // protein phosphorylation // not recorded//0006915 // apoptotic process // inferred from electronic annotation//0007049 //
1419510_at 138	0.001570	2.68	1.59	NM_021342	Kcne4	potassium voltage-gated channel, Isk-related subfamily, gene 4	0006810 // transport // inferred from electronic annotation//0006811 // ion transport // inferred from electronic annotation//0006813
1419515_at 263	0.008089	2.68	1.29	NM_001267724//NM_178283	Asb13	ankyrin repeat and SOCS box-containing 13	0016567 // protein ubiquitination // inferred from electronic annotation//0035556 // intracellular signal transduction // inferred from
1419529_at 834	0.007125	2.68	1.63	NM_011404	Sclt7a5	solute carrier family 7 (cationic amino acid transporter, y+ system), member 5	0003333 // amino acid transmembrane transport // inferred from electronic annotation//0006810 // transport // inferred from
1419532_at 161	0.000437	2.66	-1.37	NM_010171	F3	coagulation factor III	0001938 // positive regulation of endothelial cell proliferation // not recorded//0002541 // activation of plasma proteins involved in
1419537_at 214	0.003602	2.66	1.99	NM_001163621//NM_028010	Apol6	apolipoprotein L 6	0006869 // lipid transport // inferred from electronic annotation//0042157 // lipoprotein metabolic process // inferred from electronic
1419549_at 118	0.008318	2.65	1.24	NM_001160018//NM_001160	Tor1aip1	torin A interacting protein 1	0032781 // positive regulation of ATPase activity // not recorded//0034504 // protein localization to nucleus // inferred from mutant
1419569_a_at 5	0.000268	2.65	1.22	NM_133653//XM_006518450	Matl1a	methionine adenosyltransferase I, alpha	0006556 // 5-adenosylmethionine biosynthetic process // not recorded//0006730 // one-carbon metabolic process // inferred from
1419584_at 1445	0.001468	2.65	1.13	NM_199016//XM_006524130	Enpp4	ectonucleotide pyrophosphatase/phosphodiesterase 4	0007596 // blood coagulation // inferred from electronic annotation//0007599 // hemostasis // inferred from electronic
1419603_at 145	0.002131	2.63	1.11	NM_010755//XM_006520546	Maff	v-maf musculoaponeurotic fibrosarcoma oncogene family, protein F (avian)	0001701 // in utero embryonic development // inferred from genetic interaction//0006351 // transcription, DNA-templated // inferred
1419604_at 1425	0.000137	2.62	1.23	NM_001160180//NM_001160	Tor1aip2	torin A interacting protein 2	0007029 // endoplasmic reticulum organization // not recorded//0032781 // positive regulation of ATPase activity // not recorded
1419606_a_at 2	0.003247	2.62	-1.31	NM_027571//XM_006502083	P2ry12	purinergic receptor P2Y, G-protein coupled 12	0001973 // adenosine receptor signaling pathway // inferred from mutant phenotype//0001973 // adenosine receptor signaling
1419607_at 219	0.008007	2.62	2.08	NM_153505//XM_006502055	Nckap1	NCK associated protein 1 like	0001782 // B cell homeostasis // inferred from mutant phenotype//0002262 // myeloid cell homeostasis // inferred from mutant
1419609_at 1415	0.001511	2.62	1.32	NM_007962//XM_006509999	Mxrl2	myelin protein zero-like 2	0007155 // cell adhesion // inferred from electronic annotation//0016337 // single organismal cell-cell adhesion // inferred from direct
1419620_at 1424	0.005661	2.62	1.42	NM_001195025//NM_028778	Nuak2	NUAK family, SNF1-like kinase, 2	0006468 // protein phosphorylation // not recorded//0006915 // apoptotic process // inferred from electronic annotation//0009103 //
1419623_at 572	0.003915	2.62	-1.01	NM_025289	Tbrg1	transforming growth factor beta regulated gene 1	0006260 // DNA replication // not recorded//0006260 // DNA replication // inferred from sequence or structural similarity//0007049 //
1419627_s_at 14	0.000975	2.61	-1.06	NM_009244//XM_006543029	Serpina1b//Serpina1c//Serpina	serine (or cysteine) peptidase inhibitor, clade A, member 1B//serine (or	0001701 // in utero embryonic development // inferred from mutant phenotype//0006487 // protein N-linked glycosylation // inferred
1419640_at 1415	0.001241	2.60	1.86	NM_013819	H2-M3	histocompatibility 2, M region locus 3	0001916 // positive regulation of T cell mediated cytotoxicity // inferred from direct assay//0001916 // positive regulation of T cell
1419656_at 1415	0.008980	2.60	1.10	NM_007930	Enc1	ectodermal-neural cortex 1	0007275 // multicellular organismal development // inferred from electronic annotation//0001499 // proteasomal ubiquitin-
1419658_at 1445	0.000749	2.60	1.11	NM_001252568//NM_001252	Lrrc8a//Phyhd1	leucine rich repeat containing 8A//phytanoyl-CoA dioxygenase domain	0002329 // pre-B cell differentiation // inferred from mutant phenotype//0006810 // transport // inferred from electronic
1419658_at 1445	0.000749	2.60	1.12	NM_001013386//XM_006533	Ras10b	RAS-like, family 10, member B	0003050 // regulation of systemic arterial blood pressure by atrial natriuretic peptide // inferred from mutant phenotype//0006184 //
1419658_at 1445	0.000749	2.60	1.23	NM_001099217//NM_001252	Ly6c1//Ly6c2	lymphocyte antigen 6 complex, locus C1//lymphocyte antigen 6 complex,	
1419665_a_at 14	0.003273	2.59	2.00	NM_007801	Ctsh	cathepsin H	0001656 // metanephros development // inferred from sequence or structural similarity//0001656 // metanephros development //
1419676_at 178	0.001404	2.59	2.02	NM_134158//XM_006532176	Af251705	cDNA sequence AF251705	0002376 // immune system process // inferred from electronic annotation//00050715 // positive regulation of cytokine secretion //
1419684_at 203	0.000268	2.58	1.31	NM_133212//XM_006528717	Tlr8	toll-like receptor 8	0001774 // microglial cell activation // not recorded//0002224 // toll-like receptor signaling pathway // not recorded//0002282 //
1419688_at 1415	0.000897	2.57	1.00	NM_001253679//NM_001253	Sclt7a7	solute carrier family 7 (cationic amino acid transporter, y+ system), member 7	0003333 // amino acid transmembrane transport // inferred from electronic annotation//0006810 // transport // inferred from
1419691_at 127	0.005447	2.57	1.30	NM_007798	Ctsh	cathepsin B	0006508 // proteolysis // not recorded//00030574 // collagen catabolic process // not recorded//0046697 // dedicalization // inferred
1419697_at 1415	0.000296	2.57	1.71	NM_001291205//NM_001291	Rgs19	regulator of G-protein signaling 19	0009968 // negative regulation of signal transduction // inferred from electronic annotation//0038032 // termination of G-protein
1419699_at 686	0.006543	2.56	1.59	NM_001145960//NM_020258	Sclt37a2	solute carrier family 37 (glycerol-3-phosphate transporter), member 2	0006072 // glycerol-3-phosphate metabolic process // not recorded//0006127 // glycerophosphate shuttle // not recorded//0006810 //
1419703_at 1425	0.009263	2.56	1.30	NM_028791	Cmt1	cap methyltransferase 1	0006302 // double-strand break repair // inferred from electronic annotation//0006370 // 7-methylguanosine mRNA capping // not
1419706_a_at 8	0.005114	2.55	1.83	NM_001242423//NM_001242	Fam105a	family with sequence similarity 105, member A	
1419709_at 208	0.007770	2.55	1.16	XM_918370	Env	uncharacterized LOC641050	
1419714_at 605	0.001517	2.55	1.13	NM_001177792//NM_001177	Snap23	synaptosomal-associated protein 23	0006461 // protein complex assembly // not recorded//0006810 // transport // inferred from electronic annotation//0006887 //
1419721_at 808	0.004199	2.55	1.56	NM_001128601//NM_026829	Gm2382//Mthfs	predicted gene 2382//10, 10-methylenetetrahydrofolate synthetase	0009396 // folic acid-containing compound biosynthetic process // inferred from electronic annotation//0042981 // regulation of
1419725_at 239	0.000380	2.54	-1.36	NM_001024945//NM_023268	Qsok1	quiescin Q6 sulfhydryl oxidase 1	0006457 // protein folding // not recorded//0045454 // cell redox homeostasis // inferred from electronic annotation//00055114 //
1419728_at 203	0.001441	2.54	1.83	NM_010172//XM_006508696	F7	coagulation factor VII	0002690 // positive regulation of leukocyte chemotaxis // not recorded//0006508 // proteolysis // not recorded//0007596 // blood
1419738_a_at 14	0.005610	2.54	1.02	NM_133753//XM_006537088	Errf1	ERBB receptor feedback inhibitor 1	0007175 // negative regulation of epidermal growth factor-activated receptor activity // inferred from mutant phenotype//0007175 //
1419749_at 1415	0.002969	2.54	-2.22	NM_001267707//NM_130861	Sclt1a5	solute carrier organic anion transporter family, member 1a5	0003333 // amino acid transmembrane transport // not recorded//0006810 // transport // inferred from electronic

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Gene_ID	p (Corr)	FC-RSV 1 d	FC-RSV 5 d	RefSeq Transcript ID	Gene Symbol	Gene Title	Gene Ontology Biological Process
1419756_at,144c	0.007829	2.53	1.53	NM_011267	<i>Rgs16</i>	regulator of G-protein signaling 16	0007186 // G-protein coupled receptor signaling pathway // traceable author statement//0009968 // negative regulation of signal
1419764_at,142c	0.005121	2.53	1.13	NM_027869//XM_00651443	<i>Pnpt1</i>	polyribonucleotide nucleotidyltransferase 1	0000957 // mitochondrial RNA catabolic process // not recorded//0000958 // mitochondrial mRNA catabolic process // inferred from
1419815_at,142c	0.009324	2.53	1.44	NM_001004164//XM_006513	<i>Gnptab</i>	N-acetylglucosamine-1-phosphate transferase, alpha and beta subunits	0007040 // lysosome organization // not recorded//0009306 // protein secretion // inferred from mutant phenotype//0030154 // cell
1419833_s_at,14	0.008582	2.53	1.22	NM_183029	<i>Igf2bp2</i>	insulin-like growth factor 2 mRNA binding protein 2	0006417 // regulation of translation // inferred from electronic annotation//0006810 // transport // inferred from electronic
1419838_s_at,14	0.003222	2.52	1.16	NM_153573//XR_377439	<i>Fkbp14</i>	FK506 binding protein 14	0000413 // protein peptidyl-prolyl isomerization // not recorded//0006457 // protein folding // inferred from electronic
1419848_x_at,14	0.003102	2.52	1.68	NM_007969	<i>Wfdc18</i>	WAP four-disulfide core domain 18	0010466 // negative regulation of peptidase activity // inferred from electronic annotation
1419866_s_at,14	0.002734	2.52	1.28	NM_001164627//NM_001164	<i>Arhgap8</i>	Rho GTPase activating protein 8	0007165 // signal transduction // inferred from electronic annotation//0032321 // positive regulation of Rho GTPase activity // not
1419874_x_at,14	0.000277	2.52	1.95	NM_030711//XM_006517476	<i>Erap1</i>	endoplasmic reticulum aminopeptidase 1	0002376 // immune system process // inferred from electronic annotation//0006508 // proteolysis // inferred from direct
1419879_s_at,14	0.000894	2.51	1.31	NM_001164336//NM_001164	<i>S-Mar</i>	membrane-associated ring finger (C3HC4) 5	0002029 // protein ubiquitination // not recorded//0016567 // protein ubiquitination // inferred from electronic
1419914_s_at,14	0.001809	2.51	1.91	NM_001033245//NM_001206	<i>Hk3</i>	hexokinase 3	0001678 // cellular glucose homeostasis // not recorded//0005975 // carbohydrate metabolic process // inferred from electronic
1419927_s_at,14	0.002355	2.51	1.08	NM_013623//XM_006537666	<i>Orm3</i>	orosomucoid 3	0002682 // regulation of immune system process // inferred from electronic annotation//0006810 // transport // inferred from
1419949_at,142c	0.002358	2.50	-1.15	NM_027560//XM_006509740	<i>Ardc2</i>	arrestin domain containing 2	0007165 // signal transduction // inferred from electronic annotation
1420007_at,142c	0.007683	2.50	1.15	NM_021671798//NM_010840	<i>Mthfr</i>	5,10-methylenetetrahydrofolate reductase	0001666 // response to hypoxia // inferred from electronic annotation//0006555 // methionine metabolic process // inferred from
1420011_s_at,14	0.003915	2.48	1.27	NM_001169131//NM_198600	<i>Papd7</i>	PAP associated domain containing 7	0006260 // DNA replication // inferred from electronic annotation//0006261 // DNA-dependent DNA replication // inferred from
1420023_at,142c	0.008194	2.48	1.56	NM_030194//NM_175397//X	<i>Sp110</i>	Sp110 nuclear body protein	0002376 // immune system process // inferred from electronic annotation//0006351 // transcription, DNA-templated // inferred from
1420037_at,142c	0.007926	2.47	1.20	NM_001290761//NM_001290	<i>Nmral1</i>	Nmra-like family domain containing 1	0006694 // steroid biosynthetic process // inferred from electronic annotation//0006813 // potassium ion transport // inferred from
1420088_at,142c	0.005334	2.47	1.16	NM_010907	<i>Nfkbia</i>	nuclear factor of kappa light polypeptide gene enhancer in B cells inhibitor,	0000060 // protein import into nucleus, translocation // inferred from direct assay//0007253 // cytoplasmic sequestering of NF-kappaB
1420148_at,142c	0.008771	2.47	1.14	NM_019738	<i>Nupr1</i>	nuclear protein transcription regulator 1	0002526 // acute inflammatory response // inferred from mutant phenotype//0006351 // transcription, DNA-templated // inferred from
1420159_at,142c	0.005302	2.47	1.14	NM_011157//XM_006513374	<i>Srgn</i>	serglycin	0006915 // apoptotic process // inferred from electronic annotation//0008626 // granzyme-mediated apoptotic signaling pathway //
1420330_at,142c	0.000789	2.47	1.80	NM_009735	<i>B2m</i>	beta-2 microglobulin	0001916 // positive regulation of T cell mediated cytotoxicity // inferred from mutant phenotype//0002237 // response to molecule of
1420361_at,148i	0.004799	2.46	1.67	NM_028019//XM_006534272	<i>Rnf135</i>	ring finger protein 135	0002376 // immune system process // inferred from electronic annotation//0016567 // protein ubiquitination // not
1420375_at,144c	0.004353	2.46	1.49	NM_177905//XM_006510430	<i>Piwi4</i>	piwi-like RNA-mediated gene silencing 4	0006417 // regulation of translation // inferred from electronic annotation//0007126 // meiotic nuclear division // inferred from
1420376_a_at,14	0.007870	2.46	1.86	NM_133733//XM_006510602	<i>Clmp</i>	CXADR-like membrane protein	0048565 // digestive tract development // not recorded
1420376_b_at,14	0.008104	2.45	1.27	NM_023168//XM_006521249	<i>Grina</i>	glutamate receptor, ionotropic, N-methyl D-aspartate-associated protein 1	0032469 // endoplasmic reticulum calcium ion homeostasis // inferred from direct assay//1902236 // negative regulation of intrinsic
1420376_c_at,14	0.003821	2.44	1.54	NM_001128601//NM_026829	<i>Gm2382//Mthfs</i>	predicted gene 2382//10, 10-methylenetetrahydrofolate synthetase	0009396 // folic acid-containing compound biosynthetic process // inferred from electronic annotation//0042981 // regulation of
1420376_d_at,14	0.003821	2.44	1.42	NM_175401//XM_006516827	<i>Fbxw17</i>	F-box and WD-40 domain protein 17	0031146 // SCF-dependent proteasomal ubiquitin-dependent protein catabolic process // not recorded
1420376_e_at,14	0.003821	2.43	1.18	NM_001290183//NM_007837	<i>Ddit3</i>	DNA-damage inducible transcript 3	0001955 // blood vessel maturation // inferred from mutant phenotype//0006351 // transcription, DNA-templated // inferred from
1420376_f_at,14	0.003821	2.43	1.23	NM_144797	<i>Metrl</i>	meteorin, glial cell differentiation regulator-like	0009409 // response to cold // inferred from direct assay//0014850 // response to muscle activity // inferred from direct
1420377_at,144c	0.002289	2.42	1.44	NM_009926//XM_006523559	<i>Col11a2</i>	collagen, type XI, alpha 2	0001501 // skeletal system development // not recorded//0001503 // ossification // not recorded//0001894 // tissue homeostasis //
1420380_at,202c	0.000616	2.42	1.13	NM_133807	<i>Lrrc59</i>	leucine rich repeat containing 59	
1420382_at,171c	0.005670	2.42	1.08	XR_105187//XR_040705	<i>E23001322Rik</i>	RIKEN cDNA E23001322 gene	0006810 // transport // inferred from electronic annotation//0007264 // small GTPase mediated signal transduction // inferred from
1420394_s_at,14i	0.001756	2.42	1.02	NM_013759	<i>Msrb1</i>	methionine sulfoxide reductase B1	0002376 // immune system process // inferred from electronic annotation//0006979 // response to oxidative stress // inferred from
1420394_s_at,14i	0.001756	2.41	1.43	NM_021297	<i>Tlr4</i>	tol-like receptor 4	0000187 // activation of MAPK activity // inferred from mutant phenotype//0001774 // microglial cell activation // not
1420402_at,142c	0.000787	2.41	1.25	NM_001122675//NM_001122	<i>Zcchc2</i>	zinc finger, CCHC domain containing 2	0007154 // cell communication // inferred from electronic annotation
1420408_s_at,14	0.006381	2.40	1.48	NM_007695//XM_006529111	<i>Chil1</i>	chitinase-like 1	0005975 // carbohydrate metabolic process // inferred from electronic annotation//0006032 // chitin catabolic process // inferred from
1420429_at,1938	0.007125	2.40	1.23	NM_027985//XM_006535974	<i>Mad2l2</i>	MAD2 mitotic arrest deficient-like 2	0000122 // negative regulation of transcription from RNA polymerase II promoter // not recorded//0000125 // regulation of cell growth
1420437_at,159	0.006636	2.40	1.19	NM_025378	<i>Ifitm3</i>	interferon induced transmembrane protein 3	0002376 // immune system process // inferred from electronic annotation//0008285 // negative regulation of cell proliferation //
1420438_at,184i	0.000144	2.39	-1.06	NM_001159317//NM_001159	<i>Il1rap</i>	interleukin 1 receptor accessory protein	0007165 // signal transduction // inferred from electronic annotation//0019221 // cytokine-mediated signaling pathway // inferred from
1420454_at,145c	0.005500	2.38	1.20	NM_010371//XM_006518568	<i>Gzmc</i>	granzyme C	0006508 // proteolysis // not recorded//0008626 // granzyme-mediated apoptotic signaling pathway // not recorded//0019835 //
1420461_at,198	0.009892	2.38	1.57	NM_183160	<i>Tmem252</i>	transmembrane protein 252	
1420464_s_at,14i	0.004366	2.38	1.31	NM_001164071//NM_001164	<i>Tank</i>	TRAF family member-associated NF-kappa B activator	0007249 // I-kappaB kinase/NF-kappaB signaling // inferred from direct assay
1420464_s_at,14i	0.004366	2.37	1.61	NM_138310//XM_006507399	<i>Apobr</i>	apolipoprotein B receptor	0006629 // lipid metabolic process // inferred from electronic annotation//0006641 // triglyceride metabolic process // inferred from
1420464_s_at,14i	0.004366	2.37	1.57	NM_001146308//NM_001146	<i>Dnrl</i>	drebrin-like	0002376 // immune system process // inferred from electronic annotation//0006810 // transport // inferred from electronic
1420464_s_at,14i	0.004366	2.36	1.87	NM_001267808//NM_010380	<i>H2-D1//H2-L//H2-Q2//LOC676</i>	histocompatibility 2, D region locus 1//histocompatibility 2, D region locus	0001916 // positive regulation of T cell mediated cytotoxicity // inferred from direct assay//0001916 // positive regulation of T cell
1420464_s_at,14i	0.004366	2.35	2.21	NM_021334//XR_378219	<i>Iltga</i>	integrin alpha X	0007155 // cell adhesion // inferred from electronic annotation//0007229 // integrin-mediated signaling pathway // inferred from
1420464_s_at,14i	0.004366	2.35	1.37	NM_001291865//NM_009121	<i>Sat1</i>	spermidine/spermine N1-acetyl transferase 1	0001525 // angiogenesis // inferred from electronic annotation//0006595 // polyamine metabolic process // not recorded//0006598 //
1420491_at,145c	0.008839	2.35	-1.75	NM_175307	<i>Fam46b</i>	family with sequence similarity 46, member B	
1420498_a_at,14	0.009892	2.34	1.18	NM_009546	<i>Trim25</i>	tripartite motif-containing 25	0002376 // immune system process // inferred from electronic annotation//0016567 // protein ubiquitination // inferred from
1420499_at,142c	0.000915	2.34	1.20	NM_001163464//NM_025659	<i>Abi3</i>	ABI gene family, member 3	0018108 // peptidyl-tyrosine phosphorylation // not recorded//0030334 // regulation of cell migration // not recorded
1420502_at,202c	0.005236	2.34	1.35	NM_001039720//NR_108041	<i>9030619P08Rik</i>	lymphocyte antigen 6 complex pseudogene	
1420503_at,142c	0.004593	2.34	1.37	NM_001145957//NM_172767	<i>Vwa5a</i>	von Willebrand factor A domain containing 5A	0001558 // regulation of cell growth // not recorded//0006259 // DNA metabolic process // inferred from electronic
1420509_at,142c	0.003436	2.33	1.66	NM_001131054//NM_013917	<i>Pttg1</i>	pituitary tumor-transforming gene 1	0000075 // cell cycle checkpoint // inferred from sequence or structural similarity//0000724 // double-strand break repair via
1420515_s_at,145c	0.001106	2.33	1.70	NM_028696//XM_006495620	<i>Nabp1</i>	nucleic acid binding protein 1	0006810 // transport // inferred from electronic annotation//0006811 // ion transport // inferred from electronic annotation//0006821
1420532_at,145c	0.004431	2.32	1.41	NM_011930//XM_006524296	<i>Clnr7</i>	chloride channel 7	0005975 // carbohydrate metabolic process // inferred from electronic annotation//0006048 // UDP-N-acetylglucosamine biosynthetic
1420549_at,144i	0.000573	2.31	-1.13	NM_013529	<i>Gjft2</i>	glutamine fructose-6-phosphate transaminase 2	0007155 // cell adhesion // inferred from electronic annotation//0007155 // cell adhesion // --//0007157 // heterophilic cell-cell
1420566_at	0.009125	2.29	1.11	NM_177910//XM_006511759	<i>Gmpgb</i>	GDP-mannose pyrophosphorylase B	0043551 // regulation of phosphatidylinositol 3-kinase activity // inferred from electronic annotation
1420569_at,126c	0.002760	2.29	1.42	NM_011932//XM_006501518	<i>Dapp1</i>	dual adaptor for phosphotyrosine and 3-phosphoinositides 1	0006306 // DNA methylation // traceable author statement//0006351 // transcription, DNA-templated // inferred from electronic
1420579_s_at,14i	0.002809	2.29	1.13	NM_013594//XM_006525704	<i>Mbd1</i>	methyl-CpG binding domain protein 1	
1420590_at,151c	0.005609	2.29	1.39	XM_006516441//XM_006543	<i>Gm2701//LOC102631912</i>	predicted gene 2701//NADH dehydrogenase [ubiquinone] 1 beta	0001503 // ossification // inferred from electronic annotation//0001756 // somitogenesis // inferred from mutant phenotype//0002376
1420610_at,142c	0.000541	2.28	-1.34	NM_001112715//NM_026820	<i>Ifitm1</i>	interferon induced transmembrane protein 1	0001525 // angiogenesis // inferred from electronic annotation//0006412 // translation // inferred from electronic
1420628_at,143c	0.005672	2.28	3.92	NM_001164314//NM_001164	<i>Wars</i>	tryptophanyl-tRNA synthetase	0006412 // translation // inferred from electronic annotation//0006413 // translational initiation // inferred from electronic annotation
1420635_s_at,142c	0.005924	2.27	1.31	NM_010120//XM_006525626	<i>Ejfa1//B8287469//Gm4027</i>	eukaryotic translation initiation factor 1A//expressed sequence	0006810 // transport // inferred from electronic annotation//0006811 // ion transport // inferred from electronic annotation//0006812
1420639_at,142c	0.008684	2.27	1.11	NM_013927//XM_006537979	<i>Cnbg3</i>	cyclic nucleotide gated channel beta 3	0006508 // proteolysis // inferred from direct assay//0019538 // protein metabolic process // inferred from electronic annotation
1420649_at,142c	0.009552	2.27	2.19	NM_024434	<i>Lap3</i>	leucine aminopeptidase 3	0006184 // GTP catabolic process // inferred from electronic annotation//0006886 // intracellular protein transport // inferred from
1420654_a_at,14i	0.008675	2.27	-1.06	NM_009026	<i>Rasd1</i>	RAS, dexamethasone-induced 1	0000278 // mitotic cell cycle // inferred from mutant phenotype//0001816 // cytokine production // inferred from mutant
1420671_x_at,14	0.000583	2.27	1.15	NM_001048146//NM_001286	<i>Azi2</i>	5-azacytidine-induced gene 2	0006629 // lipid metabolic process // inferred from electronic annotation//0008152 // metabolic process // inferred from electronic
1420693_at,179c	0.000349	2.26	2.00	NM_146251//XM_006498014	<i>Pnp1a7</i>	patatin-like phospholipase domain containing 7	0005975 // carbohydrate metabolic process // inferred from direct assay//0008152 // metabolic process // inferred from electronic
1420697_at,165c	0.002558	2.25	1.63	NM_010368//XM_006504342	<i>Gusb</i>	glucuronidase, beta	0000122 // negative regulation of transcription from RNA polymerase II promoter // inferred from direct assay//0001658 // branching
1420723_at,264i	0.001698	2.24	1.57	NM_001136082//NM_001164	<i>Timeless</i>	timeless circadian clock 1	0007265 // Ras protein signal transduction // inferred from direct assay
1420743_a_at,14	0.006994	2.24	1.42	NM_013739	<i>Dok3</i>	docking protein 3	
1420747_at,269	0.005223	2.24	1.16	NM_145449//XM_006515758	<i>Ifi272b</i>	interferon, alpha-inducible protein 27 like 2B	0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 // regulation of transcription, DNA-templated
1420768_a_at,14	0.000378	2.23	1.18	NM_029508//XM_006527431	<i>Pcgf5</i>	polycomb group ring finger 5	0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 // regulation of transcription, DNA-templated
1420804_s_at,14i	0.001669	2.23	1.14	NM_026117//NM_207677//X	<i>Deaf2</i>	deaf death domain-containing DNA binding protein 2	0042167 // heme catabolic process // not recorded//0055114 // oxidation-reduction process // inferred from direct assay//0055114 //
1420808_at,145c	0.009319	2.22	1.28	NM_026678//XM_006498569	<i>Bilva</i>	biliverdin reductase A	0001889 // liver development // inferred from electronic annotation//0006520 // cellular amino acid metabolic process // inferred from
1420809_a_at,14	0.001858	2.22	1.32	NM_012055//XM_006505092	<i>Asns</i>	asparagine synthetase	0035556 // intracellular signal transduction // inferred from electronic annotation
1420809_a_at,14	0.001858	2.22	1.21	NM_144804	<i>Depdc7</i>	DEP domain containing 7	0006281 // DNA repair // inferred from electronic annotation//0006516 // glycoprotein catabolic process // inferred from direct
1420811_a_at,14	0.007975	2.21	1.07	NM_001163704//NM_001163	<i>Fbxo6</i>	F-box protein 6	0008152 // metabolic process // inferred from electronic annotation
1420818_at,142c	0.002771	2.21	1.11	NM_001141965//NM_026425	<i>Naa20</i>	N[alpha]-acetyltransferase 20, NatB catalytic subunit	

Table S6

Gene ID	p (Corr)	FC-RSV 1 d	FC-RSV 5 d	RefSeq Transcript ID	Gene Symbol	Gene Title	Gene Ontology Biological Process
1420831_at,142c	0.002675	2.21	1.01	NM_028749	<i>Npl</i>	N-acetylneuraminatase pyruvate lyase	0005975 // carbohydrate metabolic process // inferred from electronic annotation//0008152 // metabolic process // inferred from
1420841_at,142c	0.000541	2.21	-1.01	NM_013562	<i>lfrd1</i>	interferon-related developmental regulator 1	0007275 // multicellular organismal development // inferred from electronic annotation//0007527 // adult somatic muscle
1420852_a_at,14	0.004052	2.20	1.64	NM_001167875//NM_001167	<i>Cyp2c50</i>	cytochrome P450, family 2, subfamily c, polypeptide 50	0019369 // arachidonic acid metabolic process // inferred from direct assay//0043651 // linoleic acid metabolic process // inferred from
1420864_at,142c	0.006848	2.19	1.22	NM_001164566//NM_144882	<i>Spots21</i>	spermatogenesis associated, serine-rich 2-like	
1420878_a_at,14	0.006130	2.19	1.41	NM_194346//NM_006519062	<i>Rnf31</i>	ring finger protein 31	0000209 // protein polyubiquitination // not recorded//0008152 // metabolic process // inferred from electronic annotation//0016567
1420881_at,143c	0.004024	2.19	1.13	NM_024185//NM_006497522	<i>Fom188a</i>	family with sequence similarity 188, member A	0006915 // apoptotic process // inferred from electronic annotation
1420882_a_at,14	0.003900	2.18	1.12	NM_008927//NM_006511196	<i>Map2k1</i>	mitogen-activated protein kinase kinase 1	0000165 // MAPK cascade // inferred from mutant phenotype//0000165 // MAPK cascade // not recorded//0000187 // activation of
1420887_a_at,14	0.008793	2.18	1.12	NM_207636//NM_006519115	<i>Fndc3a</i>	fibronectin type III domain containing 3A	0007286 // spermatid development // inferred from mutant phenotype//0009566 // fertilization // inferred from mutant
1420896_at,142c	0.002933	2.18	-1.06	NM_016675//NM_006524846	<i>Cldn2</i>	claudin 2	0016338 // calcium-independent cell-cell adhesion // inferred from direct assay
1420915_at,145c	0.000226	2.18	1.16	NM_001291799//NM_010070	<i>Dok1</i>	docking protein 1	0000165 // MAPK cascade // traceable author statement//0007169 // transmembrane receptor protein tyrosine kinase signaling
1420956_at,142c	0.001936	2.18	1.43	NM_001110192//NM_001110	<i>Inpp5d</i>	inositol polyphosphate-5-phosphatase D	0002376 // immune system process // inferred from electronic annotation//0006915 // apoptotic process // inferred from electronic
1420964_at,142c	0.004189	2.17	1.23	NM_026386//NM_006526190	<i>Snx2</i>	sorting nexin 2	0006810 // transport // inferred from electronic annotation//0006886 // intracellular protein transport // not recorded//0006897 //
1420979_at,142c	0.009993	2.17	1.80	NM_001161428//NM_019449	<i>Unc93b1</i>	unc-93 homolog B1 (C. elegans)	0002224 // toll-like receptor signaling pathway // inferred from mutant phenotype//0002376 // immune system process // inferred
1420985_at,145c	0.002714	2.16	-1.05	NM_029614//NM_006508299	<i>Prss23</i>	protease, serine 23	0006508 // proteolysis // inferred from electronic annotation
1420991_at,142c	0.006602	2.15	-5.32	NM_013743	<i>Pdk4</i>	pyruvate dehydrogenase kinase, isoenzyme 4	0005975 // carbohydrate metabolic process // inferred from electronic annotation//0006006 // glucose metabolic process // inferred
1421008_at,142c	0.000953	2.15	-1.13	NM_013918//NM_006523055	<i>Usp25</i>	ubiquitin specific peptidase 25	0006508 // proteolysis // not recorded//0006511 // ubiquitin-dependent protein catabolic process // inferred from sequence or
1421014_a_at,14	0.004765	2.14	1.95	NM_001097617//NM_144938	<i>C1s1</i>	complement component 1, s subcomponent 1	0002376 // immune system process // inferred from electronic annotation//0006508 // proteolysis // not recorded//0006956 //
1421027_a_at,14	0.002544	2.14	1.28	NM_145630	<i>Pdk3</i>	pyruvate dehydrogenase kinase, isoenzyme 3	0005975 // carbohydrate metabolic process // inferred from electronic annotation//0006006 // glucose metabolic process // inferred
1421034_a_at,14	0.003367	2.13	1.32	NM_008062//NM_019468	<i>G6pdx2//G6pdx</i>	glucose-6-phosphate dehydrogenase 2//glucose-6-phosphate	0001816 // cytokine production // inferred from mutant phenotype//0001816 // cytokine production // not recorded//0001998 //
1421035_a_at,14	0.005399	2.13	1.17	NM_030889//NM_006504202	<i>Sorcs2</i>	soritin-related VPS10 domain containing receptor 2	0006810 // transport // inferred from electronic annotation
1421038_a_at,14	0.006097	2.13	1.12	NM_023377	<i>Stard5</i>	STAR-related lipid transfer (START) domain containing 5	0006694 // steroid biosynthetic process // inferred from electronic annotation//0006810 // transport // inferred from electronic
1421040_a_at,14	0.002196	2.13	-1.00	NM_198007//NM_006512923	<i>Ascc3</i>	activating signal co-integrator 1 complex subunit 3	0006200 // ATP catabolic process // not recorded//0006281 // DNA repair // inferred from electronic annotation//0006307 // DNA
1421041_s_at,14	0.004310	2.12	1.56	NM_138677//NM_006505746	<i>Edem1</i>	ER degradation enhancer, mannosidase alpha-like 1	0006986 // response to unfolded protein // inferred from electronic annotation//0030433 // ER-associated ubiquitin-dependent protein
1421041_s_at,14	0.004310	2.12	1.30	NM_029103//NM_006511843	<i>Manf</i>	mesencephalic astrocyte-derived neurotrophic factor	0002014 // vasoconstriction of artery involved in ischemic response to lowering of systemic arterial blood pressure // inferred from
1421047_at,145c	0.002458	2.12	1.36	NM_001077411//NM_008094	<i>Gba</i>	glucosidase, beta, acid	0005975 // carbohydrate metabolic process // inferred from electronic annotation//0006629 // lipid metabolic process // inferred from
1421058_at,145c	0.002971	2.12	1.34	NM_008175	<i>Grrn</i>	granulin	0000398 // mRNA splicing, via spliceosome // not recorded//0000398 // mRNA splicing, via spliceosome // ----//0001835 // blastocyst
1421067_a_at,14	0.008806	2.12	1.29	NM_007408//NM_006537557	<i>Plin2</i>	perilipin 2	0014070 // response to organic cyclic compound // inferred from electronic annotation//0015909 // long-chain fatty acid transport //
1421074_at,142c	0.002116	2.11	1.33	NM_001110498//NM_010509	<i>Ifnar2</i>	interferon (alpha and beta) receptor 2	0002376 // regulation of transcription from RNA polymerase II promoter // inferred from direct assay//0008283 // cell proliferation //
1421086_at,142c	0.000717	2.11	1.06	NM_001135149//NM_001135	<i>Slc39a8</i>	solute carrier family 39 (metal ion transporter), member 8	0006810 // transport // inferred from electronic annotation//0006811 // ion transport // inferred from electronic annotation//0006829
1421111_at,142c	0.006710	2.11	1.46	NM_001164804//NM_178893	<i>Coro2a</i>	coronin, actin binding protein 2A	0030036 // actin cytoskeleton organization // not recorded
1421111_at,142c	0.006710	2.11	1.09	NM_008380//NM_006516558	<i>Inhba</i>	inhibin beta-A	0000082 // G1/S transition of mitotic cell cycle // not recorded//0001541 // ovarian follicle development // not recorded//0001707 //
1421120_at,143c	0.004646	2.11	-1.01	NM_008489	<i>Lbp</i>	lipopolysaccharide binding protein	0002232 // leukocyte chemotaxis involved in inflammatory response // inferred from mutant phenotype//0002281 // macrophage
1421126_at,145c	0.000655	2.11	1.37	NM_011967	<i>Psmo5</i>	proteasome (prosome, macropain) subunit, alpha type 5	0006508 // proteolysis // inferred from electronic annotation//0006511 // ubiquitin-dependent protein catabolic process // inferred
1421140_a_at,14	0.005093	2.10	1.14	NM_146064//NM_006520887	<i>Soot2</i>	sterol O-acetyltransferase 2	0006629 // lipid metabolic process // inferred from electronic annotation//0008202 // steroid metabolic process // inferred from
1421145_at,142c	0.003260	2.10	1.13	NM_198664//NM_006538046	<i>Tbc1d2</i>	TBC1 domain family, member 2	0032313 // regulation of Rab GTPase activity // inferred from electronic annotation//0032851 // positive regulation of Rab GTPase
1421162_a_at,14	0.000905	2.10	1.12	NM_153523	<i>Tcstv3</i>	2-cell-stage, variable group, member 3	
1421170_a_at,14	0.003125	2.10	1.72	NM_001205339//NM_177420	<i>Psoat1</i>	phosphoserine aminotransferase 1	0006564 // L-serine biosynthetic process // inferred from electronic annotation//0008152 // metabolic process // inferred from
1421191_s_at,14	0.003281	2.10	1.28	NM_029478//NM_006534402	<i>Vmp1</i>	vacuole membrane protein 1	0006914 // autophagy // inferred from electronic annotation//0007155 // cell adhesion // inferred from electronic
1421208_at,142c	0.000583	2.09	1.71	NM_001145953//NM_010705	<i>Lgals3</i>	lectin, galactose binding, soluble 3	0001501 // skeletal system development // inferred from genetic interaction//0002376 // immune system process // inferred from
1421210_at,142c	0.004716	2.09	1.44	NM_001093754//NM_001278	<i>Denn2d2</i>	DENM/MADD domain containing 2D	0032313 // regulation of Rab GTPase activity // not recorded//0032851 // positive regulation of Rab GTPase activity // inferred from
1421215_a_at,14	0.007693	2.09	-1.13	NM_007901	<i>Slpr1</i>	sphingosine-1-phosphate receptor 1	0001525 // angiogenesis // inferred from direct assay//0001955 // blood vessel maturation // inferred from mutant
1421217_a_at,14	0.001385	2.08	5.01	NM_009892//NM_006500964	<i>Chil3//Chil4</i>	chitinase-like 3//chitinase-like 4	0000272 // polysaccharide catabolic process // inferred from electronic annotation//0005975 // carbohydrate metabolic process //
1421225_a_at,14	0.007108	2.08	1.18	NM_025894	<i>Psm1d2</i>	proteasome (prosome, macropain) 26S subunit, non-ATPase, 12	
1421228_at,142c	0.000525	2.08	1.46		<i>5730411F24Rik</i>	RIKEN cDNA 5730411F24 gene	0032321 // positive regulation of Rho GTPase activity // inferred from electronic annotation//0035023 // regulation of Rho protein
1421229_at,143c	0.003527	2.07	-1.07	NM_008654	<i>Ppp1r15a</i>	protein phosphatase 1, regulatory (inhibitor) subunit 15A	0006417 // regulation of translation // inferred from electronic annotation//0006915 // apoptotic process // inferred from electronic
1421236_at,145c	0.005089	2.07	1.34	NM_025462//NM_139293//	<i>Ece2</i>	endothelin converting enzyme 2	0006508 // proteolysis // inferred from sequence or structural similarity//0007420 // brain development // inferred from sequence or
1421253_at,181c	0.005223	2.07	1.91	NM_026362//NM_006527340	<i>Plgrkt</i>	plasmignone receptor, C-terminal lysine transmembrane protein	0006935 // chemotaxis // inferred from electronic annotation//0006954 // inflammatory response // inferred from electronic
1421254_a_at,14	0.004621	2.07	1.25	NM_001159637//NM_138671	<i>Nadk</i>	NAD kinase	0006741 // NADP biosynthetic process // inferred from electronic annotation//0008152 // metabolic process // inferred from electronic
1421256_at,149c	0.006075	2.06	1.26	NM_027513//NM_006506589	<i>Nup205</i>	nucleoporin 205	0051292 // nuclear pore complex assembly // not recorded
1421261_at,142c	0.001633	2.06	1.03	NM_001126047//NM_006495	<i>Sema4c</i>	sema domain, immunoglobulin domain (Ig), transmembrane domain (TM)	0001843 // neural tube closure // inferred from mutant phenotype//0007275 // multicellular organismal development // inferred from
1421266_s_at,14	0.005936	2.06	1.26	NM_145458//NM_178279//X	<i>Psk</i>	PX domain containing serine/threonine kinase	0006468 // protein phosphorylation // inferred from electronic annotation//0006954 // inflammatory response // not
1421284_at,142c	0.003312	2.06	1.04	NM_001103156//NM_001103	<i>Steap2</i>	six transmembrane epithelial antigen of prostate 2	0006810 // transport // inferred from electronic annotation//0006811 // ion transport // inferred from electronic annotation//0006893
1421285_at,142c	0.002211	2.05	1.07	NM_133801//NM_006525194	<i>Gtf2f1</i>	general transcription factor IIF, polypeptide 1	0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 // regulation of transcription, DNA-templated
1421289_at,142c	0.000291	2.05	1.21	NM_0011957	<i>Creb3l1</i>	cAMP responsive element binding protein 3-like 1	0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 // regulation of transcription, DNA-templated
1421291_at,145c	0.006369	2.05	1.26	NM_001114332//NM_028247	<i>Slc16a10</i>	solute carrier family 16 (monocarboxylic acid transporters), member 10	0006810 // transport // inferred from electronic annotation//0005085 // transmembrane transport // inferred from electronic
1421297_a_at,14	0.008806	2.05	1.08	NM_010235	<i>Fosl1</i>	fos-like antigen 1	0001701 // in utero embryonic development // inferred from mutant phenotype//0006355 // regulation of transcription, DNA-
1421304_at,166c	0.006907	2.05	-1.06	NM_001033487//NM_009177	<i>St3gal1</i>	ST3 beta-galactoside alpha-2,3-sialyltransferase 1	0006054 // N-acetylneuraminatase metabolic process // inferred from sequence or structural similarity//0006468 // protein
1421307_at,142c	0.000989	2.05	1.93	NM_026014	<i>Cdt1</i>	chromatin licensing and DNA replication factor 1	0000076 // DNA replication checkpoint // inferred from direct assay//0000076 // DNA replication checkpoint // not recorded//0006260
1421326_at,145c	0.002430	2.04	1.13	NM_001168525//NM_001168	<i>Sgms1</i>	sphingomyelin synthase 1	0006629 // lipid metabolic process // inferred from electronic annotation//0006665 // sphingolipid metabolic process // inferred from
1421330_at,143c	0.004334	2.04	-1.00	NM_001033310//NM_001163	<i>Cox18</i>	cytochrome c oxidase assembly protein 18	0008335 // respiratory chain complex I assembly // not recorded//00015031 // protein transport // not recorded//0051204 // protein
1421337_at,142c	0.006848	2.04	1.21	NM_133918//NM_006503648	<i>Emilin1</i>	elastin microfibril interfacer 1	0007155 // cell adhesion // inferred from electronic annotation//0010811 // positive regulation of cell-substrate adhesion // inferred
1421345_at,144c	0.008636	2.03	1.05	NM_026929	<i>Chac1</i>	ChAC, cation transport regulator 1	0006915 // apoptotic process // inferred from electronic annotation//0006986 // response to unfolded protein // inferred from
1421358_at,149c	0.005656	2.03	1.07	NM_027808//NM_006502101	<i>Alpk1</i>	alpha-kinase 1	0006468 // protein phosphorylation // inferred from electronic annotation//0016310 // phosphorylation // inferred from electronic
1421365_at,143c	0.000457	2.02	1.31	NM_001284332//NM_025858	<i>Shisa5</i>	shisa homolog 5 (Xenopus laevis)	0006915 // apoptotic process // inferred from electronic annotation//0007165 // signal transduction // not recorded//0042771 //
1421366_at,238c	0.002297	2.02	1.45	NM_011955//XR_384565	<i>Nubp1</i>	nucleotide binding protein 1	0006879 // cellular ion homeostasis // not recorded//0010826 // negative regulation of centrosome duplication // inferred from
1421376_at,142c	0.001309	2.02	1.07	NM_027514	<i>Pvr</i>	pulvinor receptor	0002860 // positive regulation of natural killer cell mediated cytotoxicity directed against tumor cell target // inferred from electronic
1421385_a_at,14	0.007145	2.02	1.09	NM_148927//NM_006541158	<i>Plekha4</i>	pleckstrin homology domain containing, family A (phosphoinositide binding	
1421392_a_at,14	0.000738	2.01	1.41	NM_026473	<i>Tubb6</i>	tubulin, beta 6 class V	0006184 // GTP catabolic process // inferred from electronic annotation//0007017 // microtubule-based process // inferred from
1421402_at,145c	0.003663	2.01	1.19	NM_148933//NM_006500547	<i>Sloc4a1</i>	solute carrier organic anion transporter family, member 4a1	0003333 // amino acid transmembrane transport // not recorded//0006810 // transport // inferred from electronic
1421408_at,807c	0.001804	2.01	1.29	NM_008334//NM_008336//	<i>Ifna11//Ifna12//Ifna15//Ifna16</i>	interferon alpha 11//interferon alpha 12//interferon alpha 15//interferon	0002250 // adaptive immune response // not recorded//0002286 // T cell activation involved in immune response // inferred from
1421451_at,170c	0.006731	2.01	1.22	NM_025443//NM_006514779	<i>Hns1</i>	partner of NOB1 homolog (S. cerevisiae)	
1421457_a_at,16	0.001295	2.01	1.09	NM_008215	<i>Pao1</i>	hyaluronan synthase1	0010764 // negative regulation of fibroblast migration // not recorded//00030213 // hyaluronan biosynthetic process // inferred from
1421468_at,144c	0.000939	2.01	1.21	NM_007465//NM_006509833	<i>Birc2</i>	baculoviral IAP repeat-containing 2	0000209 // protein polyubiquitination // not recorded//0001666 // response to hypoxia // not recorded//0001890 // placenta
1421473_at,161c	0.003482	2.01	1.27	NM_138952//NM_006537677	<i>Ripk2</i>	receptor (TNFRSF)-interacting serine-threonine kinase 2	0001961 // positive regulation of cytokine-mediated signaling pathway // inferred from mutant phenotype//0002250 // adaptive
1421488_at,143c	0.003716	2.01	1.39	NM_009373	<i>Tgm2</i>	transglutaminase 2, C polypeptide	0001974 // blood vessel remodeling // not recorded//0007186 // G-protein coupled receptor signaling pathway // traceable author
1421491_a_at,14	0.003482	2.00	-1.10	NM_009399//NM_006529381	<i>Tnfrsf11a</i>	tumor necrosis factor receptor superfamily, member 11a, NFkB activator	0001503 // ossification // inferred from mutant phenotype//0002250 // adaptive immune response // not recorded//0007275 //
1421499_a_at,14	0.005500	2.00	1.12	NM_001161845//NM_001161	<i>Sgk1</i>	serum/glucocorticoid induced kinase 1	0006468 // protein phosphorylation // inferred from direct assay//0006883 // cellular sodium ion homeostasis // not
1421542_at,142c	0.002521	2.00	1.14	NM_027098//NM_006495612	<i>Gm6238//Mrpl30</i>	predicted pseudogene 6238//mitochondrial ribosomal protein L30	

Table S6

Gene_ID	p (Corr)	FC-RSV 1 d	FC-RSV 5 d	RefSeq Transcript ID	Gene Symbol	Gene Title	Gene Ontology Biological Process
1421550_a_at,14	0.002008	2.00	1.82	NM_009137	<i>Ccl22</i>	chemokine (C-C motif) ligand 22	0006935 // chemotaxis // inferred from electronic annotation//0006954 // inflammatory response // inferred from electronic
1421550_a_at,14	0.005709	2.00	1.42	NM_001159602//NM_025376	<i>Tmem8c</i>	transmembrane protein 8C	0007517 // muscle organ development // inferred from electronic annotation//0007520 // myoblast fusion // inferred from direct
1421551_s_at,14	0.000285	2.00	1.07	XM_902421//XM_976780	<i>B230307C23rik</i>	RIKEN cDNA B230307C23 gene	0006355 // regulation of transcription, DNA-templated // inferred from electronic annotation
1421555_at,145	0.007761	2.00	1.05	NM_175118	<i>Dusp28</i>	dual specificity phosphatase 28	0006470 // protein dephosphorylation // not recorded//0007254 // INK cascade // not recorded//0016311 // dephosphorylation //
1421564_at,166	0.008945	1.99	1.16	NM_008773//XM_006507432	<i>P2ry2</i>	purinergic receptor P2Y, G-protein coupled 2	0007165 // signal transduction // inferred from electronic annotation//0007186 // G-protein coupled receptor signaling pathway // not
1421571_s_at,11	0.000099	1.98	1.14	NM_011882//NM_006529525	<i>Rnosel</i>	ribonuclease L (2', 5'-oligoadenylate synthetase-dependent)	0006364 // rRNA processing // not recorded//0006397 // mRNA processing // inferred from electronic annotation//0006468 // protein
1421571_a_at,11	0.000099	1.98	1.23	NM_019680//XM_006541526	<i>Ej4</i>	E74-like factor 4 (ets domain transcription factor)	0001787 // natural killer cell proliferation // inferred from direct assay//0001866 // NK T cell proliferation // inferred from direct
1421574_at,142	0.001624	1.98	1.26	NM_028876//XM_006535238	<i>Tmed5</i>	transmembrane emp24 protein transport domain containing 5	0006810 // transport // inferred from electronic annotation//0015031 // protein transport // inferred from electronic
1421578_at,203	0.002933	1.98	1.07	NM_025329//XM_006522448	<i>Tctex1d2</i>	Tctex1 domain containing 2	
1421582_s_at,14	0.001248	1.97	1.37	NM_001160415//NM_030255	<i>Apobec3</i>	apolipoprotein B mRNA editing enzyme, catalytic polypeptide 3	0002244 // hematopoietic progenitor cell differentiation // inferred from genetic interaction//0002376 // immune system process //
1421596_s_at,14	0.000279	1.97	1.03	NM_175175	<i>Plekfh2</i>	pleckstrin homology domain containing, family F (with FYVE domain) member	0006810 // transport // inferred from electronic annotation//0015031 // protein transport // inferred from electronic annotation
1421598_at	0.003823	1.97	-1.36	NM_013642	<i>Dusp1</i>	dual specificity phosphatase 1	0000188 // inactivation of MAPK activity // --//0000188 // inactivation of MAPK activity // inferred from sequence or structural
1421603_a_at,14	0.002436	1.96	1.17	NM_011965	<i>Pma1</i>	proteasome (prosome, macropain) subunit, alpha type 1	0002376 // immune system process // inferred from electronic annotation//0002862 // negative regulation of inflammatory response to
1421609_a_at,14	0.003455	1.96	1.57	NM_001144855//XM_006529	<i>Ppfia4</i>	protein tyrosine phosphatase, receptor type, f polypeptide (PTPRF)	
1421640_a_at,14	0.007596	1.95	1.26	NM_012030//XM_006533443	<i>Slc9a3r1</i>	solute carrier family 9 (sodium/hydrogen exchanger), member 3 regulator 1	0003096 // renal sodium ion transport // inferred from mutant phenotype//0007191 // adenylate cyclase-activating dopamine receptor
1421644_at,145	0.000533	1.95	1.24	NM_007611//XM_006526616	<i>Casp7</i>	disabled 7	0001836 // release of cytochrome c from mitochondria // inferred from genetic interaction//0006508 // proteolysis // inferred from
1421679_s_at,14	0.000181	1.95	1.12	NM_001008702//NM_001037	<i>Dab2</i>	disabled 2, mitogen-responsive phosphoprotein	0009094 // cell morphogenesis involved in differentiation // inferred from mutant phenotype//0001701 // in utero embryonic
1421685_at,142	0.004728	1.95	-1.66	NM_027519//XM_006504940	<i>Medag</i>	mesenteric estrogen dependent adipogenesis	0045600 // positive regulation of fat cell differentiation // inferred from mutant phenotype
1421694_a_at,14	0.000160	1.94	1.31	NM_026114	<i>Ejfs1</i>	eukaryotic translation initiation factor 2, subunit 1 alpha	0006412 // translation // inferred from direct assay//0006412 // translation // not recorded//0006413 // translational initiation // not
1421709_s_at,14	0.004318	1.94	1.24	NM_010493	<i>Icam1</i>	intercellular adhesion molecule 1	0001541 // ovarian follicle development // inferred from electronic annotation//0001666 // response to hypoxia // inferred from
1421734_at,127	0.005199	1.94	1.15	NM_001113562//NM_025530	<i>Cutc</i>	cutc copper transporter homology (E.coli)	0051262 // cutc tetramerization // not recorded//0055070 // copper ion homeostasis // inferred from electronic annotation
1421772_a_at,14	0.002974	1.94	1.50	NM_001177980//NM_001177	<i>Pde4b</i>	phosphodiesterase 4B, cAMP specific	0001780 // neutrophil homeostasis // inferred from mutant phenotype//0006198 // cAMP catabolic process // inferred from direct
1421783_a_at,14	0.001757	1.93	1.27	NM_001198835//NM_007728	<i>Coch</i>	coagulation factor C homolog (Limulus polyphemus)	0007605 // sensory perception of sound // inferred from mutant phenotype//0008360 // regulation of cell shape // not
1421793_at,143	0.003103	1.93	1.01	NM_009348//XM_006526902	<i>Tectb</i>	tectorin beta	0007605 // sensory perception of sound // traceable author statement
1421802_at,142	0.004646	1.93	1.07	NM_030017//XM_006516372	<i>Rdh12</i>	retinol dehydrogenase 12	0007601 // visual perception // inferred from electronic annotation//0008152 // metabolic process // inferred from electronic
1421812_at,145	0.001360	1.93	1.40	NM_026115	<i>Hat1</i>	histone aminotransferase 1	0006335 // DNA replication-dependent nucleosome assembly // not recorded//0006336 // DNA replication-independent nucleosome
1421824_at,142	0.006113	1.93	1.74	NM_011706//XM_006533165	<i>Trp2</i>	transient receptor potential cation channel, subfamily V, member 2	0006810 // transport // inferred from electronic annotation//0006811 // ion transport // inferred from electronic annotation//0006812
1421839_at,142	0.006477	1.93	1.30	NM_028275//XM_006519676	<i>1700112E06rik</i>	RIKEN cDNA 1700112E06 gene	0030154 // cell differentiation // inferred from electronic annotation//0030318 // melanocyte differentiation // not recorded
1421843_at,142	0.001757	1.92	1.07	NM_030201//NR_027492//X	<i>Hspa13</i>	heat shock protein 70 family, member 13	0000902 // cell morphogenesis // inferred from electronic annotation
1421850_at,142	0.005680	1.92	1.05	NM_178892	<i>Tiparp</i>	TCDD-inducible poly(ADP-ribose) polymerase	0001570 // vasculogenesis // inferred from mutant phenotype//0001822 // kidney development // inferred from mutant
1421876_at,142	0.003158	1.92	1.06	NM_001098271//NM_025326	<i>Tmem176a</i>	transmembrane protein 176A	2001199 // negative regulation of dendritic cell differentiation // inferred from mutant phenotype
1421911_s_at,145	0.000920	1.92	1.15	NM_028064//XM_006521427	<i>Slc39a4</i>	solute carrier family 39 (zinc transporter), member 4	0006810 // transport // inferred from electronic annotation//0006811 // ion transport // inferred from electronic annotation//0006829
1421921_at,207	0.000240	1.91	-1.19	NM_144810//XM_006529354	<i>Klhdc8a</i>	kelch domain containing 8A	
1421930_at,142	0.007007	1.91	-1.12	NM_028053//XM_006538083	<i>Transm38b</i>	transmembrane protein 38B	
1421933_at,142	0.004887	1.91	1.73	NM_011693	<i>Vcam1</i>	vascular cell adhesion molecule 1	0006810 // transport // inferred from electronic annotation//0006811 // ion transport // inferred from electronic annotation//0006813
1421936_at,142	0.004868	1.91	1.23	NM_030250	<i>Nus1</i>	nuclear undecaprenyl pyrophosphate synthase 1 homolog (S. cerevisiae)	0001666 // response to hypoxia // inferred from electronic annotation//0002526 // acute inflammatory response // inferred from
1421947_at,145	0.001225	1.91	1.18	NM_021398//XM_006499957	<i>Slc43a3</i>	solute carrier family 43, member 3	0001525 // angiogenesis // inferred from electronic annotation//0006486 // protein glycosylation // inferred from electronic
1421958_at,145	0.009788	1.90	1.33	NM_001284409//NM_009810	<i>Casp3</i>	caspase 3	0055085 // transmembrane transport // inferred from electronic annotation
1421964_at,142	0.006994	1.90	-1.03	NM_001252503//NM_001290	<i>Aftph</i>	afthiphin	0001782 // B cell homeostasis // inferred from mutant phenotype//0001836 // release of cytochrome c from mitochondria // inferred
1421968_a_at,14	0.005714	1.89	-1.02	NM_021362//XM_006537672	<i>Pappa</i>	pregnancy-associated plasma protein A	0006810 // transport // inferred from electronic annotation//0015031 // protein transport // inferred from electronic annotation
1421974_at,145	0.008007	1.89	2.36	NM_207105	<i>H2-Ab1</i>	histocompatibility 2, class II antigen A, beta 1	0006508 // proteolysis // inferred from direct assay//0006508 // proteolysis // not recorded//0030154 // cell differentiation // inferred
1421979_at,145	0.003064	1.89	2.21	NM_008196	<i>Gzmk</i>	granzyme K	0002344 // B cell affinity maturation // inferred from direct assay//0002376 // immune system process // inferred from electronic
1421985_a_at,14	0.002288	1.89	1.71	NM_001162500//NM_022321	<i>Parvg</i>	parvins, gamma	0006508 // proteolysis // not recorded
1421998_at,145	0.000099	1.89	1.18	NM_025356//XM_006501873	<i>Ube2d3</i>	ubiquitin-conjugating enzyme E2D 3	0007155 // cell adhesion // inferred from electronic annotation//0031532 // actin cytoskeleton reorganization // inferred from
1422000_at,145	0.006214	1.89	-1.12	NM_001033988//NM_001284	<i>Ncoa4</i>	nuclear receptor coactivator 4	0000209 // protein polyubiquitination // not recorded//0006281 // DNA repair // inferred from electronic annotation//0006511 //
1422002_at,143	0.004189	1.88	1.31	NM_001256130//NM_001256	<i>Nipo2</i>	not imprinted in Prader-Willi/Angelman syndrome 2 homolog (human)	0006810 // transport // inferred from electronic annotation//0006811 // ion transport // inferred from electronic annotation//0015693
1422005_at,142	0.000705	1.88	1.47	NM_009448//NR_033599	<i>Gm6882//Tuboc1</i>	tubulin, alpha 1C pseudogene//tubulin, alpha 1C	0006184 // GTP catabolic process // inferred from electronic annotation//0007017 // microtubule-based process // inferred from
1422013_at,142	0.003927	1.88	-1.03	NM_025821//XM_006522346	<i>Carhs1</i>	calcium regulated heat stable protein 1	0006355 // regulation of transcription, DNA-templated // inferred from electronic annotation//0043488 // regulation of mRNA stability
1422014_at,143	0.009319	1.87	1.26	NM_008334//NM_008336//	<i>Ifna12//Ifna15//Ifna16</i>	interferon alpha 12//interferon alpha 12//interferon alpha 15//interferon	0002250 // adaptive immune response // not recorded//0002286 // T cell activation involved in immune response // inferred from
1422020_at,142	0.001248	1.87	1.15	NM_026106	<i>Dr1</i>	down-regulator of transcription 1	0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 // regulation of transcription, DNA-templated
1422029_at,202	0.000240	1.87	1.48	NM_009068//XM_006516607	<i>Ripk1</i>	receptor (TNFRSF)-interacting serine-threonine kinase 1	0001934 // positive regulation of protein phosphorylation // not recorded//0006468 // protein phosphorylation // inferred from
1422038_a_at,14	0.004608	1.87	-1.03	NM_001253814//NM_027922	<i>Ankle2</i>	ankyrin repeat and LEM domain containing 2	0007049 // cell cycle // inferred from electronic annotation//0007067 // mitotic nuclear division // inferred from electronic
1422040_at,145	0.000277	1.87	1.08	NM_172625	<i>Ino80c</i>	INO80 complex subunit C	0006281 // DNA repair // inferred from electronic annotation//0006310 // DNA recombination // inferred from electronic
1422041_at,170	0.003814	1.87	1.10	NM_146068//XM_006522020	<i>Spidr</i>	scaffolding protein involved in DNA repair	000724 // double-strand break repair via homologous recombination // not recorded//0006281 // DNA repair // inferred from
1422044_at,142	0.000992	1.87	1.13	NM_007413	<i>Adora2b</i>	adenosine A2b receptor	0001973 // adenosine receptor signaling pathway // not recorded//0002882 // positive regulation of chronic inflammatory response to
1422046_at,164	0.003138	1.86	1.35	NM_008530//XM_006520522	<i>Ly6f</i>	lymphocyte antigen 6 complex, locus F	
1422053_at,145	0.002289	1.86	-1.07	NM_026194//XM_006538203	<i>Uf1</i>	UFM1 specific ligase 1	0001649 // osteoblast differentiation // not recorded//0031397 // negative regulation of protein ubiquitination // not
1422062_at,142	0.001332	1.86	2.10	NM_009910	<i>Cxcr3</i>	chemokine (C-X-C motif) receptor 3	0001525 // angiogenesis // inferred from electronic annotation//0001937 // negative regulation of endothelial cell proliferation // not
1422095_s_at,14	0.000226	1.85	1.04	NM_175318	<i>Spy2d1</i>	SP2, Suppressor of Ty, domain containing 1 (S. cerevisiae)	
1422123_s_at,14	0.001763	1.85	1.26	NM_023126//XM_006509565	<i>Rab8a</i>	RAB8A, member RAS oncogene family	0006184 // GTP catabolic process // not recorded//0006810 // transport // inferred from electronic annotation//0006886 //
1422126_s_at,14	0.009263	1.85	-1.14	NM_177861//NR_110955//X	<i>Tmem67</i>	transmembrane protein 67	0010826 // negative regulation of centrosome duplication // inferred from mutant phenotype//0010826 // negative regulation of
1422132_at,143	0.006369	1.84	1.17	NM_029391//XM_006539673	<i>Rab4b</i>	RAB4B, member RAS oncogene family	0006184 // GTP catabolic process // inferred from electronic annotation//0006810 // transport // inferred from electronic
1422140_at,142	0.003800	1.84	1.29	NM_146097//NR_033744	<i>Cbw1</i>	COBW domain containing 1	
1422140_at,142	0.005288	1.84	1.32	NM_001163747//NM_028427	<i>Tmem192</i>	transmembrane protein 192	
1422140_at,142	0.003800	1.84	1.13	NM_009634//XM_006520320	<i>Adsl</i>	adenylosuccinate lyase	0001666 // response to hypoxia // inferred from electronic annotation//0006163 // purine nucleotide metabolic process // not
1422140_at,142	0.003800	1.84	1.15	NM_008384//XM_006495735	<i>Inpp1</i>	inositol polyphosphate-1-phosphatase	0016311 // dephosphorylation // inferred from electronic annotation//0046854 // phosphatidylinositol phosphorylation // inferred from
1422140_at,142	0.003800	1.84	1.25	NM_010242	<i>Fut4</i>	fucosyltransferase 4	0006486 // protein glycosylation // inferred from electronic annotation//0036065 // fucosylation // not recorded
1422141_s_at,14	0.004145	1.83	1.57	NM_001037840//NM_001037	<i>Clkf</i>	chemokine-like factor	0006935 // chemotaxis // inferred from electronic annotation//0008283 // cell proliferation // not recorded//0030593 // neutrophil
1422151_s_at,145	0.006580	1.83	1.28	NM_025485	<i>Mrps22</i>	mitochondrial ribosomal protein S22	
1422158_at,144	0.007312	1.83	-1.13	NM_031252	<i>Il23a</i>	interleukin 23, alpha subunit p19	0001916 // positive regulation of T cell mediated cytotoxicity // inferred from direct assay//0002230 // positive regulation of defense
1422160_at,150	0.001575	1.83	-1.03	NM_001205052//NM_001205	<i>Jdp2</i>	Jun dimerization protein 2	0000122 // negative regulation of transcription from RNA polymerase II promoter // inferred from direct assay//0000122 // negative
1422161_at,142	0.006289	1.83	1.20	NM_178798//XM_006531135	<i>Slc7a6</i>	solute carrier family 7 (cationic amino acid transporter, y+ system), member 6	0003333 // amino acid transmembrane transport // inferred from electronic annotation//0006810 // transport // inferred from
1422163_at,142	0.003953	1.83	1.09	NM_001177669//NM_001177	<i>Golphi3</i>	golgi phosphoprotein 3-like	0007030 // Golgi organization // not recorded//0050714 // positive regulation of protein secretion // not recorded
1422170_at,143	0.000791	1.83	1.37	NM_009776//XM_006498623	<i>Serpin1</i>	serine (or cysteine) peptidase inhibitor, clade G, member 1	0001869 // negative regulation of complement activation, lectin pathway // not recorded//0002376 // immune system process //
1422184_a_at,14	0.003763	1.82	1.10	NM_001177556//NM_001177	<i>Gnq12</i>	guanine nucleotide binding protein (G protein), gamma 12	0007165 // signal transduction // inferred from electronic annotation//0007186 // G-protein coupled receptor signaling pathway //
1422190_at,143	0.006185	1.82	1.16	NM_001142357//NM_145477	<i>Alg12</i>	asparagine-linked glycosylation 12 (alpha-1,6-mannosyltransferase)	0006486 // protein glycosylation // inferred from electronic annotation//0006487 // protein N-linked glycosylation // not
1422191_at,143	0.006582	1.82	-1.22	NM_008398//XM_006513267	<i>Igta</i>	integrin alpha 7	0007155 // cell adhesion // inferred from mutant phenotype//0007155 // cell adhesion // not recorded//0007229 // integrin-mediated
1422227_at,143	0.007888	1.82	1.44	NM_001282095//NM_001282	<i>Tjp3</i>	tight junction protein 3	2000045 // regulation of G1/S transition of mitotic cell cycle // inferred from genetic interaction

Table S6

Gene_ID	p (Corr)	FC-RSV 1 d	FC-RSV 5 d	RefSeq Transcript ID	Gene Symbol	Gene Title	Gene Ontology Biological Process
1422230_s_at[1]	0.000176	1.81	1.29	NM_008334//NM_008336//	<i>Ifna1</i>	interferon alpha 1//interferon alpha 12//interferon alpha 15//interferon	0002258 // adaptive immune response // not recorded//0002286 // T cell activation involved in immune response // inferred from
1422230_s_at[1]	0.000176	1.81	1.25	NM_001289476//NM_011969	<i>Psmo7</i>	proteasome (prosome, macropain) subunit, alpha type 7	0006508 // proteolysis // inferred from electronic annotation//0006511 // ubiquitin-dependent protein catabolic process // inferred
1422245_a_at_14	0.008806	1.81	1.11	NM_001164406//NM_025291	<i>Sra1</i>	steroid receptor RNA activator 1	0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 // regulation of transcription, DNA-templated
1422259_a_at_14	0.001127	1.80	1.16	NM_001013616//XM_006508	<i>Trim6</i>	tripartite motif-containing 6	0070206 // protein trimerization // not recorded
1422270_s_at_14	0.005118	1.80	1.42	NM_001159640//NM_011593	<i>Tasp1</i>	taspace, threonine aspartase 1	0006508 // proteolysis // not recorded//0008152 // metabolic process // inferred from electronic annotation//0045893 // positive
1422280_at[149]	0.002005	1.80	1.07	NM_001285423//NM_016903	<i>Esd1</i>	esterase D/formylglutathione hydrolase//predicted pseudogene 2904	0006508 // proteolysis // inferred from electronic annotation//0046294 // formaldehyde catabolic process // inferred from electronic
1422286_a_at[2]	0.004764	1.80	1.07	NM_001285423//NM_016903	<i>Esd1</i>	esterase D/formylglutathione hydrolase//predicted pseudogene 2904	0006508 // proteolysis // inferred from electronic annotation//0046294 // formaldehyde catabolic process // inferred from electronic
1422295_s_at[142]	0.002562	1.80	1.26	NM_013586	<i>Lox1</i>	lysyl oxidase-like 3	001837 // epithelial to mesenchymal transition // not recorded//0006898 // receptor-mediated endocytosis // inferred from electronic
1422305_at[159]	0.003588	1.79	-1.03	NM_001127324//NM_007948	<i>Erc1</i>	excision repair cross-complementing rodent repair deficiency,	0007720 // pyrimidine dimer repair by nucleotide-excision repair // inferred from mutant phenotype//0000737 // DNA catabolic
1422309_s_at_14	0.000541	1.79	-1.41	NM_001162913//NM_027890	<i>Susd2</i>	sushi domain containing 2	0006898 // receptor-mediated endocytosis // inferred from electronic annotation//0006955 // immune response // inferred from
1422327_s_at_14	0.008904	1.79	-1.16	NM_011671//XM_006507579	<i>Ucp2</i>	uncoupling protein 2 (mitochondrial, proton carrier)	0000303 // response to superoxide // not recorded//0001666 // response to hypoxia // inferred from electronic annotation//0006810
1422348_at[142]	0.001823	1.79	-1.05	NM_134133//XM_006525481	<i>Smim3</i>	small integral membrane protein 3	
1422348_at[142]	0.005714	1.79	2.00	NM_009780//NM_011413//X	<i>C4a</i>	complement component 4A (Rodgers blood group)//complement	0002376 // immune system process // inferred from electronic annotation//0006954 // inflammatory response // inferred from
1422397_a_at_14	0.004489	1.79	2.00	NM_009780//NM_011413//X	<i>C4a</i>	complement component 4A (Rodgers blood group)//complement	0002376 // immune system process // inferred from electronic annotation//0006954 // inflammatory response // inferred from
1422403_at[142]	0.005866	1.79	1.01	NM_029512//NM_181734//X	<i>Ttpal</i>	tocopherol (alpha) transfer protein-like	0006810 // transport // inferred from electronic annotation
1422403_at[142]	0.006586	1.79	-1.08	NM_001114611//NM_001114	<i>Stxbp5l</i>	syntaxin binding protein 5-like	0006810 // transport // inferred from electronic annotation//0006887 // exocytosis // inferred from electronic annotation//0015031 //
1422403_at[142]	0.006586	1.78	1.65	NM_001252654//NM_001252	<i>Kcnab2</i>	potassium voltage-gated channel, shaker-related subfamily, beta member 2	0002244 // hematopoietic progenitor cell differentiation // inferred from genetic interaction//0006810 // transport // inferred from
1422403_at[142]	0.005830	1.78	1.11	NM_027135//XM_006502038	<i>Sec24d</i>	Sec24 related gene family, member D (S. cerevisiae)	0001701 // in utero embryonic development // inferred from mutant phenotype//0006810 // transport // inferred from electronic
1422403_at[142]	0.006586	1.78	1.20	NM_001164640//NM_029419	<i>Apol7a</i>	apolipoprotein L 7a//apolipoprotein L 7c//apolipoprotein L 7c pseudogene	0006869 // lipid transport // inferred from electronic annotation//0007165 // signal transduction // not recorded//0042157 //
1422403_at[142]	0.006586	1.78	1.53	NM_001130479//NM_016773	<i>Nucb2</i>	nucleobindin 2	0006874 // cellular calcium ion homeostasis // traceable author statement
1422403_at[142]	0.006586	1.77	1.13	NM_021449//NM_175357	<i>Crbn</i>	cerebellin	0006200 // ATP catabolic process // inferred from electronic annotation//0006508 // proteolysis // inferred from electronic
1422403_at[142]	0.006586	1.77	1.44	NM_009448//NR_033599//N	<i>Gm6682</i>	tubulin, alpha 1C pseudogene//tubulin, alpha 1C//tubulin, alpha 1A	0006184 // GTP catabolic process // inferred from electronic annotation//0007017 // microtubule-based process // inferred from
1422420_at[145]	0.003519	1.77	1.26	NM_001163746//NM_028352	<i>Pgm3</i>	phosphoglucosyltransferase 3	0005975 // carbohydrate metabolic process // inferred from electronic annotation//0006048 // UDP-N-acetylglucosamine biosynthetic
1422430_at[146]	0.003302	1.77	1.14	NM_001008700//NM_010557	<i>Il4ra</i>	interleukin 4 receptor, alpha	0002376 // immune system process // inferred from electronic annotation//0002532 // production of molecular mediator involved in
1422448_at[217]	0.002620	1.77	1.03	NM_010119	<i>Ehd1</i>	EH-domain containing 1	0006184 // GTP catabolic process // inferred from electronic annotation//0006886 // intracellular protein transport // not
1422460_at[561]	0.003539	1.77	1.30	NM_026454//XM_006529836	<i>Ube2f</i>	ubiquitin-conjugating enzyme E2F (putative)	0045116 // protein neddylation // inferred from mutant phenotype//0045116 // protein neddylation // not recorded
1422465_s_at_14	0.004235	1.76	1.21	NM_017401//XM_006514758	<i>Palm</i>	polymerase (DNA directed), mu	0006261 // DNA-dependent DNA replication // inferred from electronic annotation//0006281 // DNA repair // inferred from electronic
1422473_at[142]	0.001231	1.76	1.24	NM_025683//XM_006496187	<i>Rpe</i>	ribulose-5-phosphate-3-epimerase	0005975 // carbohydrate metabolic process // not recorded//0006098 // pentose-phosphate shunt // not recorded//0008152 //
1422488_at[564]	0.009250	1.76	1.17	NM_008707//XM_006532445	<i>Nmt1</i>	N-myristoyltransferase 1	0001701 // in utero embryonic development // inferred from mutant phenotype//0006499 // N-terminal protein myristoylation //
1422499_at[142]	0.003563	1.76	1.13	NM_022411//XM_006532645	<i>Slc32a2</i>	solute carrier family 13 (sodium-dependent dicarboxylate transporter),	0006810 // transport // inferred from electronic annotation//0006811 // ion transport // inferred from electronic annotation//0006814
1422506_s_at_14	0.003850	1.76	1.12	NM_030685	<i>Serp1</i>	stress-associated endoplasmic reticulum protein 1	0001501 // skeletal system development // inferred from mutant phenotype//0006006 // glucose metabolic process // inferred from
1422510_at[692]	0.005920	1.75	1.31	NM_001122595//NM_001122	<i>A630033H20Rik</i>	RIKEN cDNA A630033H20 gene	0007186 // G-protein coupled receptor signaling pathway // inferred from electronic annotation//0035589 // G-protein coupled
1422511_s_at_14	0.001995	1.75	-1.21	NM_001033954//NM_001289	<i>Calca</i>	calcitonin/calcitonin-related polypeptide, alpha	0001976 // neurological system process involved in regulation of systemic arterial blood pressure // not recorded//0001984 //
1422526_at[142]	0.005483	1.75	1.23	NM_001286002//NM_001286	<i>Scyl3</i>	SCY1-like 3 (S. cerevisiae)	0006468 // protein phosphorylation // inferred from electronic annotation
1422527_at[145]	0.002558	1.75	-1.13	NM_001136607//NM_001161	<i>Ikbkg</i>	inhibitor of kappaB kinase gamma	0001782 // B cell homeostasis // inferred from mutant phenotype//0006351 // transcription, DNA-templated // inferred from electronic
1422529_s_at[1]	0.009361	1.75	1.54	NM_026453	<i>Mak16</i>	MAK16 homolog (S. cerevisiae)	
1422533_at[142]	0.000285	1.75	1.96	NM_001033250//XM_006529	<i>Lem1</i>	LEM domain containing 1//uncharacterized LOC100505034	
1422544_at[145]	0.007108	1.74	1.12	NM_144554//NM_175093	<i>Tri3b</i>	tribbles homolog 3 (Drosophila)	0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 // regulation of transcription, DNA-templated
1422557_s_at_14	0.001314	1.74	1.36	NM_009808//XM_006509840	<i>Casp12</i>	caspase 12	0006508 // proteolysis // not recorded//0006508 // proteolysis // inferred from reviewed computational analysis//0006915 //
1422565_s_at_14	0.002274	1.74	-1.00	NM_025310	<i>Ftsj3</i>	Ftsj3 homolog 3 (E. coli)	0000453 // enzyme-directed rRNA 2'-O-methylation // inferred from electronic annotation//0001510 // RNA methylation // inferred
1422573_at[117]	0.000103	1.74	1.14	NM_001163590//NM_001163	<i>Stx11</i>	syntaxin 11	0001913 // T cell mediated cytotoxicity // inferred from mutant phenotype//0006810 // transport // inferred from electronic
1422577_at[142]	0.002386	1.74	1.26	NM_001033242	<i>Cln5</i>	ceroid-lipofuscinosis, neuronal 5	0006465 // signal peptide processing // not recorded//0007040 // lysosome organization // inferred from mutant phenotype//0007042
1422597_at[143]	0.001698	1.74	1.12	NM_011512//XM_006497828	<i>Surf4</i>	surfeit gene 4	0007030 // Golgi organization // not recorded//0010638 // positive regulation of organelle organization // not recorded
1422601_at[143]	0.001366	1.74	-1.11	NM_194333//XM_006496479	<i>Slc23a3</i>	solute carrier family 23 (nucleobase transporters), member 3	0006810 // transport // inferred from electronic annotation//0005508 // transmembrane transport // inferred from electronic
1422605_at[582]	0.004751	1.73	1.80	NM_001139516//NM_011429	<i>Rbl1</i>	retinoblastoma-like 1 (p107)	0000122 // negative regulation of transcription from RNA polymerase II promoter // inferred from mutant phenotype//0006351 //
1422606_at[817]	0.008839	1.73	-1.16	NM_008866//XM_006495471	<i>Lypla1</i>	lysophospholipase 1	0002084 // protein depalmitoylation // inferred from mutant phenotype//0006629 // lipid metabolic process // inferred from electronic
1422607_at[145]	0.008184	1.73	3.34	NM_026410	<i>Dcdc5</i>	cell division cycle associated 5	0000082 // G1/S transition of mitotic cell cycle // not recorded//0006302 // double-strand break repair // not recorded//0007049 //
1422607_at[145]	0.008184	1.73	1.31	NM_009740	<i>Bcl10</i>	B cell leukemia/lymphoma 10	0001783 // B cell apoptotic process // inferred from direct assay//0001783 // B cell apoptotic process // inferred from mutant
1422630_at[142]	0.003130	1.73	1.18	NM_001168516//NM_001168	<i>Zdhc24</i>	zinc finger, DHHC domain containing 24	0008152 // metabolic process // inferred from electronic annotation
1422631_at[145]	0.003322	1.73	1.16	NM_025478	<i>Iso1</i>	isochorismatase domain containing 1	0008152 // metabolic process // inferred from electronic annotation
1422642_at[145]	0.002265	1.72	1.17	NM_001002842//NR_028279	<i>Pram1</i>	PML-RAR alpha-regulated adaptor molecule 1	0007229 // integrin-mediated signaling pathway // inferred from mutant phenotype//0043313 // regulation of neutrophil degranulation
1422644_at[143]	0.001786	1.72	1.11	NM_172442//XM_006526816	<i>Dtx4</i>	deltex 4 homolog (Drosophila)	0007219 // Notch signaling pathway // inferred from electronic annotation//0016567 // protein ubiquitination // inferred from
1422648_at[142]	0.001755	1.72	1.50	NM_153570	<i>Noc4l</i>	nucleolar complex associated 4 homolog (S. cerevisiae)	0042254 // ribosome biogenesis // inferred from electronic annotation
1422651_at[114]	0.001511	1.72	1.07	NM_001161413//NM_008577	<i>Slc32a2</i>	solute carrier family 3 (activators of dibasic and neutral amino acid transport),	0003333 // amino acid transmembrane transport // not recorded//0005975 // carbohydrate metabolic process // inferred from
1422661_at[142]	0.008499	1.72	-1.47	NM_0011330	<i>Ct11</i>	chemokine (C-C motif) ligand 11	0001938 // positive regulation of endothelial cell proliferation // not recorded//0002544 // chronic inflammatory response // inferred
1422668_at[207]	0.000634	1.72	-1.50	NM_016913//NM_023638//	<i>Porcn</i>	porcupine homolog (Drosophila)	0009100 // glycoprotein metabolic process // inferred from direct assay//0016055 // Wnt signaling pathway // inferred from electronic
1422719_s_at_14	0.004716	1.72	1.02	NM_026738//XM_006516955	<i>1110007C09Rik</i>	RIKEN cDNA 1110007C09 gene	0042981 // regulation of apoptotic process // inferred from electronic annotation
1422730_at[142]	0.008333	1.72	1.16	NM_025546	<i>Rsl1d1</i>	ribosomal L1 domain containing 1	0001649 // osteoblast differentiation // not recorded//0006412 // translation // inferred from electronic annotation//0032880 //
1422738_at[145]	0.000645	1.71	-1.03	NM_028584//NM_212447	<i>Marveld3</i>	MARVEL (membrane-associated) domain containing 3	0045216 // cell-cell junction organization // inferred from mutant phenotype//0045216 // cell-cell junction organization // not
1422764_at[142]	0.005524	1.71	1.57	NM_178856	<i>Gins2</i>	GINS complex subunit 2 (Psf2 homolog)	0006260 // DNA replication // inferred from electronic annotation
1422781_at[142]	0.002984	1.71	1.27	NM_008915//XM_006518713	<i>Ppp3cc</i>	protein phosphatase 3, catalytic subunit, gamma isoform	0008152 // metabolic process // inferred from electronic annotation//0016311 // dephosphorylation // inferred from electronic
1422788_at[582]	0.005109	1.71	1.09	NM_010269//NR_104341//X	<i>Gdap2</i>	ganglioside-induced differentiation-associated-protein 2	0032526 // response to retinoic acid // inferred from direct assay
1422812_at[142]	0.008806	1.71	-1.09	NM_001164768//NM_001164	<i>Fbxw2</i>	F-box and WD-40 domain protein 2	
1422814_at[145]	0.005551	1.71	1.02	NM_001048207//NM_027863	<i>Gypc</i>	glycophorin C	
1422821_s_at_14	0.003619	1.71	1.03	NM_012032//XM_006499616	<i>Serinc3</i>	serine incorporator 3	1902237 // positive regulation of intrinsic apoptotic signaling pathway in response to endoplasmic reticulum stress // inferred from
1422833_at[153]	0.007368	1.71	1.66	NM_183027//XR_373542	<i>Ap1s3</i>	adaptor-related protein complex AP-1, sigma 3	0006810 // transport // inferred from electronic annotation//0006886 // intracellular protein transport // inferred from electronic
1422834_at[142]	0.004713	1.70	1.14	NM_008621	<i>Mpp1</i>	membrane protein, palmitoylated	0090022 // regulation of neutrophil chemotaxis // inferred from mutant phenotype
1422866_at[128]	0.007300	1.70	1.08	NM_001169114//NM_016888	<i>B3gnt2</i>	UDP-GlcNAc:betaGal beta1,3-N-acetylglucosaminyltransferase 2	0006486 // protein glycosylation // inferred from mutant phenotype//0006878 // cellular copper ion homeostasis // --//0007411 //
1422869_at[172]	0.006249	1.70	1.16	NM_175090//XM_006537711	<i>Slc31a1</i>	solute carrier family 31, member 1	0006810 // transport // inferred from electronic annotation//0006811 // ion transport // inferred from electronic annotation//0006825
1422875_at[144]	0.005678	1.69	1.03	NM_0011971	<i>Psmb3</i>	proteasome (prosome, macropain) subunit, beta type 3	0006508 // proteolysis // not recorded//0030163 // protein catabolic process // traceable author statement//0051603 // proteolysis
1422891_at[142]	0.001244	1.69	1.12	NM_001033194	<i>Gtf3c3</i>	general transcription factor IIIC, polypeptide 3	
1422903_at[170]	0.008757	1.69	-1.21	NM_008105//NM_023887//	<i>Gcnt2</i>	glucosaminyl (N-acetyl) transferase 2, l-branching enzyme	0006486 // protein glycosylation // not recorded//0007179 // transforming growth factor beta receptor signaling pathway // inferred from
1422924_at[219]	0.002591	1.69	-1.01	NM_001252593//NM_013742	<i>Cars</i>	cysteineyl-tRNA synthetase	0006412 // translation // inferred from electronic annotation//0006418 // tRNA aminoacylation for protein translation // inferred from
1422953_s_at[142]	0.001511	1.69	1.10	NM_019788	<i>Bloc1s6</i>	biogenesis of lysosomal organelles complex-1, subunit 6, pallidin	0006904 // vesicle docking involved in exocytosis // traceable author statement//0006906 // vesicle fusion // traceable author
1422959_s_at_14	0.001116	1.69	1.66	NM_178595//XR_374104	<i>Pthr1</i>	pituitary-tRNA hydrolase 1 homolog (S. cerevisiae)	0008152 // metabolic process // inferred from electronic annotation
1422962_s_at_14	0.000975	1.68	1.29	NM_024180//XM_006504216	<i>Gm5553</i>	predicted gene 5553//ORF1-like 2 (S. cerevisiae)	0006672 // ceramide metabolic process // not recorded//0006810 // transport // inferred from electronic annotation//0015031 //
1422965_at[146]	0.008551	1.68	1.01	NM_001291859//NM_007484	<i>Rhoc</i>	ras homolog gene family, member C	0009010 // cytokinesis // not recorded//0006184 // GTP catabolic process // inferred from electronic annotation//0007165 // signal
1422973_s_at_14	0.008665	1.67	1.97	NM_009139	<i>Ccl6</i>	chemokine (C-C motif) ligand 6	0006935 // chemotaxis // inferred from electronic annotation//0006955 // immune response // inferred from electronic

Table S6

Gene_ID	p (Corr)	FC-RSV 1 d	FC-RSV 5 d	RefSeq Transcript ID	Gene Symbol	Gene Title	Gene Ontology Biological Process
1422982_at 143	0.005640	1.67	1.29	NM_001039169//NM_001039	<i>Eif4e2</i>	eukaryotic translation initiation factor 4E member 2	0001701 // in utero embryonic development // inferred from mutant phenotype//0006412 // translation // inferred from electronic
1422988_at 143	0.009050	1.67	1.61	NM_172814//NM_006520902	<i>Lrp12</i>	low density lipoprotein-related protein 12	0006897 // endocytosis // inferred from electronic annotation
1422989_a_at 14	0.007719	1.67	1.27	NM_027412//XR_386507	<i>Ttc9c</i>	tetratricopeptide repeat domain 9C	0000413 // protein peptidyl-prolyl isomerization // ---//0018208 // peptidyl-proline modification // not recorded//0061077 //
1422991_at 142	0.009319	1.66	2.35	NM_0011311//NM_006501177	<i>S100a4</i>	S100 calcium binding protein A4	0043123 // positive regulation of I-kappaB kinase/NF-kappaB signaling // not recorded
1422999_at 143	0.004235	1.66	1.18	NM_011426//NM_006499049	<i>Siglec1</i>	sialic acid binding Ig-like lectin 1, sialoadhesin	0006897 // endocytosis // inferred from electronic annotation//0007155 // cell adhesion // inferred from electronic
1423003_at 143	0.001877	1.66	1.36	NM_016723//NM_033607//X	<i>Uchl3//Uchl4</i>	ubiquitin carboxyl-terminal esterase L3 (ubiquitin thiolesterase)//ubiquitin	0006508 // proteolysis // not recorded//0006508 // proteolysis // inferred from electronic annotation//0006511 // ubiquitin-
1423017_a_at 14	0.000885	1.65	1.50	NM_016925//NM_00653016	<i>Fanca</i>	Fanconi anemia, complementation group A	0006281 // DNA repair // inferred from electronic annotation//0006974 // cellular response to DNA damage stimulus // inferred from
1423024_at 269	0.006441	1.65	1.11	NM_008012	<i>Akr1b8</i>	aldo-keto reductase family 1, member B8	0016488 // farnesol catabolic process // not recorded//0044597 // daunosorubicin metabolic process // not recorded//0044598 //
1423024_at 145	0.006441	1.65	1.12	NM_026617	<i>Tmbim4</i>	transmembrane BAX inhibitor motif containing 4	0006915 // apoptotic process // inferred from electronic annotation//0043066 // negative regulation of apoptotic process // not
1423037_at 143	0.001102	1.65	2.31	NM_007894//NM_001012766	<i>Ear1//Ear12//Ear2//Ear3</i>	eosinophil-associated, ribonuclease A family, member 1//eosinophil-	0008152 // metabolic process // inferred from electronic annotation//0090305 // nucleic acid phosphodiester bond hydrolysis //
1423049_a_at 14	0.002138	1.65	1.06	NM_025579//NM_006539106	<i>Taf12</i>	TAF12 RNA polymerase II, TATA box binding protein (TBP)-associated factor	0006351 // transcription, DNA-templated // inferred from electronic annotation//0006352 // DNA-templated transcription, initiation //
1423069_at 115	0.003149	1.65	1.11	NM_011819//NM_006509669	<i>Gdf15</i>	growth differentiation factor 15	
1423070_at 142	0.006249	1.65	1.10	NM_030564//NM_006530512	<i>Rnf34</i>	ring finger protein 34	0006915 // apoptotic process // inferred from electronic annotation//0016567 // protein ubiquitination // not recorded//0043161 //
1423070_at 142	0.006249	1.65	1.52	NM_001163476//NM_027014	<i>Gins1</i>	GIN5 complex subunit 1 (Psf1 homolog)	0001833 // inner cell mass cell proliferation // inferred from mutant phenotype//0006260 // DNA replication // inferred from mutant
1423070_at 142	0.006249	1.64	1.45	NM_181397//NM_006525081	<i>Rftn1</i>	raftlin lipid raft linker 1	0002457 // T cell antigen processing and presentation // inferred from mutant phenotype//0032596 // protein transport into
1423070_at 142	0.006249	1.64	1.30	NM_001145821//NM_010283	<i>Ggta1</i>	glycoprotein galactosyltransferase alpha 1, 3	0005975 // carbohydrate metabolic process // inferred from electronic annotation//0006486 // protein glycosylation // inferred from
1423070_at 142	0.006249	1.64	1.22	NM_153196//NM_006504113	<i>Rbks</i>	ribokinase	0005975 // carbohydrate metabolic process // inferred from electronic annotation//0006014 // D-ribose metabolic process // inferred
1423071_a_at 14	0.004199	1.64	1.16	NM_001081401//NM_177872	<i>Adams3</i>	a disintegrin-like and metallopeptidase (repolyisin type) with	0006508 // proteolysis // inferred from direct assay//0007229 // integrin-mediated signaling pathway // inferred from electronic
1423087_a_at 14	0.005324	1.64	1.14	NM_001290413//NM_009422	<i>Traf2</i>	TNF receptor-associated factor 2	0002726 // positive regulation of T cell cytokine production // not recorded//0006461 // protein complex assembly // not
1423087_a_at 14	0.005324	1.64	1.15	NM_013784//NM_006529675	<i>Pign</i>	phosphatidylinositol glycan anchor biosynthesis, class N	0006506 // GPI anchor biosynthetic process // inferred from electronic annotation//0008152 // metabolic process // inferred from
1423092_at 142	0.003763	1.63	1.28	NM_013531//NM_006535403	<i>Gnb4</i>	guanine nucleotide binding protein (G protein), beta 4	0006184 // GTP catabolic process // not recorded//0007165 // signal transduction // inferred from electronic annotation//0007186 // G-
1423094_at 142	0.002182	1.63	1.04	NM_001290764//NM_001290	<i>Pnkp</i>	polynucleotide kinase 3'-phosphatase	0006281 // DNA repair // not recorded//0006974 // cellular response to DNA damage stimulus // inferred from electronic
1423100_at 142	0.003436	1.63	1.41	NM_001190179//NM_027091	<i>Nup35</i>	nucleoporin 35	0006810 // transport // inferred from electronic annotation//0015031 // protein transport // inferred from electronic
1423104_at 163	0.003311	1.63	1.13	NM_026899	<i>Ssu72</i>	Ssu72 RNA polymerase II CTD phosphatase homolog (yeast)	0006378 // mRNA polyadenylation // not recorded//0006397 // mRNA processing // inferred from electronic annotation//0070940 //
1423105_a_at 6	0.001125	1.63	1.10	NM_029825//NM_006516368	<i>Scfcl1</i>	Sect family domain containing 1	0001666 // response to hypoxia // inferred from electronic annotation//0006810 // transport // inferred from electronic
1423110_at 145	0.003927	1.63	1.04	NM_025706//NM_006513957	<i>Tbc1d15</i>	TBC1 domain family, member 15	0032313 // regulation of Rab GTPase activity // inferred from direct assay//0032851 // positive regulation of Rab GTPase activity //
1423112_at 142	0.000989	1.62	1.23	NM_010766	<i>Marco</i>	macrophage receptor with collagenous structure	0002376 // immune system process // inferred from electronic annotation//0006897 // endocytosis // inferred from mutant
1423119_at 100	0.005978	1.62	1.32	NM_025315	<i>Med21</i>	mediator complex subunit 21	0001824 // blastocyst development // inferred from mutant phenotype//0006351 // transcription, DNA-templated // inferred from
1423123_at 142	0.006524	1.62	1.14	NM_019936	<i>Cript</i>	cysteine-rich PDZ-binding protein	0031122 // cytoplasmic microtubule organization // not recorded//0035372 // protein localization to microtubule // not
1423125_at 142	0.002923	1.62	-1.02	NM_001199122//NM_078478	<i>Ghitm</i>	growth hormone inducible transmembrane protein	0006915 // apoptotic process // inferred from electronic annotation
1423145_a_at 2	0.002561	1.62	-1.08	NM_001163170	<i>Lix1l</i>	Lix1-like	
1423147_at 117	0.005873	1.62	1.09	NM_001077190//NM_001077	<i>Abi1</i>	abl-interactor 1	0001756 // somitogenesis // inferred from mutant phenotype//0006928 // cellular component movement // not recorded//0009987 //
1423152_at 143	0.009998	1.61	1.13	NM_019735//NM_006499926	<i>Apip</i>	APAF1 interacting protein	0006915 // apoptotic process // inferred from electronic annotation//0008652 // cellular amino acid biosynthetic process // inferred
1423156_at 142	0.004283	1.61	1.09	NM_020042//NM_028464//X	<i>Mocs1</i>	molybdenum cofactor synthesis 1	0006777 // Mo-molybdopter cofactor biosynthetic process // inferred from electronic annotation//0032324 // molybdopter cofactor
1423177_a_at 14	0.007498	1.61	1.25	NM_001113374//NM_001113	<i>Mocs2</i>	molybdenum cofactor synthesis 2	0006777 // Mo-molybdopter cofactor biosynthetic process // not recorded
1423199_at 145	0.001877	1.61	1.13	NM_024457	<i>Rap1b</i>	RAS related protein 1b	0006184 // GTP catabolic process // not recorded//0006886 // intracellular protein transport // inferred from electronic
1423200_at 142	0.000313	1.60	1.25	NM_008549//NM_006523739	<i>Man2a1</i>	mannosidase 2, alpha 1	0001701 // in utero embryonic development // inferred from genetic interaction//0001889 // liver development // inferred from
1423204_at 142	0.009722	1.60	1.02	NM_001142950//NM_027350	<i>Nars</i>	asparaginyl-tRNA synthetase	0006412 // translation // inferred from electronic annotation//0006418 // tRNA aminoacylation for protein translation // inferred from
1423215_at 145	0.005181	1.60	1.23	NM_009471//NM_006522008	<i>Umps</i>	uridine monophosphate synthetase	0006207 // 'de novo' pyrimidine nucleobase biosynthetic process // inferred from electronic annotation//0006221 // pyrimidine
1423222_at 145	0.000717	1.60	1.01	NM_181820	<i>Tnnc4</i>	transmembrane channel-like gene family 4	0006810 // transport // inferred from electronic annotation//0006811 // ion transport // inferred from electronic annotation
1423231_at 1640	0.007312	1.59	1.48	NM_144875//NM_006529434	<i>Rob29</i>	RAB29, member RAS oncogene family	0006184 // GTP catabolic process // inferred from electronic annotation//0006810 // transport // inferred from electronic
1423233_at 145	0.000999	1.59	1.42	NM_001033966//NM_016895	<i>Ak2</i>	adenylyate kinase 2	0001889 // liver development // inferred from electronic annotation//0006119 // oxidative phosphorylation // inferred from electronic
1423238_at 265	0.001570	1.59	2.28	NM_008279//NM_006539995	<i>Map4k1</i>	mitogen-activated protein kinase kinase kinase kinase 1	0000165 // MAPK cascade // not recorded//0000185 // activation of MAPKKK activity // not recorded//0006468 // protein
1423243_at 145	0.007637	1.59	1.35	NM_016896	<i>Map3k14</i>	mitogen-activated protein kinase kinase kinase kinase 14	0000165 // MAPK cascade // not recorded//0000186 // activation of MAPKK activity // not recorded//0006468 // protein
1423246_at 142	0.005256	1.59	1.04	NM_001290486//NM_010336	<i>Lpar1</i>	lysophosphatidic acid receptor 1	0000187 // activation of MAPK activity // inferred from direct assay//0007165 // signal transduction // inferred from electronic
1423259_at 142	0.006190	1.59	1.23	NM_181470//NM_006512776	<i>Ltv1</i>	LTV1 homolog (S. cerevisiae)	
1423285_at 128	0.008943	1.58	1.28	NM_024262	<i>Smg8</i>	smg8 homolog, nonsense mediated mRNA decay factor (C. elegans)	0000184 // nuclear-transcribed mRNA catabolic process, nonsense-mediated decay // not recorded//0045859 // regulation of protein
1423306_at 106	0.009151	1.58	1.07	NM_027570//NM_006531183	<i>Ldhd</i>	lactate dehydrogenase D	0006754 // ATP biosynthetic process // non-traceable author statement//0055114 // oxidation-reduction process // non-traceable
1423316_at 144	0.002931	1.58	1.15	NM_001289535//NM_001289	<i>Stx18</i>	syntaxin 18	0006810 // transport // inferred from electronic annotation//0006886 // intracellular protein transport // inferred from electronic
1423323_at 567	0.004844	1.58	-1.14	NM_007539	<i>Bdkrb1</i>	bradykinin receptor, beta 1	0001933 // negative regulation of protein phosphorylation // not recorded//0002687 // positive regulation of leukocyte migration // not
1423358_at 142	0.002787	1.58	-1.03	NM_001271607//NM_007722	<i>Ackr3</i>	atypical chemokine receptor 3	0001525 // angiogenesis // inferred from electronic annotation//0001570 // vasculogenesis // inferred from electronic
1423359_at 145	0.004060	1.57	1.00	NM_001039185//NM_001039	<i>Ceacam1//Ceacam2</i>	carcinoembryonic antigen-related cell adhesion molecule	0007156 // homophilic cell adhesion // inferred from direct assay//0009615 // response to virus // inferred from electronic
1423362_at 142	0.005363	1.57	2.55	NM_017480//NM_006498618	<i>Icos</i>	inducible T cell co-stimulator	0002517 // T cell tolerance induction // not recorded//0016337 // single organismal cell-cell adhesion // not recorded//0031295 // T
1423392_at 142	0.000738	1.57	1.01	NM_053015//NM_006529231	<i>Mrph</i>	melanophilin	0006605 // protein targeting // inferred from mutant phenotype//0006886 // intracellular protein transport // inferred from electronic
1423398_at 1664	0.000380	1.57	1.22	NM_001271416//NM_001271	<i>Ly6a</i>	lymphocyte antigen 6 complex, locus A	
1423403_at 145	0.008539	1.57	1.07	NM_080288//NM_198093//X	<i>Elmo1</i>	engulfment and cell motility 1	0006909 // phagocytosis // inferred from direct assay//0006911 // phagocytosis, engulfment // not recorded//0006911 //
1423407_a_at 1	0.005423	1.57	1.01	NM_001256104//NM_145406	<i>Sic10a3</i>	solute carrier family 10 (sodium/bile acid cotransporter family), member 3	0006810 // transport // inferred from electronic annotation//0006814 // sodium ion transport // inferred from electronic
1423433_at 143	0.002912	1.57	-1.18	NM_007381	<i>Acadl</i>	acyl-Coenzyme A dehydrogenase, long-chain	0001659 // temperature homeostasis // inferred from mutant phenotype//0006629 // lipid metabolic process // inferred from
1423434_at 142	0.001877	1.57	1.04	NM_133847//NM_006500476	<i>Tm9sf4</i>	transmembrane 9 superfamily protein member 4	
1423442_a_at 14	0.005279	1.57	1.27	NM_029582//NM_134105//X	<i>Tnxd11</i>	thioredoxin domain containing 11	0006457 // protein folding // not recorded//0034976 // response to endoplasmic reticulum stress // not recorded//0045454 // cell
1423459_at 143	0.006156	1.57	-1.03	NM_001271730//NM_013842	<i>Xbp1</i>	X-box binding protein 1	0002070 // epithelial cell maturation // inferred from mutant phenotype//0006351 // transcription, DNA-templated // inferred from
1423463_a_at 14	0.002333	1.57	-1.08	NM_001079847//NM_001079	<i>Gpr64</i>	G protein-coupled receptor 64	0007165 // signal transduction // inferred from electronic annotation//0007166 // cell surface receptor signaling pathway // inferred
1423484_at 143	0.003312	1.57	1.47	NM_001006122//NM_001039	<i>Leo1</i>	Leo1, Pafl/RNA polymerase II complex component, homolog (S. cerevisiae)	0001711 // endodermal cell fate commitment // inferred from mutant phenotype//0006351 // transcription, DNA-templated // inferred
1423500_a_at 14	0.004728	1.56	-1.04	NM_008587//NM_006498618	<i>Merkv</i>	c-met proto-oncogene tyrosine kinase	0001779 // natural killer cell differentiation // inferred from genetic interaction//0006468 // protein phosphorylation // not
1423505_at 213	0.005669	1.56	1.57	NM_133898//NM_006504900	<i>N4bp2l1</i>	NEDD4 binding protein 2-like 1	
1423545_a_at 14	0.006808	1.56	1.30	NM_001033978//NM_006524	<i>H2-Eb2</i>	histocompatibility 2, class II antigen E beta2	0002376 // immune system process // inferred from electronic annotation//0002504 // antigen processing and presentation of peptide
1423551_at 143	0.001102	1.56	1.15	NM_008945	<i>Psmb4</i>	proteasome (prosome, macropain) subunit, beta type 4	0002862 // negative regulation of inflammatory response to antigenic stimulus // inferred from mutant phenotype//0006508 //
1423551_at 9	0.000103	1.56	1.23	NM_001025312//NM_133865	<i>Dclre1b</i>	DNA cross-link repair 1B, PS02 homolog (S. cerevisiae)	0000075 // cell cycle checkpoint // not recorded//0000723 // telomere maintenance // not recorded//0006281 // DNA repair //
1423567_a_at 14	0.003539	1.56	1.13	NM_001205286//NM_001205	<i>Tmem39a</i>	transmembrane protein 39a	
1423571_at 136	0.002933	1.56	1.33	NM_001081314//NM_006511	<i>C2cd4b</i>	C2 calcium-dependent domain containing 4B	
1423578_at 128	0.009767	1.56	1.15	NM_009642//NM_006535911	<i>Agrap</i>	angiotensin II, type I receptor-associated protein	0001666 // response to hypoxia // inferred from electronic annotation//0008217 // regulation of blood pressure // inferred from
1423586_at 263	0.004300	1.56	1.17	NM_00113248//NM_009188	<i>Sin3b</i>	transcriptional regulator, SIN3B (yeast)	0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 // regulation of transcription, DNA-templated
1423596_at 142	0.002620	1.56	1.42	NM_001029837//NM_001164	<i>Plk3cd</i>	phosphatidylinositol 3-kinase catalytic delta polypeptide	0001782 // B cell homeostasis // inferred from mutant phenotype//0002376 // immune system process // inferred from electronic
1423619_at 194	0.001466	1.55	1.22	NM_134033	<i>Ccdc117</i>	coiled-coil domain containing 117	
1423628_s_at 14	0.007601	1.55	3.44	NM_010386//NM_006523684	<i>H2-Dma</i>	histocompatibility 2, class II, locus Dma	0002376 // immune system process // inferred from electronic annotation//0002504 // antigen processing and presentation of peptide
1423664_at 143	0.006186	1.55	1.23	NM_027828	<i>Fam110c</i>	family with sequence similarity 110, member C	0030335 // positive regulation of cell migration // not recorded//0051897 // positive regulation of protein kinase B signaling // not
1423665_a_at 14	0.001526	1.55	1.31	NM_030565//NM_006504775	<i>Fam20c</i>	family with sequence similarity 20, member C	0001501 // skeletal system development // inferred from mutant phenotype//0006468 // protein phosphorylation // not
1423665_a_at 14	0.001526	1.55	1.21	NM_023635//NM_006510780	<i>Rab27a</i>	RAB27A, member RAS oncogene family	0006184 // GTP catabolic process // inferred from direct assay//0006605 // protein targeting // inferred from mutant

Table S6

Gene_ID	p (Corr)	FC-RSV 1 d	FC-RSV 5 d	RefSeq Transcript ID	Gene Symbol	Gene Title	Gene Ontology Biological Process
1423669_at 145f	0.001877	1.55	-1.09	NM_018754	<i>Sfn</i>	stratifin	000079 // regulation of cyclin-dependent protein serine/threonine kinase activity // inferred from direct assay//0001836 // release of
1423671_at 145f	0.008611	1.55	1.05	NM_001085383//NM_023628	<i>Anxa9</i>	annexin A9	0007165 // signal transduction // not recorded//0007268 // synaptic transmission // not recorded//0016337 // single organismal cell-
1423672_at 172d	0.008753	1.55	1.02	NM_016881//XM_006522360	<i>Pmm2</i>	phosphomannomutase 2	0008152 // metabolic process // inferred from electronic annotation//0009298 // GDP-mannose biosynthetic process // inferred from
1423676_at 143f	0.003787	1.55	1.12	NM_172697//XM_006502985	<i>Prpf38a</i>	PRP38 pre-mRNA processing factor 38 (yeast) domain containing A	0006397 // mRNA processing // inferred from electronic annotation//0008380 // RNA splicing // inferred from electronic annotation
1423681_at 145f	0.001536	1.55	1.16	NM_001164357//NM_001164	<i>Slc25a25</i>	solute carrier family 25 (mitochondrial carrier, phosphate carrier), member	0002021 // response to dietary excess // inferred from mutant phenotype//0006810 // transport // inferred from electronic
1423707_at 1779	0.000268	1.54	1.24	NM_001003913//NM_001171	<i>Mars</i>	methionine-tRNA synthetase	0006412 // translation // inferred from electronic annotation//0006418 // tRNA aminoacylation for protein translation // inferred from
1423724_at 142f	0.002143	1.54	-1.19	NM_001177464//NM_183033	<i>Zfp516</i>	zinc finger protein 516	0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 // regulation of transcription, DNA-templated
1423726_at 143f	0.003226	1.54	1.27	NM_001290688//NM_020000	<i>Med8</i>	mediator complex subunit 8	0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 // regulation of transcription, DNA-templated
1423727_at 127f	0.001785	1.54	1.70	NM_001290716//NM_011514	<i>Suv39h1</i>	suppressor of variegation 3-9 homolog 1 (Drosophila)	0000183 // chromatin silencing at rDNA // not recorded//0006323 // DNA packaging // traceable author statement//0006342 //
1423747_s_at 14	0.002469	1.54	1.06	NM_026040//XR_386008	<i>Srfbp1</i>	serum response factor binding protein 1	0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 // regulation of transcription, DNA-templated
1423768_at 544	0.007380	1.54	1.02	NM_019425//XM_006519273	<i>Gnpnat1</i>	glucosamine-phosphate N-acetyltransferase 1	0001889 // liver development // inferred from electronic annotation//0006041 // glucosamine metabolic process // not
1423774_s_at 14	0.002923	1.54	1.04	NM_023680//XM_006508662	<i>Tnfrsf22//Tnfrsf23</i>	tumor necrosis factor receptor superfamily, member 22//tumor necrosis	0009502 // RNA phosphodiester bond hydrolysis, endonucleolytic // inferred from electronic annotation//1902042 // negative
1423783_at 143f	0.004366	1.54	1.34	NM_153783//XM_006536166	<i>Paox</i>	polyamine oxidase (exo-N4-amino)	0006598 // polyamine catabolic process // inferred from direct assay//0006598 // polyamine catabolic process // not
1423812_s_at 14	0.006775	1.53	1.45	NM_001145979//NM_019581	<i>Gtpbp2</i>	GTP binding protein 2	0006184 // GTP catabolic process // inferred from electronic annotation
1423813_at 143f	0.005043	1.53	1.07	NM_001166457//NM_001166	<i>Brcr3</i>	BRCA1/BRCA2-containing complex, subunit 3	0006281 // DNA repair // inferred from electronic annotation//0006302 // double-strand break repair // not recorded//0006508 //
1423826_at 142f	0.005818	1.53	1.01	NM_013778//XM_006516482	<i>Akr1c13//Akr1c12</i>	aldo-keto reductase family 1, member C13//aldo-keto reductase family 1,	0006805 // xenobiotic metabolic process // traceable author statement//0055114 // oxidation-reduction process // inferred from
1423829_at 143f	0.005780	1.53	1.32	NM_201357//XM_006515120	<i>Tssc1</i>	tumor suppressing subtransmembrane candidate 1	
1423831_at 142f	0.009474	1.53	-1.04	NM_026186	<i>Cwc25</i>	CWC25 spliceosome-associated protein homolog (S. cerevisiae)	
1423841_at 145f	0.008641	1.53	1.28	NM_025417//XM_006511343	<i>Comm4d</i>	COMM domain containing 4	
1423849_a_at 11i	0.004053	1.53	1.15	NM_001172136//NM_172456	<i>Exog</i>	endo/exonuclease (5'-3'), endonuclease G-like	0000737 // DNA catabolic process, endonucleolytic // not recorded
1423851_s_at 14	0.001507	1.53	1.65	NM_001048060//NM_198004	<i>Idnk</i>	idnk glucokinase homolog (E. coli)	0005975 // carbohydrate metabolic process // inferred from electronic annotation//0016310 // phosphorylation // inferred from
1423854_a_at 6i	0.005765	1.53	1.05	NM_020610	<i>Nrip3</i>	nuclear receptor interacting protein 3	0006508 // proteolysis // inferred from electronic annotation
1423855_x_at 14	0.004199	1.53	1.13	NM_177638//XM_006524163	<i>Crb3</i>	crumbs homolog 3 (Drosophila)	0045198 // establishment of epithelial cell apical/basal polarity // not recorded//0045216 // cell-cell junction organization // not
1423855_s_at 14	0.004199	1.53	1.08	NM_001098227//NM_018807	<i>Sdcbp</i>	syndecan binding protein	0007265 // Ras protein signal transduction // inferred from physical interaction//0042327 // positive regulation of phosphorylation //
1423855_s_at 14	0.004199	1.52	1.10	NM_010773//XM_006525710	<i>Mbd2</i>	methy1-CpG binding domain protein 2	0000122 // negative regulation of transcription from RNA polymerase II promoter // inferred from mutant phenotype//0006351 //
1423855_s_at 14	0.004199	1.52	1.38	NM_009256//XM_006516625	<i>Serpinb9</i>	serine (or cysteine) peptidase inhibitor, clade B, member 9	0001913 // T cell mediated cytotoxicity // inferred from mutant phenotype//0002438 // acute inflammatory response to antigenic
1423855_s_at 14	0.004199	1.52	1.11	NM_144866//XM_006525859	<i>Etf1</i>	eukaryotic translation termination factor 1	0000184 // nuclear-transcribed mRNA catabolic process, nonsense-mediated decay // inferred from electronic annotation//0006412 //
1423855_s_at 14	0.003306	1.52	1.19	NM_145510	<i>Rabif</i>	RAB interacting factor	0006810 // transport // inferred from electronic annotation//0007264 // small GTPase mediated signal transduction // inferred from
1423857_at 144f	0.003207	1.51	1.21	NM_019727	<i>Snx1</i>	sorting nexin 1	0006810 // transport // inferred from electronic annotation//0006886 // intracellular protein transport // not recorded//0007154 //
1423857_at 144f	0.003207	1.51	1.06	NM_001164207//NM_001164	<i>Tmem176b</i>	transmembrane protein 176b	0030154 // cell differentiation // inferred from electronic annotation//2001199 // negative regulation of dendritic cell differentiation //
1423861_at 142f	0.008762	1.51	1.46	NM_009226//XM_001481166	<i>Gm14277//Snrpd1</i>	predicted gene 14277//small nuclear ribonucleoprotein D1	000387 // spliceosomal snRNP assembly // not recorded//0006397 // mRNA processing // inferred from electronic
1423873_at 144f	0.005256	1.51	-1.04	NM_178925//XM_006521671	<i>Nsun3</i>	NOL1/NOP2/Sun domain family member 3	0002259 // methylation // inferred from electronic annotation
1423878_at 1716f	0.003058	1.51	1.21	NM_001163671//NM_001163	<i>Mapk9</i>	mitogen-activated protein kinase 9	0000165 // MAPK cascade // inferred from electronic annotation//0001836 // release of cytochrome c from mitochondria // not
1423881_at 142f	0.002971	1.50	1.27	NM_019752	<i>Htra2</i>	HtrA serine peptidase 2	0006508 // proteolysis // not recorded//0006672 // ceramide metabolic process // inferred from electronic annotation//0006915 //
1423902_s_at 14	0.001652	1.50	1.29	NM_021529//XR_381536	<i>Ppp2r3c</i>	protein phosphatase 2, regulatory subunit B', gamma	0001782 // B cell homeostasis // inferred from mutant phenotype//0002759 // regulation of antimicrobial humoral response // inferred
1423903_at 142f	0.001877	1.50	-1.73	NM_030166//XM_006519699	<i>Galnt15</i>	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-	0006486 // protein glycosylation // inferred from electronic annotation//0008152 // metabolic process // inferred from electronic
1423909_at 142f	0.001570	1.50	1.10	NM_026519	<i>Emc4</i>	ER membrane protein complex subunit 4	0006915 // apoptotic process // inferred from electronic annotation
1423912_at 145f	0.006033	1.50	1.09	NM_080554//XM_006498238	<i>Psmd5</i>	proteasome (prosome, macropain) 26S subunit, non-ATPase, 5	0006457 // protein folding // inferred from electronic annotation
1423919_at 231	0.006692	1.50	1.35	NM_023040//NM_212443//X	<i>Gfer</i>	growth factor, erv1 (S. cerevisiae)-like (augmenter of liver regeneration)	0055114 // oxidation-reduction process // not recorded
1423941_at 142f	0.004366	1.50	1.07	NM_175127	<i>Fbxo28</i>	F-box protein 28	
1423944_at 154f	0.000099	1.49	-1.07	NM_001113368//NM_001113	<i>Ceacam2//Ceacam1</i>	carcinoembryonic antigen-related cell adhesion molecule	0007156 // homophilic cell adhesion // inferred from direct assay//0016032 // viral process // inferred from electronic
1423954_at 122f	0.000470	1.49	-1.22	NM_175236//NR_027664//X	<i>Adhfe1</i>	alcohol dehydrogenase, iron containing, 1	0015993 // molecular hydrogen transport // not recorded//0055114 // oxidation-reduction process // not recorded
1423957_at 145f	0.005308	1.49	2.27	NM_010689//XM_006507396	<i>Lat</i>	linker for activation of T cells	0002260 // lymphocyte homeostasis // inferred from mutant phenotype//0002376 // immune system process // inferred from
1423974_at 142f	0.002292	1.49	1.69	NM_016750//XR_105012//X	<i>Gm203//H2afz</i>	predicted pseudogene 8203//H2A histone family, member Z	0006334 // nucleosome assembly // inferred from electronic annotation//0007275 // multicellular organismal development // inferred
1423976_at 142f	0.008741	1.49	1.09	NM_001293683//NM_001293	<i>Zwint</i>	ZW10 interactor	0000070 // mitotic sister chromatid segregation // not recorded//0007049 // cell cycle // inferred from electronic annotation//0007067
1423986_s_at 14	0.003565	1.49	-1.00	NM_028248//XM_006500243	<i>Tmem87b</i>	transmembrane protein 87b	
1423994_at 142f	0.001385	1.49	1.24	NM_053157//XM_006503494	<i>Tm2d1</i>	TM2 domain containing 1	0006915 // apoptotic process // inferred from electronic annotation//0006974 // cellular response to DNA damage stimulus // inferred
1424007_at 145f	0.004540	1.49	1.45	NM_009786	<i>Cacybp</i>	calyculin binding protein	0007507 // heart development // inferred from electronic annotation//0007568 // aging // inferred from electronic
1424008_a_at 7f	0.006239	1.49	1.11	NM_134000//XM_006512495	<i>Traf3ip2</i>	TRAF3 interacting protein 2	0001783 // B cell apoptotic process // inferred from mutant phenotype//0006959 // humoral immune response // inferred from mutant
1424008_a_at 11i	0.006239	1.49	-2.51	NM_153576	<i>Cxcl17</i>	chemokine (C-X-C motif) ligand 17	0001525 // angiogenesis // inferred from electronic annotation//0006935 // chemotaxis // inferred from electronic
1424032_at 740f	0.003140	1.48	1.08	NM_013684	<i>Tbp</i>	TATA box binding protein	0006351 // transcription, DNA-templated // inferred from electronic annotation//0006352 // DNA-templated transcription, initiation //
1424041_s_at 5f	0.001823	1.48	-1.11	NM_001290684//NM_001290	<i>Shroom2</i>	shroom family member 2	0000902 // cell morphogenesis // inferred from direct assay//0002089 // lens morphogenesis in camera-type eye // inferred from
1424050_s_at 14	0.001570	1.48	1.66	NM_030060//XM_006497182	<i>Batf3</i>	basic leucine zipper transcription factor, ATF-like 3	0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 // regulation of transcription, DNA-templated
1424055_at 228f	0.008405	1.48	1.10	NM_023409	<i>Npc2</i>	Niemann-Pick type C2	0006629 // lipid metabolic process // inferred from electronic annotation//0008202 // steroid metabolic process // inferred from
1424057_at 145f	0.002018	1.48	1.12	NM_001162939//NM_026531	<i>Aen</i>	apoptosis enhancing nuclease	0006915 // apoptotic process // inferred from electronic annotation//0006974 // cellular response to DNA damage stimulus // inferred
1424065_at 145f	0.006151	1.48	1.05	NM_025668//XM_006508117	<i>Spcs2</i>	signal peptidase complex subunit 2 homolog (S. cerevisiae)	0006465 // signal peptide processing // inferred from electronic annotation//0006508 // proteolysis // inferred from electronic
1424067_at 158f	0.003519	1.48	-1.13	NM_011898	<i>Spry4</i>	sprouty homolog 4 (Drosophila)	0007275 // multicellular organismal development // inferred from electronic annotation//0009966 // regulation of signal transduction //
1424078_s_at 14	0.004347	1.47	1.35	NM_028632	<i>Fcf1</i>	FCF1 small subunit (SSU) processome component homolog (S. cerevisiae)	0006364 // rRNA processing // inferred from electronic annotation//0042254 // ribosome biogenesis // inferred from electronic
1424097_at 142f	0.001757	1.47	-1.02	NM_133225	<i>Acbd3</i>	acyl-Coenzyme A binding domain containing 3	0006629 // lipid metabolic process // inferred from electronic annotation//0006694 // steroid biosynthetic process // inferred from
1424118_s_at 14	0.002150	1.47	1.11	NM_001033499//NM_012009	<i>Sh2d1b1//Sh2d1b2</i>	SH2 domain protein 1B1//SH2 domain protein 1B2	0002366 // leukocyte activation involved in immune response // inferred from direct assay//0002717 // positive regulation of natural
1424129_at 143f	0.004689	1.47	1.02	NM_013777//NM_013778//X	<i>Akr1c12//Akr1c13</i>	aldo-keto reductase family 1, member C12//aldo-keto reductase family 1,	0006805 // xenobiotic metabolic process // traceable author statement//0055114 // oxidation-reduction process // inferred from
1424131_at 128f	0.005006	1.47	1.15	NM_019734	<i>Asah1</i>	N-acylsphingosine amidohydrolase 1	0006629 // lipid metabolic process // inferred from electronic annotation//0008152 // metabolic process // inferred from direct
1424143_s_at 14	0.005610	1.46	-1.01	NM_025445//XM_006521253	<i>Arfgap3</i>	ADP-ribosylation factor GTPase activating protein 3	0006810 // transport // inferred from electronic annotation//0009306 // protein secretion // inferred from electronic
1424165_s_at 142f	0.008318	1.46	2.27	NM_001163510//NM_008433	<i>Kcnk4</i>	potassium intermediate/small conductance calcium-activated channel,	0002376 // immune system process // inferred from electronic annotation//0006810 // transport // inferred from electronic
1424165_s_at 14	0.001003	1.46	1.04	NM_018829//XM_006519292	<i>Ap3m1</i>	adaptor-related protein complex 3, mu 1 subunit	0006810 // transport // inferred from electronic annotation//0006886 // intracellular protein transport // inferred from electronic
1424177_at 142f	0.003991	1.46	1.25	NM_011843//XM_006513650	<i>Eys1t1</i>	extended synaptotagmin-like protein 1	0006810 // transport // inferred from electronic annotation//0006869 // lipid transport // inferred from electronic annotation
1424220_s_at 5f	0.003814	1.46	1.06	NM_019586//XM_006538107	<i>Ube2j1</i>	ubiquitin-conjugating enzyme E2j 1	0008152 // metabolic process // inferred from electronic annotation//0016567 // protein ubiquitination // inferred from sequence or
1424233_at 142f	0.008587	1.46	1.11	NM_025701	<i>Trappc5</i>	trafficking protein particle complex 5	0006810 // transport // inferred from electronic annotation//0016192 // vesicle-mediated transport // inferred from electronic
1424235_at 433f	0.001446	1.45	1.26	NM_001004761//NM_175706	<i>Gpr158</i>	G protein-coupled receptor 158	0007165 // signal transduction // inferred from electronic annotation//0007186 // G-protein coupled receptor signaling pathway //
1424239_at 756f	0.001720	1.45	1.03	NM_019442//XM_006524640	<i>Stk19</i>	serine/threonine kinase 19	0006468 // protein phosphorylation // inferred from electronic annotation//0016310 // phosphorylation // inferred from electronic
1424254_at 687f	0.003013	1.45	1.29	NM_026992//NR_033993	<i>Dnajc24</i>	DnaJ (Hsp40) homolog, subfamily C, member 24	0006810 // transport // inferred from electronic annotation//0017183 // peptidyl-diphthamide biosynthetic process from peptidyl-
1424256_at 143f	0.001160	1.45	1.10	NM_001163430//NM_181586	<i>Sirt6</i>	sirtuin 6	0006471 // protein ADP-ribosylation // inferred from direct assay//0010569 // regulation of double-strand break repair via homologous
1424257_at 145f	0.009684	1.45	1.16	NM_031203//XM_006520749	<i>Tstc3</i>	tissue specific transplantation antigen P358	0008152 // metabolic process // inferred from electronic annotation//0019673 // GDP-mannose metabolic process // not
1424265_at 740f	0.001202	1.45	1.15	NM_025288	<i>Sfzf3</i>	stefin A3	0010466 // negative regulation of peptidase activity // inferred from electronic annotation//0010951 // negative regulation of
1424266_s_at 2f	0.001796	1.45	-1.00	NM_133913	<i>Chpf2</i>	chondroitin polymerizing factor 2	0008152 // metabolic process // inferred from electronic annotation
1424278_s_at 1f	0.006496	1.44	-1.05	NM_175675	<i>Sc15c36</i>	solute carrier family 35, member F6	0006810 // transport // inferred from electronic annotation//0008284 // positive regulation of cell proliferation // not
1424303_at 211f	0.006660	1.44	-1.10	NM_001160208//NM_001160	<i>Blzf1</i>	basic leucine zipper nuclear factor 1	0006810 // transport // inferred from electronic annotation//0007030 // Golgi organization // not recorded//0010531 // protein
1424309_a_at 14	0.003294	1.44	-1.09	NM_001289716//NM_001289	<i>Bcl2l1</i>	BCL2-like 1	0000910 // cytokinesis // not recorded//0001541 // ovarian follicle development // inferred from genetic interaction//0001541 //

Table S6

Gene_ID	p (Corr)	FC-RSV 1 d	FC-RSV 5 d	RefSeq Transcript ID	Gene Symbol	Gene Title	Gene Ontology Biological Process
1424313_a_at,14	0.004914	1.44	1.33	NM_028128//XM_006530465	<i>Rfc5</i>	replication factor C (activator 1) 5	0006260 // DNA replication // inferred from electronic annotation//0006281 // DNA repair // inferred from electronic
1424314_at,1707	0.001780	1.44	-1.03	NM_178616	<i>Psm11</i>	proteasome (prosome, macropain) 26S subunit, non-ATPase, 11	0006511 // ubiquitin-dependent protein catabolic process // not recorded//0043248 // proteasome assembly // not
1424319_at,1444	0.000422	1.43	1.30	NM_177780//XM_006519491	<i>Dock5</i>	dedicator of cytokinesis 5	0007264 // small GTPase mediated signal transduction // inferred from electronic annotation//0043087 // regulation of GTPase activity
1424339_at,231	0.000878	1.43	1.14	NM_001243748//NM_019713	<i>Rassf1</i>	Ras association (RalGDS/AF-6) domain family member 1	0006974 // cellular response to DNA damage stimulus // not recorded//0007049 // cell cycle // inferred from electronic
1424340_at,1444	0.006067	1.43	1.37	NM_178907//XM_006511616	<i>Mapkapk3</i>	mitogen-activated protein kinase-activated protein kinase 3	0002224 // toll-like receptor signaling pathway // inferred from mutant phenotype//0006468 // protein phosphorylation // inferred
1424343_a_at,14	0.000144	1.43	1.86	NM_011539//XM_006505873	<i>Tbxas1</i>	thromboxane A synthase 1, platelet	0001516 // prostaglandin biosynthetic process // inferred from electronic annotation//0006629 // lipid metabolic process // inferred
1424352_at,1277	0.001384	1.43	4.05	NM_030712//XM_006512401	<i>Cxcr6</i>	chemokine (C-X-C motif) receptor 6	0006935 // chemotaxis // inferred from electronic annotation//0006954 // inflammatory response // inferred from electronic
1424354_at,1444	0.000295	1.43	1.11	NM_027193//XM_006502039	<i>Dph5</i>	DPH5 homolog (S. cerevisiae)	0008152 // metabolic process // inferred from electronic annotation//0007183 // peptidyl-dipthamide biosynthetic process from
1424359_a_at,14	0.001324	1.43	2.07	NM_010381//XM_003688950	<i>H2-Ea-ps</i>	histocompatibility 2, class II antigen E alpha, pseudogene	0002376 // immune system process // inferred from electronic annotation//0002504 // antigen processing and presentation of peptide
1424356_a_at,14	0.005109	1.42	1.11	NM_133708//XM_006496530	<i>Gmpaa</i>	GDP-mannose pyrophosphorylase A	0009058 // biosynthetic process // inferred from electronic annotation//0009298 // GDP-mannose biosynthetic process // inferred from
1424407_s_at,14	0.002293	1.42	1.12	NM_024215	<i>Zfp593</i>	zinc finger protein 593	0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 // regulation of transcription, DNA-templated
1424420_at,142C	0.006498	1.42	1.07	NM_133783	<i>Ptges2</i>	prostaglandin E synthase 2	0001516 // prostaglandin biosynthetic process // inferred from electronic annotation//0006629 // lipid metabolic process // inferred
1424440_at,1444	0.002063	1.42	1.11	NM_027123//XM_006517364	<i>Fastkd3</i>	FAST kinase domains 3	0006468 // protein phosphorylation // inferred from electronic annotation//0045333 // cellular respiration // not recorded//0045333
1424444_a_at,14	0.008501	1.42	1.26	NM_028038	<i>Ddx28</i>	DEAD (Asp-Glu-Ala-Asp) box polypeptide 28	0008152 // metabolic process // inferred from electronic annotation
1424448_at,1454	0.004782	1.41	-1.07	NM_001008232//XM_006538	<i>Asop3</i>	ArfGAP with SH3 domain, ankyrin repeat and PH domain 3	0016477 // cell migration // not recorded//0032312 // regulation of ARF GTPase activity // inferred from electronic
1424455_at,1444	0.004183	1.41	1.05	NM_001033448//XM_006531	<i>ApSb1</i>	adaptor-related protein complex 5, beta 1 subunit	0006810 // transport // inferred from electronic annotation//0015031 // protein transport // inferred from electronic
1424459_at,1424	0.001312	1.41	1.15	NM_001287261//NM_009074	<i>Mstr1</i>	macrophage stimulating 1 receptor (c-met-related tyrosine kinase)	0002376 // immune system process // inferred from electronic annotation//0006468 // protein phosphorylation // inferred from
1424488_a_at,17	0.001384	1.41	-1.21	NM_013885	<i>Clic4</i>	chloride intracellular channel 4 (mitochondrial)	0001525 // angiogenesis // inferred from mutant phenotype//0001886 // endothelial cell morphogenesis // inferred from mutant
1424495_a_at,14	0.005094	1.41	-0.06	NM_026267	<i>Necap1</i>	NECAP endocytosis associated 1	0006810 // transport // inferred from electronic annotation//0006897 // endocytosis // inferred from mutant phenotype//0015031 //
1424496_at,1435	0.004608	1.41	2.16	NM_008566//XM_006530750	<i>Mcm5</i>	minichromosome maintenance deficient 5, cell division cycle 46 (S.	0006260 // DNA replication // inferred from electronic annotation//0006270 // DNA replication initiation // inferred from electronic
1424509_at,1688	0.002931	1.41	1.36	NM_146159	<i>Haua3</i>	HAUS augmin-like complex, subunit 3	0006260 // DNA replication // inferred from electronic annotation//0006261 // DNA-dependent DNA replication // ---//0006281 // DNA
1424511_at,1444	0.001383	1.41	1.23	NM_016714	<i>Nup50</i>	nucleoporin 50	0001841 // neural tube formation // inferred from mutant phenotype//0006810 // transport // inferred from electronic
1424518_at,1718	0.000583	1.41	1.06	NM_011820//XM_006513647	<i>Ggt5</i>	gamma-glutamyltransferase 5	0006508 // proteolysis // inferred from electronic annotation//0006749 // glutathione metabolic process // inferred from electronic
1424518_at,223	0.000583	1.40	1.10	NM_029572//XM_006538341	<i>Erp44</i>	endoplasmic reticulum protein 44	0006457 // protein folding // not recorded//0006950 // response to stress // inferred from electronic annotation//0006986 // response
1424523_at,145C	0.003802	1.40	1.01	NM_00113188//NM_001113	<i>Fxr1</i>	fragile X mental retardation gene 1, autosomal homolog	0007275 // multicellular organismal development // inferred from electronic annotation//0007517 // muscle organ development //
1424524_at,1717	0.006672	1.40	1.57	NM_007633	<i>Cnc1</i>	cyclin E1	0000079 // regulation of cyclin-dependent protein serine/threonine kinase activity // inferred from electronic annotation//0000082 //
1424531_a_at,2	0.006659	1.40	-1.04	NM_001195023//NM_199469	<i>Nploc4</i>	nuclear protein localization 4 homolog (S. cerevisiae)	0007030 // Golgi organization // not recorded//0030433 // ER-associated ubiquitin-dependent protein catabolic process // inferred
1424542_at,201	0.002196	1.40	1.16	NM_001172096//NM_001172	<i>Cacul1</i>	CDK2 associated, cyclin domain 1	0000082 // G1/S transition of mitotic cell cycle // not recorded//0006511 // ubiquitin-dependent protein catabolic process // inferred
1424555_at,230	0.009131	1.40	1.11	NM_028850	<i>Chic2</i> //B930098A02rkl	cysteine-rich hydrophobic domain 2//RIKEN cDNA B930098A02 gene	0006893 // Golgi to plasma membrane transport // traceable author statement
1424560_at,192	0.008673	1.40	1.85	NM_028131//XM_006531387	<i>Cenp2</i>	centromere protein N	0007059 // chromosome segregation // inferred from electronic annotation//0007067 // mitotic nuclear division // inferred from
1424562_a_at,14	0.000416	1.39	-1.02	NM_019769//XM_003085105	<i>Chp1</i> //Gm20056	calcineurin-like EF hand protein 1//predicted gene, 20056	0001578 // microtubule bundle formation // not recorded//0001933 // negative regulation of protein phosphorylation // not
1424594_at,1424	0.005199	1.39	1.03	NM_001252543//NM_001252	<i>Sec23b</i>	SEC23B (S. cerevisiae)	0006810 // transport // inferred from electronic annotation//0006886 // intracellular protein transport // inferred from electronic
1424601_at,1424	0.000240	1.39	1.20	NM_025813	<i>Mfsd1</i>	major facilitator superfamily domain containing 1	0006810 // transport // inferred from electronic annotation//0005508 // transmembrane transport // inferred from electronic
1424613_at,1451	0.004434	1.39	-1.11	NM_001252547//NM_013781	<i>Sh2d3c</i>	SH2 domain containing 3C	0007165 // signal transduction // traceable author statement//0007169 // transmembrane receptor protein tyrosine kinase signaling
1424617_at,1444	0.000324	1.38	1.02	NM_172695	<i>Pla2</i>	phospholipase A2, activating protein	0006954 // inflammatory response // inferred from direct assay//0043085 // positive regulation of catalytic activity // inferred from
1424628_a_at,17	0.006780	1.38	1.10	NM_029001//XM_006517778	<i>Elov7</i>	ELOVL family member 7, elongation of long chain fatty acids (yeast)	0006629 // lipid metabolic process // inferred from electronic annotation//0006631 // fatty acid metabolic process // inferred from
1424652_at,232	0.001680	1.38	1.69	NM_001014996//XM_006518	<i>Cenp3</i>	centromere protein J	0007099 // centriole replication // not recorded//0030954 // astral microtubule nucleation // not recorded//0046427 // positive
1424659_at,1451	0.008427	1.38	1.09	NM_001130169//NM_001130	<i>Zfp207</i>	zinc finger protein 207	0000070 // mitotic sister chromatid segregation // not recorded//0007049 // cell cycle // inferred from electronic annotation//0007059
1424667_a_at,14	0.008819	1.38	1.03	NM_025433	<i>Rpl7l</i>	ribosomal protein L7-like 1	0008284 // positive regulation of cell proliferation // not recorded//0010536 // positive regulation of activation of Janus kinase activity
1424681_a_at,14	0.003356	1.38	-1.10	NM_010559//XM_006501045	<i>Il6ra</i>	interleukin 6 receptor, alpha	0006364 // rRNA processing // inferred from mutant phenotype
1424698_s_at,14	0.005446	1.38	1.05	NM_026464//XR_386010	<i>Wdr55</i>	WD repeat domain 55	0001649 // osteoblast differentiation // not recorded//0008152 // metabolic process // inferred from electronic annotation//0008152
1424713_at,1756	0.003438	1.37	1.11	NM_019553//XR_380417	<i>Ddx21</i>	DEAD (Asp-Glu-Ala-Asp) box polypeptide 21	0006412 // translation // inferred from electronic annotation//0006418 // rRNA aminoacylation for protein translation // inferred from
1424726_at,232	0.001205	1.37	-1.02	NM_153591//XM_006507816	<i>Nars2</i>	asparaginyl-tRNA synthetase 2 (mitochondrial)(putative)	0006508 // proteolysis // not recorded//0006511 // ubiquitin-dependent protein catabolic process // inferred from electronic
1424732_a_at,14	0.006151	1.37	1.35	NM_001128169//NM_001128	<i>Cyld</i>	cylindromatosis (turban tumor syndrome)	0008152 // metabolic process // inferred from electronic annotation
1424733_at,140	0.004675	1.37	1.29	NM_178870//XM_006532296	<i>Hs23ta1</i>	heparan sulfate (chondrosamine) 3-O-sulfotransferase 3A1	0007005 // mitochondrion organization // inferred from mutant phenotype//0007420 // brain development // inferred from electronic
1424735_at,1444	0.007141	1.37	1.25	NM_025340//XM_006520263	<i>Sharpin</i>	SHANK-associated R7 domain interacting protein	0010225 // response to UV-C // not recorded//0010332 // response to gamma radiation // not recorded//0030308 // negative
1424746_at,1424	0.008247	1.37	1.02	NM_001163703//NM_173408	<i>Ocurn1d3</i>	DCN1, defective in collagen neddylation 1, domain containing 3 (S. cerevisiae)	0001764 // neuron migration // inferred from genetic interaction//0006468 // protein phosphorylation // inferred from electronic
1424754_at,1444	0.005231	1.36	1.59	NM_001111051//NM_001111	<i>Dclk1</i>	doublecortin-like kinase 1	0003014 // renal system process // not recorded//0006469 // negative regulation of protein kinase activity // inferred from direct
1424775_at,1246	0.000126	1.36	1.28	NM_025774	<i>Prkrip1</i>	Prkr interacting protein 1 (IL11 inducible)	0006457 // protein folding // inferred from electronic annotation//0006950 // response to stress // inferred from electronic
1424783_a_at,14	0.002719	1.36	1.33	NM_018808//XM_006531518	<i>Dnajb1</i>	DnaJ (Hsp40) homolog, subfamily B, member 1	0042254 // ribosome biogenesis // inferred from electronic annotation
1424783_a_at,14	0.002719	1.36	1.21	NM_024193//XM_006500062	<i>Nop56</i>	NOP56 ribonucleoprotein	0000917 // barrier septum assembly // inferred from electronic annotation//0006184 // GTP catabolic process // inferred from
1424783_a_at,14	0.002719	1.35	1.32	NM_145972//XM_006521971	<i>BC027231</i>	cDNA sequence BC027231	0006810 // transport // inferred from electronic annotation//0006914 // autophagy // traceable author statement//0007289 //
1424783_a_at,14	0.002719	1.35	-1.11	NM_001082483//XM_006515	<i>Efrab</i>	EFR3 homolog B (S. cerevisiae)	000122 // negative regulation of transcription from RNA polymerase II promoter // not recorded//0008283 // cell proliferation //
1424783_a_at,14	0.002719	1.35	-1.02	NM_001199272//NM_003187	<i>Gopc</i>	golgi associated PDZ and coiled-coil motif containing	0001916 // positive regulation of T cell mediated cytotoxicity // inferred from direct assay//0002376 // immune system process //
1424783_a_at,14	0.002719	1.35	1.08	NM_001285507//NM_001285	<i>Cops2</i>	COP9 (constitutive photomorphogenic) homolog, subunit 2 (Arabidopsis	0008152 // metabolic process // inferred from electronic annotation
1424784_at,1451	0.005610	1.35	2.03	NM_007639//XM_006500958	<i>Cd1d1</i>	CD1d1 antigen	0006364 // rRNA processing // inferred from electronic annotation//0031047 // gene silencing by RNA // inferred from electronic
1424805_a_at,14	0.006412	1.35	1.22	NM_001081077//XM_006527	<i>Cwf19l1</i>	CWF19-like 1, cell cycle control (S. pombe)	0009002 // cell morphogenesis // inferred from electronic annotation
1424809_at,1434	0.008784	1.35	1.29	NM_026067	<i>Erl1</i>	exoribonuclease 1	0008152 // metabolic process // inferred from electronic annotation
1424810_at,1451	0.001683	1.34	1.25	NM_001037542//NM_015765	<i>Hspa14</i>	heat shock protein 14	0003976 // response to endoplasmic reticulum stress // not recorded//0071569 // protein ufymylation // inferred from direct
1424814_a_at,14	0.005154	1.34	1.23	NM_026341//XM_006519462	<i>Nudt13</i>	nudix (nucleoside diphosphate linked moiety X)-type motif 13	0001561 // fatty acid alpha-oxidation // inferred from direct assay//0001561 // fatty acid alpha-oxidation // not recorded//0006631 //
1424817_at,1444	0.001024	1.34	1.16	NM_027315	<i>Ube2q1</i>	ubiquitin-conjugating enzyme E2Q (putative) 1	0006353 // transcription, DNA-templated // inferred from electronic annotation//0006355 // regulation of transcription, DNA-templated
1424818_at,1427	0.003018	1.34	1.05	NM_026435	<i>Ufm1</i>	ubiquitin-fold modifier 1	0001967 // suckling behavior // inferred from mutant phenotype//0007566 // embryo implantation // inferred from mutant
1424826_s_at,14	0.000296	1.34	-1.26	NM_010726	<i>Phyh</i>	phytanoyl-CoA hydroxylase	0034976 // response to endoplasmic reticulum stress // not recorded//0071569 // protein ufymylation // inferred from direct
1424840_at,1424	0.005324	1.34	1.24	NM_144933//XM_006510157	<i>Med17</i>	mediator complex subunit 17	0001561 // fatty acid alpha-oxidation // inferred from direct assay//0001561 // fatty acid alpha-oxidation // not recorded//0006631 //
1424871_s_at,21	0.007007	1.34	1.28	NM_001281871//NM_026312	<i>Pbdc1</i>	polysaccharide biosynthesis domain containing 1	0006353 // transcription, DNA-templated // inferred from electronic annotation//0006355 // regulation of transcription, DNA-templated
1424885_at,1444	0.006175	1.34	1.26	NM_152800//NR_045485//X	<i>Tor2a</i>	tor1 family 2, member A	0051085 // chaperone mediated protein folding requiring cofactor // inferred from electronic annotation//0051260 // protein
1424886_at,1424	0.003366	1.33	-1.15	NM_010305	<i>Gna11</i>	guanine nucleotide binding protein (G protein), alpha inhibiting 1	0006184 // GTP catabolic process // not recorded//0007049 // cell cycle // inferred from electronic annotation//0007165 // signal
1424895_at,1761	0.003172	1.33	1.01	NM_031869//XM_006530201	<i>Prkab1</i>	protein kinase, AMP-activated, beta 1 non-catalytic subunit	0006468 // protein phosphorylation // not recorded//0006468 // protein phosphorylation // traceable author statement//0006629 //
1424921_at,1695	0.001145	1.33	1.52	NM_001289724//NM_001289	<i>Silp3</i>	stem-loop binding protein	0006397 // mRNA processing // inferred from electronic annotation//0006398 // histone mRNA 3'-end processing // inferred from
1424932_at,1434	0.002115	1.33	1.99	NM_031247	<i>Gimap3</i>	GTPase, IMAP family member 3	003955 // mitochondrial DNA inheritance // inferred from mutant phenotype
1424936_a_at,14	0.001069	1.32	1.25	NM_001164705//NM_028113	<i>Amer2</i>	APC membrane recruitment 2	0007398 // ectoderm development // inferred from sequence or structural similarity//0016055 // Wnt signaling pathway // inferred
1424937_at,1444	0.006153	1.32	1.13	NM_027332//NM_027371//X	<i>Rpf1</i>	ribosome production factor 1 homolog (S. cerevisiae)	0006364 // rRNA processing // inferred from electronic annotation//0042254 // ribosome biogenesis // inferred from electronic
1424942_a_at,11	0.001995	1.32	1.10	NM_133749//XM_006500254	<i>Ermc7</i>	ER membrane protein complex subunit 7	0006397 // mRNA processing // inferred from electronic annotation//0008380 // RNA splicing // inferred from electronic annotation
1424948_x_at,14	0.002358	1.32	1.20	NM_133939	<i>Lsm8</i>	LSM8 homolog, U6 small nuclear RNA associated (S. cerevisiae)	0042254 // ribosome biogenesis // inferred from electronic annotation
1424948_x_at,11	0.005500	1.31	1.05	NM_026396	<i>Brix1</i>	BRX1, biogenesis of ribosomes, homolog (S. cerevisiae)	0010833 // telomere maintenance via telomere lengthening // not recorded//0010836 // negative regulation of protein ADP-
1424961_at,1451	0.006381	1.31	1.19	NM_145705//XM_006519080	<i>Tinf2</i>	TRF1 (TRF1)-interacting nuclear factor 2	0006364 // rRNA processing // inferred from electronic annotation//0016075 // rRNA catabolic process // not recorded//0043087 //
1424965_at,107	0.003436	1.31	1.25	NM_028315//XM_006519601	<i>Dis3</i>	DIS3 mitotic control homolog (S. cerevisiae)	0006520 // cellular amino acid metabolic process // inferred from electronic annotation//0006544 // glycine metabolic process //
1424968_at,1723	0.001347	1.31	1.29	NM_138595	<i>Gldc</i>	glycine decarboxylase	

Table S6

Gene_ID	p (Corr)	FC-RSV 1 d	FC-RSV 5 d	RefSeq Transcript ID	Gene Symbol	Gene Title	Gene Ontology Biological Process
1424972_at,145	0.001457	1.31	1.90	NM_023294	<i>Ndc80</i>	NDC80 homolog, kinetochore complex component (S. cerevisiae)	0000070 // mitotic sister chromatid segregation // not recorded///0000132 // establishment of mitotic spindle orientation // not
1424982_a_at,14	0.004781	1.31	1.24	NM_001110159///NM_019761	<i>Nxt1</i>	NTF2-related export protein 1	0006405 // RNA export from nucleus // inferred from direct assay///0006611 // protein export from nucleus // inferred from direct
1424998_at,145	0.004199	1.30	1.22	NM_007859///XM_006538517	<i>Dffb</i>	DNA fragmentation factor, beta subunit	0006309 // apoptotic DNA fragmentation // not recorded///0006915 // apoptotic process // inferred from electronic
1425008_a_at,14	0.001894	1.30	1.76	NM_011676///XM_006533162	<i>Unc119</i>	unc-119 homolog (C. elegans)	0006810 // transport // inferred from electronic annotation///0007109 // cytokinesis, completion of separation // not
1425008_a_at,14	0.002045	1.30	1.11	NM_027181///XM_003945587	<i>Gm6851-1</i>	predicted pseudogene 6851///predicted gene 7301///protein (peptidyl-prolyl	0000413 // protein peptidyl-prolyl isomerization // inferred from electronic annotation///0006364 // rRNA processing // not
1425025_at,143	0.002295	1.30	-1.20	NM_144899///XM_006501367	<i>Adomts14</i>	ADAMTS-like 4	0006508 // proteolysis // inferred from electronic annotation///0006915 // apoptotic process // inferred from electronic
1425050_at,142	0.005367	1.30	1.10	NM_010094	<i>Lefty1</i>	left right determination factor 1	0000122 // negative regulation of transcription from RNA polymerase II promoter // inferred from direct assay///0003007 // heart
1425052_at	0.009610	1.29	1.31	NM_001291071///NM_019703	<i>Pfkfb</i>	phosphofructokinase, platelet	0006002 // fructose 6-phosphate metabolic process // not recorded///0006096 // glycolytic process // not recorded///0006096 //
1425065_at,146	0.000738	1.29	1.03	NM_025778///XM_006506484	<i>Bcl2l14</i>	BCL2-like 14 (apoptosis facilitator)	0006915 // apoptotic process // not recorded///0006915 // apoptotic process // inferred from reviewed computational
1425097_a_at,14	0.003194	1.29	1.06	NM_178760///XM_006498097	<i>Gpr107</i>	G protein-coupled receptor 107	0006400 // tRNA modification // not recorded///0008033 // tRNA processing // inferred from electronic annotation///0030488 // tRNA
1425099_a_at,1	0.004595	1.29	1.03	NM_010792///XM_006513312	<i>Mettl1</i>	methyltransferase like 1	0006508 // proteolysis // inferred from electronic annotation
1425113_x_at	0.001914	1.29	1.35	NM_028660///XM_006540537	<i>Klk9</i>	kallikrein related-peptidase 9	0006810 // transport // inferred from electronic annotation///0006886 // intracellular protein transport // inferred from electronic
1425119_at,239	0.002811	1.28	-1.11	NM_019667///XM_006498198	<i>Stam2</i>	signal transducing adaptor molecule (SH3 domain and ITAM motif) 2	0006508 // proteolysis // not recorded///0032496 // response to lipopolysaccharide // inferred from sequence or structural
1425120_x_at,2	0.004194	1.28	1.01	NM_001290536///NM_001290	<i>Otu5d</i>	OTU domain containing 5	0000122 // negative regulation of transcription from RNA polymerase II promoter // not recorded///0000209 // protein
1425154_a_at,14	0.001646	1.27	-1.08	NM_009424///XM_006499156	<i>Traf6</i>	TNF receptor-associated factor 6	0001676 // long-chain fatty acid metabolic process // not recorded///0006006 // glucose metabolic process // not recorded///0006629 //
1425156_at,143	0.001877	1.27	-1.08	NM_013495///XM_006531654	<i>Cpt1a</i>	carnitine palmitoyltransferase 1a, liver	0006351 // transcription, DNA-templated // inferred from electronic annotation///0006355 // regulation of transcription, DNA-templated
1425173_s_at,14	0.006553	1.27	1.05	NM_197992	<i>Pcgef1</i>	polycorn group ring finger 1	0006915 // apoptotic process // inferred from electronic annotation
1425193_at,145	0.002566	1.27	-1.01	NM_144525///XM_006504090	<i>Tmem214</i>	transmembrane protein 214	000724 // double-strand break repair via homologous recombination // inferred from direct assay///0000724 // double-strand break
1425202_a_at,14	0.006201	1.27	2.15	NM_0011234	<i>Rad51</i>	RAD51 homolog	0006184 // GTP catabolic process // inferred from electronic annotation///0006810 // transport // inferred from electronic
1425218_a_at,1	0.002040	1.27	1.54	NM_134050///XM_006515367	<i>Rab15</i>	RAB15, member RAS oncogene family	0002376 // immune system process // inferred from electronic annotation///0002474 // antigen processing and presentation of peptide
1425225_at,146	0.002146	1.26	1.32	NM_001289524///NM_001289	<i>Lrrc40</i>	leucine rich repeat containing 40	0007009 // plasma membrane organization // inferred from mutant phenotype///0042462 // eye photoreceptor cell development //
1425233_at,783	0.000749	1.26	1.94	NM_010378///XM_006536522	<i>H2-Aa</i>	histocompatibility 2, class II antigen A, alpha	0000122 // negative regulation of transcription from RNA polymerase II promoter // inferred from direct assay///0000723 // telomere
1425256_a_at,14	0.001116	1.26	1.12	NM_133239///XM_006529217	<i>Crb1</i>	crumbs homolog 1 (Drosophila)	0008152 // metabolic process // inferred from electronic annotation///0043085 // positive regulation of catalytic activity // not recorded
1425284_a_at,14	0.008486	1.26	1.07	NM_001012638///XM_00653	<i>Acd</i>	adrenocortical dysplasia	0000079 // regulation of cyclin-dependent protein serine/threonine kinase activity // inferred from electronic annotation///0000082 //
1425313_at,146	0.003235	1.26	1.11	NM_133763///XM_006500368	<i>Dntt1p1</i>	deoxynucleotidyltransferase, terminal, interacting protein 1	0006706 // protein import into nucleus // not recorded///0006810 // transport // inferred from electronic annotation///0007030 // Golgi
1425341_at,142	0.009166	1.26	1.06	NM_025525	<i>Rnf113a2</i>	ring finger protein 113A2	0007275 // multicellular organismal development // inferred from electronic annotation///0007420 // brain development // inferred
1425364_a_at,1	0.004839	1.25	1.21	NM_028184///XM_006508649	<i>Oraov1</i>	oral cancer overexpressed 1	0006897 // endocytosis // inferred from electronic annotation///0007010 // cytoskeleton organization // not recorded///0007275 //
1425374_at,146	0.001102	1.25	1.01	NM_001291286///NM_001291	<i>Trn6b</i>	lethal, Chr 7, Rinchik 6	0007179 // transforming growth factor beta receptor signaling pathway // traceable author statement
1425382_a_at,14	0.002242	1.25	-1.03	NM_023054	<i>Utp3</i>	UTP3, small subunit (SSU) processome component, homolog (S. cerevisiae)	0001975 // response to amphetamine // inferred from electronic annotation///0006306 // DNA methylation // inferred from electronic
1425383_a_at,14	0.000240	1.25	1.10	NM_001276684///NM_018790	<i>Arc</i>	activity regulated cytoskeletal-associated protein	0006810 // transport // inferred from electronic annotation///0006811 // ion transport // inferred from electronic annotation///0009268
1425394_at,1667	0.003675	1.25	-1.28	NM_019919///NM_206958///X	<i>Ltbp1</i>	latent transforming growth factor beta binding protein 1	0006747 // FAD biosynthetic process // inferred from electronic annotation///0006777 // Mo-molybdopterin cofactor biosynthetic
1425405_a_at,14	0.001347	1.24	-1.01	NM_010067///XM_006497324	<i>Tdrmt1</i>	tRNA aspartic acid methyltransferase 1	0006569 // tryptophan catabolic process // not recorded///0008152 // metabolic process // inferred from electronic
1425411_at,143	0.004366	1.24	1.75	NM_001042489///NM_028752	<i>Flad1</i>	hydrogen voltage-gated channel 1	0009405 // pathogenesis // not recorded
1425421_at,100	0.006071	1.24	1.03	NM_020517///NM_177041	<i>Flad1</i>	Rfad1, flavin adenine dinucleotide synthetase, homolog (yeast)///lens	0002329 // pre-B cell differentiation // inferred from mutant phenotype///0006810 // transport // inferred from electronic
1425450_at,142	0.009206	1.24	1.75	NM_001289593///NM_001289	<i>Kynu</i>	kynureninase (L-kynurenine hydrolase)	003208b // negative regulation of NF-kappaB transcription factor activity // not recorded///0033209 // tumor necrosis factor-mediated
1425452_s_at,11	0.003018	1.24	-1.01	NM_001033178///NM_001045	<i>Tmem181a</i>	transmembrane protein 181A///transmembrane protein 181B,	0010960 // magnesium ion homeostasis // inferred from mutant phenotype///0032259 // methylation // inferred from electronic
1425475_at,142	0.005720	1.24	1.21	NM_001001798///NM_001037	<i>Atp11c</i>	ATPase, class VI, type 11C	0006508 // proteolysis // not recorded///0007283 // spermatogenesis // traceable author statement
1425496_at,145	0.005519	1.23	1.16	NM_001195390///NM_133850	<i>Ccmd7</i>	COMM domain containing 7	0001649 // osteoblast differentiation // inferred from genetic interaction///0006334 // nucleosome assembly // inferred from electronic
1425546_a_at,2	0.007260	1.23	1.15	NM_175389///XM_006500842	<i>Trmt10a</i>	tRNA methyltransferase 10A	0001701 // in utero embryonic development // inferred from mutant phenotype///0001944 // vasculature development // inferred from
1425577_at,144	0.005767	1.23	1.09	NM_020487	<i>Prss21</i>	protease, serine 21	0006417 // regulation of translation // inferred from electronic annotation///0016070 // RNA metabolic process // inferred from
1425583_at	0.000749	1.22	1.11	NM_026579	<i>D10Wsu102e</i>	DNA segment, Chr 10, Wayne State University 102, expressed	0001649 // osteoblast differentiation // inferred from genetic interaction///0006334 // nucleosome assembly // inferred from electronic
1425584_x_at	0.000268	1.22	-1.05	NM_001081019///NM_008210	<i>Gm12657</i>	predicted gene 12657///predicted gene 12657///predicted pseudogene	0000122 // negative regulation of transcription from RNA polymerase II promoter // not recorded///0006351 // transcription, DNA-
1425586_a_at,14	0.006612	1.22	-1.23	NM_009551///XM_006527058	<i>Zfand5</i>	zinc finger, AN1-type domain 5	0006886 // intracellular protein transport // inferred from direct assay///0042593 // glucose homeostasis // inferred from direct
1425601_a_at,2	0.006602	1.22	1.12	NM_001243584///NM_001243	<i>Mif4gd</i>	MIF4G domain containing	0001649 // osteoblast differentiation // inferred from genetic interaction///0006334 // nucleosome assembly // inferred from electronic
1425609_at,145	0.008466	1.22	-1.05	NM_001081019///NM_008210	<i>Gm12657</i>	predicted gene 12657///predicted gene 12657///predicted pseudogene	0000398 // mRNA splicing, via spliceosome // inferred from electronic annotation///0006397 // mRNA processing // inferred from
1425631_at,143	0.002853	1.22	3.33	NM_001243760///NM_001243	<i>Ctla</i>	class II transactivator	0001701 // in utero embryonic development // inferred from mutant phenotype///0002328 // pro-B cell differentiation // inferred from
1425649_at,142	0.000383	1.22	-1.07	NM_001164224///NM_026877	<i>Aspscr1</i>	alveolar soft part sarcoma chromosome region, candidate 1 (human)	0006810 // transport // inferred from electronic annotation///0002900 // electron transport chain // inferred from electronic
1425673_at,143	0.002268	1.22	-1.05	NM_001081019///NM_008210	<i>Gm12657</i>	predicted gene 12657///predicted gene 12657///predicted pseudogene	0000460 // maturation of 5.8S rRNA // not recorded///0006364 // rRNA processing // inferred from electronic annotation///0016310 //
1425674_a_at,14	0.006907	1.21	1.28	NM_027541///XM_006502079	<i>Prpf3</i>	PRP3 pre-mRNA processing factor 3 homolog (yeast)	0006953 // acute-phase response // inferred from electronic annotation
1425676_a_at,14	0.002666	1.21	-1.04	NM_028012///XM_006517041	<i>Xrcc4</i>	X-ray repair complementing defective repair in Chinese hamster cells 4	0030198 // extracellular matrix organization // inferred from direct assay///0030324 // lung development // inferred from electronic
1425678_a_at,14	0.003130	1.21	-1.40	NM_007805///XM_006532129	<i>Cyb561</i>	cytochrome b-561	0006281 // DNA repair // inferred from electronic annotation///0006289 // nucleotide-excision repair // not recorded///0006974 //
1425714_a_at,14	0.005308	1.21	1.11	NM_001159599///NM_028727	<i>Nola9</i>	nucleolar protein 9	0006629 // lipid metabolic process // inferred from electronic annotation///0006694 // steroid biosynthetic process // not
1425719_a_at,16	0.000506	1.21	1.04	NM_030233///XM_006541317	<i>Saal1</i>	serum amyloid A-like 1	0002376 // immune system process // inferred from electronic annotation///0002504 // antigen processing and presentation of peptide
1425732_a_at,14	0.007559	1.21	-1.61	NM_030209///XM_006531507	<i>Crispld2</i>	cysteine-rich secretory protein LCCL domain containing 2	0006508 // proteolysis // inferred from electronic annotation///0009987 // cellular process // inferred from electronic
1425742_a_at,14	0.003455	1.20	-1.17	NM_009010///XM_006530774	<i>Rad23a</i>	RAD23a homolog (S. cerevisiae)	0007155 // cell adhesion // inferred from electronic annotation
1425747_at,143	0.007986	1.20	1.17	NM_020010	<i>Cyp51</i>	cytochrome P450, family 51	0001510 // RNA methylation // inferred from electronic annotation///0006396 // RNA processing // inferred from electronic
1425767_a_at,14	0.003455	1.20	2.06	NM_010382	<i>H2-Eb1</i>	histocompatibility 2, class II antigen E beta	0001878 // response to yeast // inferred from direct assay///0001879 // detection of yeast // inferred from direct assay///0002221 //
1425772_at,144	0.009123	1.19	1.09	NM_026490	<i>Mrp19</i>	mitochondrial ribosomal protein L19	0006897 // endocytosis // inferred from electronic annotation
1425806_a_at,11	0.005427	1.19	1.13	NM_175224	<i>Metap1</i>	methionyl aminopeptidase 1	0006200 // ATP catabolic process // not recorded///0006281 // DNA repair // inferred from electronic annotation///0006351 //
1425815_a_at,14	0.003473	1.19	1.36	NM_001162506///NM_030159	<i>Troap</i>	troponin associated protein	0006810 // transport // inferred from electronic annotation///0015031 // protein transport // inferred from electronic annotation
1425821_at,145	0.002727	1.19	1.17	NM_001080999///NM_001081	<i>Trmt2a</i>	TRM2 RNA methyltransferase 2A	0006915 // apoptotic process // inferred from electronic annotation
1425829_a_at,14	0.000103	1.19	3.94	NM_020008	<i>Clec7a</i>	C-type lectin domain family 7, member a	0006355 // regulation of transcription, DNA-templated // inferred from electronic annotation///0008284 // positive regulation of cell
1425861_a_at,14	0.002406	1.19	1.89	NM_013825	<i>Ly75</i>	lymphocyte antigen 75	000397 // mRNA processing // inferred from electronic annotation///0007399 // nervous system development // inferred from
1425866_a_at,14	0.002562	1.18	1.20	NM_009874	<i>Cdk7</i>	cyclin-dependent kinase 7	0001934 // positive regulation of protein phosphorylation // inferred from mutant phenotype///0007165 // signal transduction //
1425883_at,143	0.007181	1.18	1.10	NM_026918///XM_006508175	<i>Zg16</i>	zymogen granule protein 16	0000070 // mitotic sister chromatid segregation // not recorded///0000090 // mitotic anaphase // inferred from sequence or structural
1425890_at,157	0.000176	1.18	1.02	NM_026273///XM_006522489	<i>4930453N24Rik</i>	RIKEN cDNA 4930453N24 gene	0006260 // DNA replication // inferred from electronic annotation///0009186 // deoxyribonucleoside diphosphate metabolic process //
1425913_a_at,14	0.000240	1.18	1.21	NM_001171052///NM_001171	<i>Mta3</i>	metastasis associated 3	0000070 // mitotic sister chromatid segregation // inferred from mutant phenotype///0007049 // cell cycle // inferred from electronic
1425918_at	0.002544	1.18	-1.04	NM_001081633///NM_022408	<i>Dgcr14</i>	DIGeorge syndrome critical region gene 14	0000186 // activation of MAPKK activity // not recorded///0000902 // cell morphogenesis // inferred from genetic interaction///0001889
1425958_at,215	0.001248	1.18	-1.21	NM_001195774///NM_022420	<i>Gprc5b</i>	G protein-coupled receptor, family C, group 5, member B	0001398 // positive regulation of protein ubiquitination // not recorded///0003207 // negative regulation of TOR signaling // inferred
1426037_s_at,14	0.006996	1.17	1.72	NM_017407///XM_006533747	<i>Spag5</i>	sperm associated antigen 5	0001558 // regulation of cell growth // not recorded///0006694 // steroid biosynthetic process // inferred from electronic
1426053_s_at,14	0.006144	1.17	3.71	NM_009104	<i>Rrm2</i>	ribonucleotide reductase M2	0006810 // transport // inferred from electronic annotation///0005508 // transmembrane transport // inferred from electronic
1426062_a_at,14	0.006840	1.17	1.99	NM_019499///XM_006506406	<i>Mad2l1</i>	MAD2 mitotic arrest deficient-like 1	0006508 // proteolysis // inferred from direct assay///0035609 // C-terminal protein deglutamylation // inferred from direct
1426065_a_at,14	0.009788	1.17	-1.11	NM_007912///NM_207655///X	<i>Egfr</i>	epidermal growth factor receptor	
1426112_a_at,1	0.003158	1.16	1.07	NM_001252639///NM_001252	<i>Tbclad7</i>	TBCL domain family, member 7	
1426165_a_at,14	0.008852	1.16	1.34	NM_001040684///NM_133943	<i>Hsd3b7</i>	hydroxy-delta-5-steroid dehydrogenase, 3 beta- and steroid delta-isomerase	
1426215_at,143	0.004335	1.16	1.06	NM_001145876///NM_001145	<i>Slc25a44</i>	solute carrier family 25, member 44	
1426218_at,145	0.000930	1.16	1.07	NM_001159650///NM_002352	<i>Crybb3</i>	crystallin, beta B3	
1426220_at,143	0.003542	1.15	1.06	NM_001048189///NM_001284	<i>Agb14</i>	ATP/GTP binding protein-like 4	

Table S6

Gene_ID	p (Corr)	FC-RSV 1 d	FC-RSV 5 d	RefSeq Transcript ID	Gene Symbol	Gene Title	Gene Ontology Biological Process
1426221_at 142E	0.002566	1.15	1.51	NM_029249//XM_006514267	<i>Parpbp</i>	PARP1 binding protein	0006281 // DNA repair // inferred from electronic annotation//0006974 // cellular response to DNA damage stimulus // inferred from
1426223_at 144I	0.000573	1.14	3.37	NM_001081117//XM_006507	<i>Mki67</i>	antigen identified by monoclonal antibody Ki 67	0006259 // DNA metabolic process // inferred from electronic annotation//0007126 // meiotic nuclear division // inferred from direct
1426225_at 196F	0.003763	1.14	-1.24	NM_145132	<i>Mchr1</i>	melanin-concentrating hormone receptor 1	0007165 // signal transduction // inferred from electronic annotation//0007166 // cell surface receptor signaling pathway // not
1426254_at 145I	0.006067	1.13	1.32	NM_001164557//NM_001164	<i>Pdzk1ip1</i>	PDK1 interacting protein 1	
1426258_at 146E	0.004626	1.12	1.85	NM_016692//XM_006526707	<i>Incnp</i>	inner centromere protein	0000910 // cytokinesis // not recorded//0007049 // cell cycle // inferred from electronic annotation//0007059 // chromosome
1426285_at 167	0.005097	1.12	1.14	NM_153583//XM_006510184	<i>Atg4d</i>	autophagy related 4D, cysteine peptidase	0006508 // proteolysis // inferred from sequence or structural similarity//0006810 // transport // inferred from electronic
1426299_at 716F	0.008516	1.12	1.93	NM_011496//XM_006532725	<i>Aurkb</i>	aurora kinase B	0000122 // negative regulation of transcription from RNA polymerase II promoter // not recorded//0000910 // cytokinesis // inferred
1426300_at 142E	0.000717	1.11	-1.04	NM_001164242//NM_001164	<i>Prpsap2</i>	phosphoribosyl pyrophosphate synthetase-associated protein 2	0009165 // nucleotide biosynthetic process // inferred from electronic annotation//0006348 // bone development // inferred from
1426307_at 266F	0.006907	1.11	1.32	NM_026032	<i>Lsm1</i>	LSM1 homolog, U6 small nuclear RNA associated (S. cerevisiae)	0006397 // mRNA processing // inferred from electronic annotation//0008380 // RNA splicing // inferred from electronic
1426378_at 142E	0.002296	1.11	1.38	NM_012012//XM_006496862	<i>Exo1</i>	exonuclease 1	0000737 // DNA catabolic process, endonucleolytic // not recorded//0000738 // DNA catabolic process, exonucleolytic // not
1426386_at 145E	0.004347	1.11	1.22	NM_001159724//NM_008990	<i>Pvrl2</i>	poliovirus receptor-related 2	0001675 // acrosome assembly // inferred from mutant phenotype//0002860 // positive regulation of natural killer cell mediated
1426399_at 246	0.003915	1.10	3.27	NM_009394	<i>Tnnc2</i>	troponin C2, fast	003009 // skeletal muscle contraction // not recorded//0007165 // signal transduction // inferred from electronic annotation
1426410_at 236F	0.003959	1.10	-1.46	NM_001164567//NM_011700	<i>Vill</i>	villin-like	0007010 // cytoskeleton organization // inferred from electronic annotation//00051693 // actin filament capping // inferred from
1426411_a_at 14	0.003004	1.09	1.27	NM_008876//XM_006532483	<i>Plid2</i>	phospholipase D2	0001666 // response to hypoxia // not recorded//0002031 // G-protein coupled receptor internalization // inferred from direct
1426426_at 679F	0.009324	1.09	1.29	NM_001025371//XM_006499	<i>Serinc4//Eil3</i>	serine incorporator 4//elongation factor RNA polymerase II-like 3	0006629 // lipid metabolic process // inferred from electronic annotation//0008654 // phospholipid biosynthetic process // inferred
1426447_at 694F	0.001757	1.08	1.12	NM_026591//XM_006501939	<i>Mrlp24</i>	mitochondrial ribosomal protein L24	0006412 // translation // inferred from electronic annotation
1426452_a_at 7I	0.006400	1.08	1.34	NM_001122958//NM_001122	<i>Rad54l</i>	RAD54 like (S. cerevisiae)	0000724 // double-strand break repair via homologous recombination // inferred from genetic interaction//0000733 // DNA strand
1426464_at 217	0.001539	1.08	1.54	NM_001159538//NM_013710	<i>Fgd2</i>	FYVE, RhoGEF and PH domain containing 2	0003231 // positive regulation of Rho GTPase activity // inferred from electronic annotation//00035023 // regulation of Rho protein
1426469_a_at 2	0.008175	1.07	2.27	NM_016904	<i>Cks1b</i>	Cdk2 protein kinase 1b	0007049 // cell cycle // inferred from electronic annotation//0004589 // regulation of protein kinase activity // inferred from electronic
1426473_at 108F	0.005749	1.07	1.22	NM_013765	<i>Rps26</i>	ribosomal protein S26	0006412 // translation // inferred from electronic annotation//00033119 // negative regulation of RNA splicing // not recorded
1426482_at 142E	0.007886	1.07	1.18	NM_009087//NM_181730	<i>Polr1d</i>	polymerase (RNA) 1 polypeptide D	0006351 // transcription, DNA-templated // inferred from electronic annotation//0006360 // transcription from RNA polymerase I
1426496_at 679F	0.007696	1.07	2.76	NM_001204201//NM_001204	<i>Spp1</i>	secreted phosphoprotein 1	0001503 // ossification // inferred from electronic annotation//0001649 // osteoblast differentiation // not recorded//0006954 //
1426501_a_at 2	0.007415	1.07	1.03	NM_001163552//NM_001163	<i>Ap4b1</i>	adaptor-related protein complex AP-4, beta 1	0006810 // transport // inferred from electronic annotation//0006886 // intracellular protein transport // traceable author
1426505_at 142E	0.005546	1.06	1.39	NM_013783	<i>Mme11</i>	membrane metallo-endopeptidase-like 1	0005508 // proteolysis // inferred from sequence or structural similarity
1426506_at 145E	0.004311	1.06	-1.41	NM_001039515//NM_007487	<i>Ar14a</i>	ADP-ribosylation factor-like 4A	0006184 // GTP catalytic process // traceable author statement//0007264 // small GTPase mediated signal transduction // inferred
1426511_at 717F	0.006412	1.06	1.54	NM_009987	<i>Cx3cr1</i>	chemokine (C-X3-C motif) receptor 1	0002282 // microglial cell activation involved in immune response // inferred from mutant phenotype//0006935 // chemotaxis //
1426528_at 143E	0.002727	1.05	1.39	NM_026329	<i>Polr2g</i>	polymerase (RNA) (DNA directed) polypeptide G	0000291 // nuclear-transcribed mRNA catabolic process, exonucleolytic // not recorded//0006351 // transcription, DNA-templated //
1426533_at 145E	0.007637	1.04	-1.34	NM_028803	<i>Gbe1</i>	glucan (1,4-alpha-), branching enzyme 1	0005975 // carbohydrate metabolic process // inferred from electronic annotation//0005978 // glycogen biosynthetic process // not
1426534_a_at 14	0.002040	1.02	1.36	NM_172453//XM_006510913	<i>Pif1</i>	P1F1 5'-to-3' DNA helicase homolog (S. cerevisiae)	0000002 // mitochondrial genome maintenance // inferred from electronic annotation//0000723 // telomere maintenance // inferred
1426545_at 143E	0.001698	1.01	1.13	NM_009077//XM_006540720	<i>Rpl18</i>	ribosomal protein L18	0006412 // translation // inferred from electronic annotation
1426556_at 145E	0.005097	1.01	1.81	NM_001291185//NM_011497	<i>Aurka</i>	aurora kinase A	0000212 // meiotic spindle organization // inferred from mutant phenotype//0000226 // microtubule cytoskeleton organization //
1426575_at 142E	0.004081	1.01	-1.41	NM_181407//XM_006507189	<i>Me3</i>	malic enzyme 3, NAD(P+)-dependent, mitochondrial	0006090 // pyruvate metabolic process // not recorded//0006108 // malate metabolic process // not recorded//0005114 // oxidation-
1426603_at 142E	0.003941	1.00	1.49	NM_011035//XM_006507434	<i>Pak1</i>	p21 protein (Cdc42/Rac)-activated kinase 1	0001666 // response to hypoxia // not recorded//0001934 // positive regulation of protein phosphorylation // not recorded//0006468
1426605_at 143E	0.001295	1.00	1.19	NM_026533//XM_001480802	<i>Gm15483//LOC102642137//Rp</i>	predicted gene 15483//40S ribosomal protein S13-like//ribosomal protein	0006412 // translation // inferred from electronic annotation//00033119 // negative regulation of RNA splicing // not recorded
1426624_a_at 6I	0.009125	-1.00	2.81	NM_026560	<i>Cdca8</i>	cell division cycle associated 8	0000089 // mitotic metaphase // not recorded//0007049 // cell cycle // inferred from electronic annotation//0007067 // mitotic
1426635_at 145E	0.009788	-1.00	1.57	NM_001146022//XM_006519	<i>Wdfy4</i>	WD repeat and FYVE domain containing 4	
1426708_at 719F	0.000573	-1.01	-1.41	NM_009275//NM_133977	<i>Sprb//Trf</i>	signal recognition particle receptor, B subunit//transferrin	0006810 // transport // inferred from electronic annotation//0006811 // ion transport // inferred from electronic annotation//0006826
1426716_at 145E	0.000583	-1.01	1.29	NM_001039215//NM_001039	<i>Pfkfb4</i>	6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 4	0006000 // fructose metabolic process // inferred from electronic annotation//0006003 // fructose 2,6-biphosphate metabolic process
1426721_s_at 14	0.005881	-1.02	1.47	NM_026412//XM_006498984	<i>Knstrn</i>	kinetochore-localized astrin/SPAG5 binding	0000070 // mitotic sister chromatid segregation // not recorded//0000090 // mitotic anaphase // inferred from sequence or structural
1426731_at 142E	0.002131	-1.02	1.31	NM_027878//XM_006514149	<i>Dram1</i>	DNA-damage regulated autophagy modulator 1	0006914 // autophagy // inferred from electronic annotation//0006915 // apoptotic process // inferred from electronic
1426765_at 145E	0.003953	-1.02	1.44	NM_001272097//NM_001272	<i>Fabp5</i>	fatty acid binding protein 5, epidermal	0006006 // glucose metabolic process // inferred from mutant phenotype//0006629 // lipid metabolic process // inferred from mutant
1426767_at 106F	0.006178	-1.03	1.50	NM_001163687//NM_025972	<i>Naaa</i>	N-acylthanolamine acid amidase	0006629 // lipid metabolic process // inferred from electronic annotation
1426773_at 144E	0.008004	-1.03	1.95	NM_172301//XM_006541329	<i>Ccnb1//Gm5593</i>	cyclin B1//predicted gene 5593	0000079 // regulation of cyclin-dependent protein serine/threonine kinase activity // inferred from electronic annotation//0000278 //
1426774_at 243	0.001511	-1.03	1.33	NM_172564	<i>Tns4</i>	tensin 4	0006915 // apoptotic process // inferred from electronic annotation//0008104 // protein localization // not recorded
1426794_at 142E	0.002131	-1.03	1.07	NM_026007//XM_00394551	<i>Eef1g//LOC101055956</i>	eukaryotic translation elongation factor 1 gamma//elongation factor 1-	0006412 // translation // inferred from electronic annotation//0006414 // translational elongation // inferred from electronic
1426820_at 145E	0.004484	-1.03	1.22	NM_001163485//NM_009083	<i>Gm12191//Gm5481//Gm6109</i>	ribosomal protein L30 pseudogene//predicted gene 5481//predicted gene	0006412 // translation // inferred from electronic annotation
1426874_at 234F	0.006412	-1.03	1.16	NM_001029990//XM_006519	<i>Mettl7</i>	methyltransferase like 17	0006412 // translation // inferred from electronic annotation//0008152 // metabolic process // inferred from electronic
1426880_at 145E	0.007918	-1.03	1.22	NM_001163485//NM_009083	<i>Gm12191//Gm5481//Gm6109</i>	ribosomal protein L30 pseudogene//predicted gene 5481//predicted gene	0006412 // translation // inferred from electronic annotation
1426886_at 211F	0.008460	-1.03	1.10	NM_024195//XM_006511199	<i>Cyb5r4</i>	cytochrome b5 reductase 4	0006091 // generation of precursor metabolites and energy // not recorded//0006739 // NADP metabolic process // not
1426892_at 142E	0.002153	-1.03	1.85	NM_001163359//NM_001163	<i>Fignl1</i>	figedin-like 1	0001649 // osteoblast differentiation // inferred from mutant phenotype//0006281 // DNA repair // inferred from electronic
1426898_at 166E	0.007856	-1.04	1.14	NM_178005	<i>Lrrtm2</i>	leucine rich repeat transmembrane neuronal 2	0002091 // negative regulation of receptor internalization // inferred from genetic interaction//0005808 // synapse organization //
1426903_at 144E	0.009094	-1.04	1.73	NM_011495//NM_173169//	<i>Plk4</i>	polo-like kinase 4	0006468 // protein phosphorylation // inferred from direct assay//0007099 // centriole replication // inferred from mutant
1426906_at 145E	0.003800	-1.05	1.30	NM_018730//XM_001480721	<i>Gm4604//Rpl36</i>	predicted gene 4604//ribosomal protein L36	0006412 // translation // inferred from electronic annotation
1426947_s_at 14	0.003594	-1.05	2.15	NM_172301//XM_006541329	<i>Ccnb1//Gm5593</i>	cyclin B1//predicted gene 5593	0000079 // regulation of cyclin-dependent protein serine/threonine kinase activity // inferred from electronic annotation//0000278 //
1426959_at 145E	0.008738	-1.07	1.84	NM_001199123//NM_001199	<i>Spc25</i>	SPC25, NDC80 kinetochore complex component, homolog (S. cerevisiae)	0007049 // cell cycle // inferred from electronic annotation//0007052 // mitotic spindle organization // not recorded//0007059 //
1426970_a_at 14	0.001400	-1.07	1.07	NM_001170981//NM_001170	<i>Hnmpc</i>	heterogeneous nuclear ribonucleoprotein C	0001649 // osteoblast differentiation // not recorded//0006397 // mRNA processing // inferred from electronic annotation//0008380
1426972_at 696F	0.006558	-1.07	1.56	NM_001256081//NM_001256	<i>Myo7b</i>	myosin VIIA	0001845 // phagolysosome assembly // inferred from mutant phenotype//0006200 // ATP catalytic process // not recorded//0006810
1426995_s_at 14	0.001213	-1.08	1.06	NM_009438//NM_013520//	<i>Rpl30//Fit3//Gm11478</i>	ribosomal protein L30A//FMS-like tyrosine kinase 3 ligand//60S ribosomal	0006412 // translation // inferred from electronic annotation//0006417 // regulation of translation // inferred from electronic
1427008_at 207	0.004621	-1.08	1.18	NM_016853//XM_006512016	<i>Stac</i>	src homolog three (SH3) and cysteine rich domain	0034605 // cellular response to heat // inferred from direct assay//0005556 // intracellular signal transduction // inferred from
1427019_at 145E	0.007411	-1.08	1.45	NM_001110162//NM_175384	<i>Cdca2</i>	cell division cycle associated 2	0007049 // cell cycle // inferred from electronic annotation//0007059 // chromosome segregation // inferred from direct
1427020_at 219	0.000285	-1.08	3.36	NM_007659	<i>Cdk1</i>	cyclin-dependent kinase 1	0000278 // mitotic cell cycle // inferred from electronic annotation//0006461 // protein complex assembly // not recorded//0006468 //
1427028_at 143E	0.000457	-1.09	1.55	NM_172616//XM_006522091	<i>C330027C09Rik</i>	RIKEN cDNA C330027C09 gene	0007283 // spermatogenesis // inferred from mutant phenotype//2000179 // positive regulation of neural precursor cell proliferation //
1427045_at 143A	0.009319	-1.09	1.09	NM_009096//XM_001003926	<i>Rps6//Rps6-ps4//LOC10264325</i>	ribosomal protein S6//ribosomal protein S6, pseudogene 4//40S ribosomal	0000082 // G1/S transition of mitotic cell cycle // inferred from mutant phenotype//0001890 // placenta development // inferred from
1427053_s_at 142E	0.002163	-1.09	1.09	NM_009076//XM_006496393	<i>LOC102635048//LOC102635049</i>	60S ribosomal protein L12-like//uncharacterized LOC102635049//ribosomal	0006412 // translation // inferred from electronic annotation
1427063_at 144E	0.001917	-1.09	1.56	NM_010436	<i>H2afx</i>	H2A histone family, member X	0000077 // DNA damage checkpoint // inferred from mutant phenotype//0000724 // double-strand break repair via homologous
1427076_a_at 13I	0.000305	-1.09	1.26	NM_029766//XM_006497212	<i>Dtl</i>	denticleless homolog (Drosophila)	0002029 // protein polyubiquitination // not recorded//0006260 // DNA replication // inferred from electronic annotation//0006511 //
1427069_at 142E	0.001332	-1.10	2.21	NM_001253808//NM_001253	<i>Racgap1</i>	src GTPase-activating protein 1	0000281 // mitotic cytokinesis // not recorded//0000910 // cytokinesis // inferred from sequence or structural similarity//0000915 //
1427073_at 215F	0.003991	-1.10	1.36	NM_027976//XM_006527178	<i>Acsf5</i>	acyl-CoA synthetase long-chain family member 5	0000676 // long-chain fatty acid metabolic process // not recorded//0006629 // lipid metabolic process // inferred from electronic
1427076_at 174	0.002448	-1.10	3.24	NM_001164362//NM_028293	<i>Cep55</i>	centrosomal protein 55	0000281 // mitotic cytokinesis // not recorded//0000910 // cytokinesis // inferred from electronic annotation//0007049 // cell cycle //
1427088_at 142E	0.009722	-1.10	2.65	NM_026515//XR_379450	<i>2810417H13Rik</i>	RIKEN cDNA 2810417H13 gene	0006260 // DNA replication // not recorded//0006281 // DNA repair // inferred from electronic annotation//0006974 // cellular
1427091_at 989F	0.001296	-1.10	1.37	NM_134081	<i>Dnajc9</i>	DNA (Hsp40) homolog, subfamily C, member 9	0035176 // social behavior // inferred from electronic annotation
1427102_at 145E	0.000295	-1.11	-1.62	NM_001190852//NM_001190	<i>Pdlim5</i>	PDL and LIM domain 5	0051963 // regulation of synapse assembly // not recorded//0061001 // regulation of dendritic spine morphogenesis // not recorded
1427105_at 145E	0.002780	-1.11	1.58	NM_013552//XM_006532276	<i>Hmnm</i>	hyaluronan mediated motility receptor (RHAMM)	0000160 // phosphorelay signal transduction system // inferred from electronic annotation
1427122_at 142E	0.007559	-1.11	1.03	NM_019883//NM_029366	<i>Kdx1//Uba52</i>	KdXL motif containing 1//ubiquitin A-52 residue ribosomal protein fusion	0006412 // translation // inferred from electronic annotation//0010992 // ubiquitin homeostasis // inferred from genetic
1427149_at 240	0.000905	-1.11	1.87	NM_009773//XM_006498622	<i>Bub1b</i>	ubiquitin unbinding by benzimidazole S-1 homolog, beta (S. cerevisiae)	0006468 // protein phosphorylation // inferred from electronic annotation//0006915 // apoptotic process // inferred from electronic
1427150_at 143A	0.006794	-1.12	1.00	NM_009429//XM_006518913	<i>Tpt1</i>	tumor protein, translationally-controlled 1	0009615 // response to virus // inferred from electronic annotation//0019827 // stem cell maintenance // inferred from mutant
1427161_at 145E	0.000181	-1.12	-1.00	NM_026718//XM_006530454	<i>Ankrd13a</i>	ankyrin repeat domain 13a	
1427168_a_at 14	0.001400	-1.12	1.16	NM_019953//XM_006513901	<i>Cnpy2</i>	canopy 2 homolog (zebrafish)	0010629 // negative regulation of gene expression // inferred from mutant phenotype//0010988 // regulation of low-density lipoprotein

Table S6

Gene_ID	p (Corr)	FC-RSV 1 d	FC-RSV 5 d	RefSeq Transcript ID	Gene Symbol	Gene Title	Gene Ontology Biological Process
1427178_at[353]	0.004753	-1.13	-1.11	NM_016800//XM_006516088	Vti1b	vesicle transport through interaction with t-SNAREs 1B	0006810 // transport // inferred from electronic annotation//0006886 // intracellular protein transport // inferred from electronic
1427191_at[230]	0.004130	-1.13	1.14	NM_011295//XM_001473380	Gm12571//Rps12//Rps12-ps10	predicted gene, 21571//ribosomal protein S12//ribosomal protein S12,	0006412 // translation // inferred from electronic annotation
1427301_at[1259]	0.006857	-1.13	1.83	NM_001146689//NM_007971	Ezh2	enhancer of zeste homolog 2 (Drosophila)	0000122 // negative regulation of transcription from RNA polymerase II promoter // inferred from direct assay//0000122 // negative
1427310_at[1427]	0.001036	-1.13	1.34	NM_181589//XM_006500158	Ckap2l	cytoskeleton associated protein 2-like	
1427312_at[764]	0.005747	-1.13	2.02	NM_001113179//NM_009772	Bub1	structurally uninhibited by benimidazole 1 homolog (S. cerevisiae)	0006468 // protein phosphorylation // inferred from electronic annotation//0006915 // apoptotic process // inferred from electronic
1427327_at[231]	0.002149	-1.14	1.50	NM_008017//XM_006537610	Smc2	structural maintenance of chromosomes 2	0006281 // DNA repair // inferred from electronic annotation//0006310 // DNA recombination // inferred from electronic
1427330_at[1452]	0.006780	-1.14	1.29	NM_001081102//NM_001177	Whsc1	Wolf-Hirschhorn syndrome candidate 1 (human)	0000122 // negative regulation of transcription from RNA polymerase II promoter // inferred from genetic interaction//0003149 //
1427345_a_at[2]	0.007499	-1.14	1.38	NM_010655	Kpna2	karyopherin (importin) alpha 2	0006606 // protein import into nucleus // inferred from direct assay//0006607 // NLS-bearing protein import into nucleus //
1427348_at[1442]	0.002080	-1.14	1.03	NM_008774	Pabpc1	poly(A) binding protein, cytoplasmic 1	0000184 // nuclear-transcribed mRNA catabolic process, nonsense-mediated decay // inferred from electronic annotation//0006397 //
1427353_at[1452]	0.000296	-1.14	2.17	NM_001042652//NM_133851	Nusap1	nucleolar and spindle associated protein 1	0000070 // mitotic sister chromatid segregation // not recorded//0000226 // microtubule cytoskeleton organization // inferred from
1427355_at[1452]	0.005627	-1.14	1.14	NM_001005859//NM_001199	Gm4705//Gm6404//Rpl34//R	predicted gene 4705//predicted gene 6404//ribosomal protein	0006412 // translation // inferred from electronic annotation
1427382_a_at[14]	0.007434	-1.15	1.10	NM_016980//XM_001004898	Rpl5//Rpl5-ps2	ribosomal protein L5//ribosomal protein L5, pseudogene 2	0006364 // rRNA processing // not recorded//0006412 // translation // inferred from electronic annotation//0010922 // positive
1427429_at[129]	0.000255	-1.15	1.70	NM_027435//NM_153199//X	Atad2	ATPase family, AAA domain containing 2	0006200 // ATP catabolic process // not recorded//0006351 // transcription, DNA-templated // inferred from electronic
1427445_a_at[14]	0.006178	-1.16	1.42	NM_028232//XM_006524969	Sgo1	shugoshin-like 1 (S. pombe)	0007049 // cell cycle // inferred from electronic annotation//0007059 // chromosome segregation // not recorded//0007067 // mitotic
1427463_at[1451]	0.002148	-1.16	1.21	NM_019941//XM_006540229	Zfp235	zinc finger protein 235	0006355 // regulation of transcription, DNA-templated // inferred from electronic annotation
1427465_at[1434]	0.001575	-1.16	1.53	NM_009791//XM_006529108	Aspm	asp (abnormal spindle)-like, microcephaly associated (Drosophila)	0001764 // neuron migration // inferred from genetic interaction//0001764 // neuron migration // inferred from mutant
1427469_at[1452]	0.000541	-1.16	-3.84	NM_013468	Ankrd1	ankyrin repeat domain 1 (cardiac muscle)	0000122 // negative regulation of transcription from RNA polymerase II promoter // not recorded//0006357 // regulation of
1427485_at[936]	0.005978	-1.16	-1.04	NM_001168497//NM_023564	Plscr3	phospholipid scramblase 3	0006915 // apoptotic process // inferred from electronic annotation//0042593 // glucose homeostasis // inferred from mutant
1427495_at[1432]	0.003563	-1.16	-1.17	NM_001278415//NM_028388	Ndufv2	NADH dehydrogenase (ubiquinone) flavoprotein 2	0006120 // mitochondrial electron transport, NADH to ubiquinone // not recorded//0006810 // transport // inferred from electronic
1427498_a_at[14]	0.007857	-1.16	1.01	NM_018794	Atp6ap1	ATPase, H ⁺ transporting, lysosomal accessory protein 1	0006810 // transport // inferred from electronic annotation//0006811 // ion transport // inferred from electronic annotation//0008219
1427510_at[1434]	0.001624	-1.16	1.05	NM_013762//XM_001475733	Gm12816//Gm5879//Rpl3	predicted gene 12816//predicted gene 5879//ribosomal protein L3	0006412 // translation // inferred from electronic annotation//0071353 // cellular response to interleukin-4 // inferred from direct assay
1427514_at[624]	0.004383	-1.17	1.14	NM_001277113//NM_001277	Rpl22	ribosomal protein L22	0006412 // translation // inferred from electronic annotation//0046632 // alpha-beta T cell differentiation // inferred from mutant
1427528_a_at[14]	0.002104	-1.17	1.39	NM_010421//XR_379397	Hexa	hexosaminidase A	0001501 // skeletal system development // inferred from genetic interaction//0005975 // carbohydrate metabolic process // inferred
1427562_a_at[14]	0.008841	-1.17	-1.04	NM_001113545//NM_023063	Lima1	LIM domain and actin binding 1	0003843 // negative regulation of actin filament depolymerization // not recorded//00031529 // ruffle organization // not
1427568_a_at[14]	0.004603	-1.18	1.11	NM_011801	Cfdp1	craniofacial development protein 1	0007155 // cell adhesion // inferred from direct assay//0007275 // multicellular organismal development // inferred from electronic
1427592_at[1442]	0.001183	-1.18	1.13	NM_009092//XR_141401//X	Gm14586//Rps17	predicted gene 14586//ribosomal protein S17	0000028 // ribosomal small subunit assembly // not recorded//0006364 // rRNA processing // not recorded//0006412 // translation //
1427600_at	0.003991	-1.18	1.01	NM_001017966//NM_023544	Ddix1//Rsc1a1	DNA-damage inducible protein 2//regulatory solute carrier protein, family 1,	0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 // regulation of transcription, DNA-templated
1427610_at[1432]	0.003001	-1.18	-1.21	NM_025362	Dnajc30	DnaI (Hsp40) homolog, subfamily C, member 30	
1427633_a_at[14]	0.007125	-1.18	-1.09	NM_001007589//NM_026019	Akirin2	akirin 2	0000122 // negative regulation of transcription from RNA polymerase II promoter // not recorded//0002376 // immune system process
1427640_a_at[14]	0.003809	-1.18	1.04	NM_175101	Emc3	ER membrane protein complex subunit 3	
1427691_a_at[14]	0.003908	-1.18	1.04	NM_001242580//NM_012049	Nit1	nitrilase 1	0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 // regulation of transcription, DNA-templated
1427724_at[1454]	0.001334	-1.18	1.08	NM_009092//XR_141401//X	Gm14586//Rps17	predicted gene 14586//ribosomal protein S17	0000028 // ribosomal small subunit assembly // not recorded//0006364 // rRNA processing // not recorded//0006412 // translation //
1427736_a_at[5]	0.002826	-1.19	-1.11	NM_001165902//NM_007614	Ctnnb1	catenin (cadherin associated protein), beta 1	0000122 // negative regulation of transcription from RNA polymerase II promoter // inferred from direct assay//0000578 // embryonic
1427737_a_at[7]	0.009177	-1.19	1.30	NM_029494//XM_006508293	Rab30	RAB30, member RAS oncogene family	0006184 // GTP catabolic process // inferred from electronic annotation//0006886 // intracellular protein transport // inferred from
1427747_a_at[10]	0.000196	-1.19	1.05	NM_001110217//NM_013647	LOC100862433//Rps16//Rps16	40S ribosomal protein S16-like//ribosomal protein S16//ribosomal protein	0006364 // rRNA processing // not recorded//0006412 // translation // inferred from electronic annotation//0042274 // ribosomal
1427875_a_at[14]	0.007725	-1.20	1.00	NM_026697	Rab14	RAB14, member RAS oncogene family	0006184 // GTP catabolic process // not recorded//0006810 // transport // inferred from electronic annotation//0006886 //
1427875_a_at[14]	0.007725	-1.20	1.00	NM_026697	Rab14	RAB14, member RAS oncogene family	0000079 // regulation of cyclin-dependent protein serine/threonine kinase activity // inferred from electronic annotation//0001701 // in
1427875_a_at[14]	0.007725	-1.20	1.06	NM_008750	Nxn	nucleoredoxin	0007275 // multicellular organismal development // inferred from electronic annotation//0016055 // Wnt signaling pathway // inferred
1427883_a_at[14]	0.005121	-1.20	1.26	NM_025592	Rpl35	ribosomal protein L35	0006412 // translation // inferred from electronic annotation
1427911_at[1442]	0.007753	-1.20	1.00	NM_007896	Mapre1	microtubule-associated protein, RP/EB family, member 1	0007049 // cell cycle // inferred from electronic annotation//0007067 // mitotic nuclear division // inferred from electronic
1427921_a_at[14]	0.002290	-1.20	-1.07	NM_025316//XM_006535514	Ndufb5	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 5	0006810 // transport // inferred from electronic annotation//0055114 // oxidation-reduction process // inferred from electronic
1427932_a_at[7]	0.002038	-1.21	1.03	NM_001002239//XM_006521	Gm10362//LOC101056140//LO	predicted gene 10362//60S ribosomal protein L17-like//ribosomal protein	0006412 // translation // inferred from electronic annotation//0042391 // regulation of membrane potential // inferred from genetic
1427932_a_at[14]	0.001273	-1.21	2.81	NM_011623//XM_006533153	Tp2a	topoisomerase (DNA) II alpha	0000712 // resolution of meiotic recombination intermediates // not recorded//0000819 // sister chromatid segregation // not
1427932_a_at[14]	0.002150	-1.22	1.82	NM_001004140//XM_006509	Ckap2	cytoskeleton associated protein 2	0000281 // mitotic cytokinesis // not recorded//0006915 // apoptotic process // inferred from electronic annotation//0007026 //
1427945_at[1427]	0.008329	-1.22	1.20	NM_007713//XM_006510739	Clk3	CDC-like kinase 3	0006468 // protein phosphorylation // inferred from direct assay//0006468 // protein phosphorylation // not recorded//0016310 //
1427956_at[698]	0.004034	-1.22	1.09	NM_016738//XM_001474690	Gm10071//Rpl13//Tax1bp3	predicted gene 10071//ribosomal protein L13//Taxi (human T cell leukemia	0006412 // translation // inferred from electronic annotation//0007266 // Rho protein signal transduction // not recorded//0008285 //
1427981_a_at[2]	0.003294	-1.23	-1.26	NM_001101433	Zcchc24	zinc finger, CCHC domain containing 24	014013 // regulation of gliogenesis // not recorded
1427982_s_at[14]	0.003823	-1.23	1.04	NM_025345//XM_006522450	Fopn1	Fgfr10p N-terminal like	0030030 // cell projection organization // inferred from electronic annotation//0034453 // microtubule anchoring // inferred from
1427986_a_at[10]	0.004800	-1.23	-1.25	NM_175015//XM_006499199	Atp5g3	ATP synthase, H ⁺ transporting, mitochondrial F0 complex, subunit C3	0006810 // transport // inferred from electronic annotation//0006811 // ion transport // inferred from electronic annotation//0015986
1427994_at[246]	0.002734	-1.23	-1.17	NM_026444	Cs	citrate synthase	0005975 // carbohydrate metabolic process // not recorded//0006084 // acetyl-CoA metabolic process // not recorded//0006099 //
1428002_at[1422]	0.003695	-1.24	1.05	NM_001002239//XM_006521	Gm10362//LOC101056140//LO	predicted gene 10362//60S ribosomal protein L17-like//ribosomal protein	0006412 // translation // inferred from electronic annotation//0042391 // regulation of membrane potential // inferred from genetic
1428025_s_at[14]	0.002079	-1.24	-1.35	NM_024197	Ndufa10	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex 10	0006139 // nucleobase-containing compound metabolic process // inferred from electronic annotation//0006810 // transport //
1428031_at[1454]	0.006440	-1.24	-1.20	NM_007505	Atp5a1	ATP synthase, H ⁺ transporting, mitochondrial F1 complex, alpha subunit 1	0001937 // negative regulation of endothelial cell proliferation // not recorded//0006172 // ADP biosynthetic process // not
1428034_a_at[14]	0.001248	-1.25	1.03	NM_009801//XM_006530050	Car2	carbonic anhydrase 2	0001822 // kidney development // inferred from electronic annotation//0002009 // morphogenesis of an epithelium // inferred from
1428050_a_at[14]	0.001559	-1.25	-1.06	NM_177045//XM_006503152	Cc2d1b	coiled-coil and C2 domain containing 1B	0000122 // negative regulation of transcription from RNA polymerase II promoter // inferred from direct assay//0006351 //
1428057_a_at[14]	0.001771	-1.25	1.18	NM_197981//NR_027359//N	Rhno1	RAD9-HUS1-RAD1 interacting nuclear orphan 1	0000077 // DNA damage checkpoint // inferred from electronic annotation//0000725 // recombinational repair // inferred from
1428061_at[107]	0.004864	-1.26	-1.11	NM_010072//NM_009628	Dpm1//Adnp	dolichol-phosphate (beta-D) mannosyltransferase 1//activity-dependent	0006486 // protein glycosylation // inferred from electronic annotation//0006506 // GPI anchor biosynthetic process // inferred from
1428069_at[1442]	0.001512	-1.26	2.25	NM_145588//XM_006507201	Klf22	kinase family member 22	0006281 // DNA repair // inferred from electronic annotation//0007018 // microtubule-based movement // inferred from electronic
1428074_at[1432]	0.003307	-1.26	-1.20	NM_018753//XM_006499909	Ywhab	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, LIM domains containing 1	0006605 // protein targeting // inferred from direct assay//00035308 // negative regulation of protein dephosphorylation // not
1428077_at[721]	0.002138	-1.26	1.10	NM_013860//XM_006512151	Limd1	LIM domains containing 1	0001666 // response to hypoxia // not recorded//0002076 // osteoblast development // inferred from mutant phenotype//0006351 //
1428082_at[433]	0.008668	-1.26	2.15	NM_021050//XM_006504977	Gtf	cystic fibrosis transmembrane conductance regulator	0006200 // ATP catabolic process // inferred from electronic annotation//0006695 // cholesterol biosynthetic process // inferred from
1428097_at[1444]	0.004811	-1.26	1.14	NM_019647//XM_001480280	Gm10045//Gm11703//Gm1365	predicted pseudogene 10045//predicted gene 11703//predicted gene	0006412 // translation // inferred from electronic annotation
1428258_at[702]	0.004583	-1.26	-1.33	NM_001276358//NM_030716	Kcnip2	Kv channel-interacting protein 2	0006810 // transport // inferred from electronic annotation//0006811 // ion transport // inferred from electronic annotation//0006813
1428283_at[741]	0.005975	-1.26	-1.27	NM_010480//XM_006515485	Hsp90aa1	heat shock protein 90, alpha (cytosolic), class A member 1	0001764 // neuron migration // not recorded//0003009 // skeletal muscle contraction // inferred from electronic annotation//0006200
1428286_at[1432]	0.001383	-1.26	2.30	NM_023209//XM_006519257	Pbk	PDZ binding kinase	0001937 // negative regulation of protein phosphorylation // inferred from mutant phenotype//0006468 // protein phosphorylation //
1428306_at[747]	0.002908	-1.26	-1.12	NM_020582	Atp5j2//AK164124	ATP synthase, H ⁺ transporting, mitochondrial F0 complex, subunit F2//Mus	0006200 // ATP catabolic process // not recorded//0006754 // ATP biosynthetic process // inferred from electronic
1428327_at[1452]	0.001564	-1.26	1.07	NM_001160235//NM_001160	Fam168b	family with sequence similarity 168, member B	
1428346_at[231]	0.001436	-1.27	1.91	NM_001285997//NM_001285	Prc1	protein regulator of cytokinesis 1	0000226 // microtubule cytoskeleton organization // inferred from electronic annotation//0000910 // cytokinesis // not
1428358_at[1422]	0.007352	-1.27	1.01	NM_025709//XM_006498231	Gapvd1	GTPase activating protein and VPS9 domains 1	0006897 // endocytosis // inferred from electronic annotation//0007165 // signal transduction // inferred from electronic
1428368_at[1422]	0.008318	-1.27	-1.08	NM_001145804//NM_175294	Nucks1	nuclear casein kinase and cyclin-dependent kinase substrate 1	
1428372_at[769]	0.005670	-1.27	-1.59	NM_009846	Cd24a	CD24a antigen	0001666 // response to hypoxia // inferred from sequence or structural similarity//0001775 // cell activation // inferred from sequence
1428394_at[227]	0.001490	-1.28	2.31	NM_011369	Shcbp1	Shc SH2-domain binding protein 1	0008543 // fibroblast growth factor receptor signaling pathway // inferred from mutant phenotype//0000177 // regulation of neural
1428492_at[1452]	0.003455	-1.28	1.10	NM_011919//XM_006508802	Ing1	inhibitor of growth family, member 1	0006606 // protein import into nucleus // inferred from mutant phenotype//0007049 // cell cycle // inferred from electronic
1428500_at[1451]	0.000467	-1.28	2.23	NM_024245//XM_006511452	Klf23	kinase family member 23	0000910 // cytokinesis // not recorded//0007018 // microtubule-based movement // inferred from electronic annotation//0007049 //
1428505_at[663]	0.008611	-1.28	1.03	NM_017463	Pbx2	pre B cell leukemia homeobox 2	0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 // regulation of transcription, DNA-templated
1428510_at[1452]	0.001582	-1.29	-1.04	NM_001160229//NM_031494	Zfp275	zinc finger protein 275	0006355 // regulation of transcription, DNA-templated // inferred from electronic annotation
1428577_at[1422]	0.006866	-1.29	1.10	NM_001190258//NM_027015	Rps27//Rps27rt	ribosomal protein S27//ribosomal protein S27, retrogene	0006412 // translation // inferred from electronic annotation
1428580_at[109]	0.002620	-1.29	1.04	NM_009084//NR_030451	Rpl37a//Mir682	ribosomal protein L37a//microRNA 682	0006412 // translation // inferred from electronic annotation

Table S6

Gene_ID	p (Corr)	FC-RSV 1 d	FC-RSV 5 d	RefSeq Transcript ID	Gene Symbol	Gene Title	Gene Ontology Biological Process
1428666_at,145	0.002689	-1.29	-1.06	NM_025842///NM_152234	<i>Ubp1n1</i>	ubiquitin 1	0006289 // nucleotide-excision repair // inferred from electronic annotation///00031396 // regulation of protein ubiquitination // not
1428709_a_at,6	0.008268	-1.29	1.02	NM_009930	<i>Cal3a1</i>	collagen, type III, alpha 1	0001501 // skeletal system development // inferred from electronic annotation///0001568 // blood vessel development // inferred from
1428772_at,142	0.009144	-1.29	1.06	NM_001161369///NM_001161	<i>Scs18</i>	synovial sarcoma translocation, Chromosome 18	0000226 // microtubule cytoskeleton organization // inferred from direct assay///0000902 // cell morphogenesis // inferred from direct
1428776_at,757	0.002458	-1.29	-1.21	NM_024186///NM_024272///X	<i>Scs2</i>	single-stranded DNA binding protein 2	0006351 // transcription, DNA-templated // inferred from electronic annotation///0006355 // regulation of transcription, DNA-templated
1428786_at,142	0.007181	-1.29	1.10	NM_001190258///NM_027015	<i>Rps27r1/Rps27rt</i>	ribosomal protein S27///ribosomal protein S27, retrogene	0006412 // translation // inferred from electronic annotation
1428835_at,719	0.004753	-1.30	-1.20	NM_010771	<i>Matr3</i>	matrin 3	
1428838_a_at,14	0.005199	-1.30	-1.10	NM_181594///XM_006530901	<i>Edc4</i>	enhancer of mRNA decapping 4	0003351 // epithelial cilium movement // inferred from mutant phenotype///0007283 // spermatogenesis // inferred from mutant
1428843_at,143	0.002754	-1.30	-1.11	NM_172639///XM_006527006	<i>Dpdc</i>	deleted in primary ciliary dyskinesia	0033617 // mitochondrial respiratory chain complex IV assembly // not recorded
1428847_a_at,14	0.001468	-1.30	-1.11	NM_183256///XM_003945320	<i>Cox14//LOC101055854</i>	cytochrome c oxidase assembly protein 14//cytochrome c oxidase assembly	0006810 // transport // inferred from electronic annotation///0006886 // intracellular protein transport // inferred from electronic
1429005_at,143	0.003455	-1.30	-1.01	NM_001102423///NM_001102	<i>Stx16</i>	syntaxin 16	0006897 // endocytosis // inferred from electronic annotation///0006898 // receptor-mediated endocytosis // inferred from direct
1429244_at,330	0.004117	-1.31	-1.04	NM_008512	<i>Lrp1</i>	low density lipoprotein receptor-related protein 1	0006351 // transcription, DNA-templated // inferred from electronic annotation///0006355 // regulation of transcription, DNA-templated
1429321_at,677	0.005953	-1.31	1.21	NM_026570	<i>Yeats4</i>	YEATS domain containing 4	0006351 // transcription, DNA-templated // inferred from electronic annotation///0006355 // regulation of transcription, DNA-templated
1429370_a_at,14	0.001575	-1.31	1.02	NM_001166033///NM_172977	<i>Gtf3c4</i>	general transcription factor IIIC, polypeptide 4	0006351 // transcription, DNA-templated // inferred from electronic annotation///0006355 // regulation of transcription, DNA-templated
1429379_at,145	0.000914	-1.31	-1.29	NM_009201///XM_006539695	<i>Sic1a5</i>	solute carrier family 1 (neutral amino acid transporter), member 5	0003333 // amino acid transmembrane transport // inferred from direct assay///0003333 // amino acid transmembrane transport // not
1429562_at,142	0.002971	-1.32	-1.38	NM_025609///XM_006521259	<i>Tab1</i>	TGF-beta activated kinase 1/MAP3K7 binding protein 1	0000185 // activation of MAPKKK activity // inferred from mutant phenotype///0001701 // in utero embryonic development // inferred
1429568_x_at,14	0.006413	-1.32	-1.21	NM_175114///XM_006512221	<i>Trak1</i>	trafficking protein, kinesin binding 1	0006357 // regulation of transcription from RNA polymerase II promoter // inferred from sequence or structural similarity///0006493 //
1429707_at,143	0.005690	-1.32	-1.28	NM_001164198///NM_001164	<i>Prkab</i>	protein kinase, cAMP dependent, catalytic, beta	0001843 // neural tube closure // inferred from genetic interaction///0006468 // protein phosphorylation // inferred from direct
1429907_at,144	0.009162	-1.32	-1.04	NM_172866///XM_006537909	<i>Rgp1</i>	RGP1 retrograde golgi transport homolog (S. cerevisiae)	
1430332_a_at,14	0.007702	-1.33	-1.06	NM_027862///XM_006534254	<i>Atp5h</i>	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit D	0006200 // ATP catabolic process // not recorded///0006810 // transport // inferred from electronic annotation///0006811 // ion
1430447_x_at,14	0.005659	-1.33	1.76	NM_146171///XM_006506531	<i>Ncapd2</i>	non-SMC condensin I complex, subunit D2	0007049 // cell cycle // inferred from electronic annotation///0007067 // mitotic nuclear division // inferred from electronic
1430526_a_at,14	0.005812	-1.33	1.06	NM_025597	<i>Nduf3b</i>	NADH dehydrogenase (ubiquinone) 1 beta subcomplex 3	0006810 // transport // inferred from electronic annotation///0002900 // electron transport chain // inferred from electronic
1430700_a_at,12	0.003602	-1.33	-1.13	NM_147776	<i>Vwv1</i>	von Willebrand factor A domain containing 1	0030198 // extracellular matrix organization // inferred from direct assay///0030198 // extracellular matrix organization // inferred from
1430718_s_at,14	0.004195	-1.33	1.22	NM_012047///XM_006531046	<i>Brd7</i>	bromodomain containing 7	0006351 // transcription, DNA-templated // inferred from electronic annotation///0006355 // regulation of transcription, DNA-templated
1430912_a_at,12	0.007989	-1.33	-1.25	NM_001033489///XM_006539	<i>Rnf207</i>	ring finger protein 207	
1430989_a_at,14	0.005747	-1.34	-1.04	NM_016721///XM_006540950	<i>Igapp1//LOC102641119</i>	IQ motif containing GTPase activating protein 1//uncharacterized	0001817 // regulation of cytokine production // inferred from mutant phenotype///0007165 // signal transduction // inferred from
1431008_at,145	0.001570	-1.34	1.23	NM_013454///XM_006537554	<i>Abca1</i>	ATP-binding cassette, sub-family A (ABC1), member 1	0002790 // peptide secretion // inferred from mutant phenotype///0006200 // ATP catabolic process // not recorded///0006497 //
1431008_at,145	0.001570	-1.34	1.15	NM_001163766///NM_134124	<i>Wdr90</i>	WD repeat domain 90	
1431008_at,145	0.001570	-1.35	1.02	NM_001012477///NM_013655	<i>Cxcl12</i>	chemokine (C-X-C motif) ligand 12	0001569 // patterning of blood vessels // inferred from mutant phenotype///0001666 // response to hypoxia // inferred from electronic
1431032_at,143	0.002918	-1.35	-1.05	NM_011251///NM_029169///X	<i>Rbm6</i>	RNA binding motif protein 6	
1431055_a_at,14	0.001511	-1.35	1.22	NM_026616	<i>Rnaseh2c</i>	ribonuclease H2, subunit C	0006401 // RNA catabolic process // not recorded
1431057_x_at,14	0.003991	-1.35	1.21	NM_025587///XM_006500702	<i>Gm5963//Rps21</i>	predicted pseudogene 5963///ribosomal protein S21	0000447 // endonucleolytic cleavage in ITS1 to separate SSU-rRNA from 5.8S rRNA and LSU-rRNA from tricornicrRNA transcript (SSU-
1431336_at,145	0.002727	-1.35	1.06	NM_134089///XM_006520238	<i>Scrib</i>	scribbled homolog (Drosophila)	0001843 // neural tube closure // inferred from mutant phenotype///0001843 // neural tube closure // not recorded///0001921 //
1431359_x_at,6	0.001533	-1.36	-1.13	NM_001290696///NM_172699	<i>Foxj3</i>	forkhead box J3	0000122 // negative regulation of transcription from RNA polymerase II promoter // --//0006351 // transcription, DNA-templated //
1431423_x_at,14	0.005161	-1.36	-1.44	NM_008095///XM_006504279	<i>Gbas</i>	glioblastoma amplified sequence	0005119 // oxidative phosphorylation // not recorded///0006754 // ATP biosynthetic process // not recorded///0000984 // negative
1431464_a_at,14	0.003830	-1.36	-1.35	NM_009447///XM_006496478	<i>Tuba4a</i>	tubulin, alpha 4A	0006384 // GTP catabolic process // inferred from electronic annotation///0007017 // microtubule-based process // inferred from
1431554_x_at,7	0.006864	-1.36	1.23	NM_027288///XM_006500908	<i>Manba</i>	mannosidase, beta A, lysosomal	0005975 // carbohydrate metabolic process // inferred from electronic annotation///0006516 // glycoprotein catabolic process //
1431591_s_at,14	0.000658	-1.36	1.04	NM_001205214///NM_001205	<i>Rxb1</i>	retinoid X receptor beta	0001701 // in utero embryonic development // inferred from genetic interaction///0001893 // maternal placenta development //
1431591_s_at,11	0.000789	-1.36	-1.13	NM_019743///NM_893519	<i>Gm6910//Rybp</i>	predicted gene 6910//RING1 and YY1 binding protein	0000122 // negative regulation of transcription from RNA polymerase II promoter // inferred from direct assay///0006351 //
1431705_a_at,6	0.004267	-1.37	-1.09	NM_133804///XM_006527503	<i>Tmem132a</i>	transmembrane protein 132A	0043069 // negative regulation of programmed cell death // not recorded
1431724_a_at,7	0.008329	-1.37	1.12	NM_011438	<i>Sox12</i>	SRV (sex determining region Y)-box 12	0006351 // transcription, DNA-templated // inferred from electronic annotation///0006355 // regulation of transcription, DNA-templated
1431808_a_at,11	0.000296	-1.37	-1.09	NR_033626	<i>1810010001Rik</i>	RIKEN cDNA 1810010001 gene	0006810 // transport // inferred from electronic annotation///0006811 // ion transport // inferred from electronic annotation///0006816
1431822_a_at,14	0.002923	-1.37	1.74	NM_001190333///NM_001190	<i>Ccr6</i>	chemokine (C-C motif) receptor 6	0006935 // chemotaxis // inferred from electronic annotation///0006955 // immune response // inferred from electronic
1431843_a_at,14	0.001958	-1.37	-1.50	NM_00113559///NM_001243	<i>Sox5</i>	SRV (sex determining region Y)-box 5	0001701 // in utero embryonic development // inferred from mutant phenotype///0006351 // transcription, DNA-templated // inferred
1431890_a_at,14	0.006230	-1.37	-1.04	NM_001081359///NM_001112	<i>Ubr5</i>	ubiquitin protein ligase E3 component n-recognin 5	0000209 // protein polyubiquitination // not recorded///0006281 // DNA repair // inferred from electronic annotation///0006974 //
1431995_at,145	0.000268	-1.38	-1.12	NM_001289477///NM_001289	<i>Papss1</i>	3'-phosphoadenosine 5'-phosphosulfate synthase 1	0000103 // sulfate assimilation // inferred from electronic annotation///0008152 // metabolic process // inferred from electronic
1432235_at,145	0.001698	-1.38	-2.50	NM_001281845///NM_013473	<i>Anxa8</i>	annexin A8	0007596 // blood coagulation // inferred from electronic annotation///0007599 // hemostasis // inferred from electronic annotation
1432466_a_at,1	0.008259	-1.38	-1.04	NM_021494///XM_006507463	<i>Dendd5a</i>	DENN/MADD domain containing 5A	0032313 // regulation of Rab GTPase activity // not recorded///0032851 // positive regulation of Rab GTPase activity // --//0032851 //
1433448_at,143	0.002358	-1.38	-1.24	NM_026452	<i>Caq9</i>	coenzyme Q9 homolog (yeast)	0006120 // mitochondrial electron transport, NADH to ubiquinone // inferred from mutant phenotype///0006744 // ubiquinone
1433467_at,146	0.002907	-1.38	-1.26	NM_001081979///NM_010788	<i>Mecp2</i>	methyl CpG binding protein 2	0000122 // negative regulation of transcription from RNA polymerase II promoter // not recorded///0001662 // behavioral fear response
1433494_at,143	0.000913	-1.38	1.84	NM_001012335///NM_001012	<i>Mdk</i>	midkine	0001662 // behavioral fear response // inferred from mutant phenotype///0007275 // multicellular organismal development // inferred
1433504_at,110	0.004217	-1.38	-1.08	NM_011273	<i>Xpr1</i>	xenotropic and polytropic retrovirus receptor 1	0009615 // response to virus // inferred from direct assay///0009615 // response to virus // not recorded
1433519_at,144	0.005243	-1.38	-1.09	NM_001081080///NM_025871	<i>Phf3</i>	PHD finger protein 3	0006351 // transcription, DNA-templated // inferred from electronic annotation
1433549_x_at,14	0.008570	-1.38	2.08	NM_025806///XM_006506485	<i>Pib1d1</i>	phospholipase B domain containing 1	0006629 // lipid metabolic process // inferred from electronic annotation///0016042 // lipid catabolic process // inferred from electronic
1433549_x_at,14	0.008570	-1.39	-1.01	NM_001166553///NM_028862	<i>Rnf145</i>	ring finger protein 145	
1433565_at,144	0.006460	-1.39	-1.16	NM_001164729///NM_001290	<i>Prickle4//Tomm6</i>	prickle homolog 4 (Drosophila)//translocase of outer mitochondrial	0006810 // transport // inferred from electronic annotation///0015031 // protein transport // inferred from electronic annotation
1433706_a_at,14	0.005137	-1.39	-1.28	NM_009483///XM_006527594	<i>Kdm6a</i>	lysine (K)-specific demethylase 6A	0001701 // in utero embryonic development // inferred from mutant phenotype///0001843 // neural tube closure // inferred from
1433720_s_at,14	0.000593	-1.40	1.05	NM_018822	<i>Sgsh</i>	N-sulfoglucosamine sulfohydrolase (sulfamidase)	0000152 // metabolic process // inferred from electronic annotation///0030201 // heparan sulfate proteoglycan metabolic process //
1433750_at,145	0.000807	-1.40	3.37	NM_001012272///NM_001012	<i>Birc5</i>	baculoviral IAP repeat-containing 5	0000086 // G2/M transition of mitotic cell cycle // not recorded///0000226 // microtubule cytoskeleton organization // inferred from
1433757_x_at,14	0.002146	-1.40	-1.33	NM_009949	<i>Cpt2</i>	carmitin palmitoyltransferase 2	0006629 // lipid metabolic process // inferred from electronic annotation///0006631 // fatty acid catabolic process // inferred from
1433834_at,144	0.008641	-1.40	1.08	NM_025314	<i>Dtd1</i>	D-tyrosyl-tRNA deacylase 1	0006260 // DNA replication // inferred from electronic annotation///0019478 // D-amino acid catabolic process // inferred from
1433859_at,225	0.001511	-1.41	-1.11	NM_001291233///NM_001291	<i>Cux1</i>	cut-like homeobox 1	0000122 // negative regulation of transcription from RNA polymerase II promoter // inferred from direct assay///0000301 // retrograde
1433918_at,143	0.001646	-1.41	-1.12	NM_001029850///NM_001083	<i>Mag1</i>	membrane associated guanylate kinase, WW and PDZ domain containing 1	0070997 // neuron death // not recorded
1433966_x_at,14	0.006870	-1.41	1.06	NM_001162913///NM_025515	<i>Cdc90b</i>	coiled-coil domain containing 90B	
1434027_x_at,145	0.008184	-1.41	-1.14	NM_001290993///NM_011774	<i>Sic30a4</i>	solute carrier family 30 (zinc transporter), member 4	0006810 // transport // inferred from electronic annotation///0006811 // ion transport // inferred from electronic annotation///0006812
1434066_at,143	0.003001	-1.41	1.05	NM_001111059///NM_133654	<i>Cd34</i>	CD34 antigen	0001894 // tissue homeostasis // not recorded///0001935 // endothelial cell proliferation // not recorded///0003094 // glomerular
1434099_at,143	0.002562	-1.41	-1.12	NM_009628///NM_010072	<i>Adnp//Dpm1</i>	activity-dependent neuroprotective protein//dolichol-phosphate (beta-D)	0006351 // transcription, DNA-templated // inferred from electronic annotation///0006355 // regulation of transcription, DNA-templated
1434261_at,244	0.002436	-1.41	-3.33	NM_009700///XM_006525540	<i>Aqp4</i>	aquaporin 4	0006810 // transport // inferred from electronic annotation///0006833 // water transport // inferred from direct assay///0006833 //
1434273_at,100	0.001221	-1.41	1.05	NM_001042491///NM_001289	<i>Anapc5</i>	anaphase-promoting complex subunit 5	0007049 // cell cycle // inferred from electronic annotation///0007067 // mitotic nuclear division // inferred from electronic
1434320_at,143	0.006618	-1.41	-1.01	NM_001039138///NM_001039	<i>Camk2g</i>	calcium/calmodulin-dependent protein kinase II gamma	0000082 // G1/S transition of mitotic cell cycle // inferred from mutant phenotype///0001666 // response to hypoxia // not
1434330_at,145	0.000196	-1.41	-1.26	NM_013541	<i>Gstp1</i>	glutathione S-transferase, pi 1	0000302 // response to reactive oxygen species // inferred from direct assay///0002674 // negative regulation of acute inflammatory
1434335_at,144	0.007350	-1.41	-1.01	NM_146168///XM_006505951	<i>Vopp1</i>	vesicular, overexpressed in cancer, pro-survival protein 1	0006351 // transcription, DNA-templated // inferred from electronic annotation///0006355 // regulation of transcription, DNA-templated
1434372_at,107	0.003694	-1.41	-1.08	NM_011385///XM_006538685	<i>Ski</i>	ski sarcoma viral oncogene homolog (avian)	0000122 // negative regulation of transcription from RNA polymerase II promoter // inferred from genetic interaction///0000122 //
1434392_at,143	0.000914	-1.42	1.48	NM_007681///XM_006503708	<i>Cenpa</i>	centromere protein A	0000132 // establishment of mitotic spindle orientation // not recorded///0006334 // nucleosome assembly // inferred from electronic
1434484_at,66	0.001021	-1.42	-1.96	NM_007981///XM_006509262	<i>Acs1l</i>	acyl-CoA synthetase long-chain family member 1	0001676 // long-chain fatty acid metabolic process // not recorded///0006629 // lipid metabolic process // inferred from electronic
1434507_at,228	0.005114	-1.42	-1.00	NM_016861	<i>Pdlim1</i>	PDZ and LIM domain 1 (eflin)	0001666 // response to hypoxia // inferred from electronic annotation///0006355 // regulation of transcription, DNA-templated //
1434511_at,102	0.007753	-1.42	-1.31	NM_023831///XM_006510671	<i>Ifi46</i>	intraflagellar transport 46	0007224 // smoothened signaling pathway // inferred from mutant phenotype///0015031 // protein transport // not
1434528_at,239	0.006838	-1.42	-1.13	NM_029272///XM_006514270	<i>Ndufs7</i>	NADH dehydrogenase (ubiquinone) Fe-S protein 7	0006810 // transport // inferred from electronic annotation///0002981 // mitochondrial respiratory chain complex I assembly // not
1434633_at,143	0.002341	-1.42	-1.15	NM_001253813///NM_175344	<i>Ano6</i>	anoctamin 6	0002407 // dendritic cell chemotaxis // inferred from mutant phenotype///0002543 // activation of blood coagulation via clotting

Table S6

Gene_ID	p (Corr)	FC-RSV 1 d	FC-RSV 5 d	RefSeq Transcript ID	Gene Symbol	Gene Title	Gene Ontology Biological Process
1434690_at[225]	0.003763	-1.43	-1.38	NM_001081330//NM_177617	<i>Dnah2</i>	dynein, axonemal, heavy chain 2	0001539 // cilium or flagellum-dependent cell motility // inferred from electronic annotation//0006200 // ATP catabolic process //
1434695_at[145]	0.003594	-1.43	-1.32	NM_175467//NM_006499295	<i>Sptlc3</i>	serine palmitoyltransferase, long chain base subunit 3	0006629 // lipid metabolic process // inferred from electronic annotation//0006665 // sphingolipid metabolic process // inferred from
1434709_at[143]	0.005097	-1.43	-1.10	NM_0191771	<i>Dstn</i>	desmin	0000910 // cytokinesis // inferred from mutant phenotype//0006928 // cellular component movement // inferred from mutant
1434735_at[143]	0.002338	-1.43	-1.01	NM_007725	<i>Cnn2</i>	calponin 2	0010628 // positive regulation of gene expression // inferred from mutant phenotype//0030097 // hemopoiesis // inferred from mutant
1434748_at[809]	0.004338	-1.43	1.11	NM_001197046//NM_201230	<i>Fgfr10p</i>	Fgfr1 oncogene partner	0006469 // negative regulation of protein kinase activity // not recorded//0008284 // positive regulation of cell proliferation // not
1434772_at[145]	0.006413	-1.43	1.22	NM_145607//NM_006530965	<i>Tctc13</i>	tetratricopeptide repeat domain 13	
1434859_at[145]	0.003821	-1.43	1.77	NM_001081363//NM_006497	<i>Cenpf</i>	centromere protein F	0000085 // mitotic G2 phase // not recorded//0000087 // mitotic M phase // not recorded//0000278 // mitotic cell cycle // not
1434866_x_at[14]	0.002971	-1.43	-1.09	NM_001293559//NM_009941	<i>Cox4l1</i>	cytochrome c oxidase subunit IV isoform 1	0007584 // response to nutrient // inferred from electronic annotation//1902600 // hydrogen ion transmembrane transport // inferred
1434888_a_at[14]	0.008420	-1.44	-1.06	NM_001286158//NM_027326	<i>MLL3</i>	myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, 5-adenosylmethionine decarboxylase 1	0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 // regulation of transcription, DNA-templated
1434930_at[145]	0.002665	-1.44	-1.02	NM_009665	<i>Amd1</i>	S-adenosylmethionine decarboxylase 1	0001701 // in utero embryonic development // inferred from mutant phenotype//0006557 // S-adenosylmethionine biosynthetic
1434931_at[144]	0.008611	-1.44	-1.18	NM_011871	<i>Prkra</i>	protein kinase, interferon inducible double stranded RNA dependent	0006468 // protein phosphorylation // inferred from direct assay//0008284 // positive regulation of cell proliferation // not
1435026_at[145]	0.007312	-1.44	-1.36	NM_001001326//NM_029811	<i>St5</i>	suppression of tumorigenicity 5	0032313 // regulation of Rab GTPase activity // not recorded//0032851 // positive regulation of Rab GTPase activity // inferred from
1435110_at[145]	0.004310	-1.44	1.06	NM_178772	<i>Nceh1</i>	neutral cholesterol ester hydrolase 1	0006470 // protein dephosphorylation // inferred from direct assay//0006629 // lipid metabolic process // inferred from electronic
1435239_at[144]	0.006815	-1.45	-1.27	NM_001199484//NM_001199	<i>4931406C07Rik</i>	RIKEN cDNA 4931406C07 gene	0008152 // metabolic process // not recorded
1435272_at[144]	0.000556	-1.45	-1.73	NM_001077348//NM_025874	<i>Plin5</i>	perilipin 5	0006629 // lipid metabolic process // inferred from electronic annotation//0010867 // positive regulation of triglyceride biosynthetic
1435290_x_at[14]	0.001408	-1.45	-1.33	NM_001033287//NM_008976	<i>Ptpn14</i>	protein tyrosine phosphatase, non-receptor type 14	0001946 // lymphangiogenesis // inferred from mutant phenotype//0001946 // lymphangiogenesis // not recorded//0006351 //
1435330_at[143]	0.001408	-1.45	1.02	NM_028410//NM_006508223	<i>Prkr</i>	protein-kinase, interferon-inducible double stranded RNA dependent	0016310 // phosphorylation // inferred from electronic annotation
1435335_x_at[14]	0.003563	-1.45	-1.26	NM_001136260//NM_001197	<i>Slc4a4</i>	solute carrier family 4 (anion exchanger), member 4	0006810 // transport // inferred from electronic annotation//0006811 // ion transport // inferred from electronic annotation//0006814
1435362_at[143]	0.004921	-1.46	-1.12	NM_001025432//NM_006521	<i>Crebbp</i>	CREB binding protein	0000122 // negative regulation of transcription from RNA polymerase II promoter // not recorded//0006351 // transcription, DNA-
1435375_at[144]	0.003716	-1.46	-1.01	NM_138748//NM_006497608	<i>Ppp2r4</i>	protein phosphatase 2A activator, regulatory subunit B	0000413 // protein peptidyl-prolyl isomerization // not recorded//0006200 // ATP catabolic process // not recorded//0006457 //
1435394_x_at[14]	0.002983	-1.46	-1.16	NM_011078//NM_006516880	<i>Phf2</i>	PHD finger protein 2	0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 // regulation of transcription, DNA-templated
1435420_at[232]	0.002492	-1.46	-1.03	NM_145625	<i>Eif4b</i>	eukaryotic translation initiation factor 4B	0006412 // translation // inferred from electronic annotation//0006413 // translational initiation // inferred from electronic annotation
1435454_a_at[2]	0.009832	-1.46	-1.14	NM_172606	<i>6-Mar</i>	membrane-associated ring finger (C3HC4) 6	0016567 // protein ubiquitination // inferred from electronic annotation//0070936 // protein K48-linked ubiquitination // not recorded
1435476_a_at[14]	0.003941	-1.47	-1.07	NM_001081379//NR_037865	<i>Ankrd11</i>	ankyrin repeat domain 11	0001701 // in utero embryonic development // inferred from mutant phenotype//0001894 // tissue homeostasis // inferred from
1435518_at[143]	0.008682	-1.47	1.02	NM_134054	<i>Sptssa</i>	serine palmitoyltransferase, small subunit A	0006629 // lipid metabolic process // inferred from electronic annotation//0006665 // sphingolipid metabolic process // inferred from
1435524_at[144]	0.004195	-1.47	1.10	NM_019435//NM_006527554	<i>Ndufb11</i>	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 11	0006810 // transport // inferred from electronic annotation//0055114 // oxidation-reduction process // inferred from electronic
1435551_at[225]	0.005202	-1.47	-1.08	NM_145488	<i>Pex6</i>	peroxisomal biogenesis factor 6	0006200 // ATP catabolic process // not recorded//0006625 // protein targeting to peroxisome // not recorded//0007031 //
1435572_at[143]	0.000461	-1.47	-1.05	NM_025347//NM_026875//Xp	<i>Ypel3</i>	yippe-like 3 (Drosophila)	0006915 // apoptotic process // inferred from electronic annotation
1435622_at[154]	0.006839	-1.47	-1.09	NM_026993//NM_006502024	<i>Ddah1</i>	dimethylarginine dimethylaminohydrolase 1	0000052 // citrulline metabolic process // not recorded//0003073 // regulation of systemic arterial blood pressure // inferred from
1435725_x_at[11]	0.005670	-1.47	-1.06	NM_146131//NM_00650123	<i>Bxp1p</i>	pre B cell leukemia transcription factor interacting protein 1	0045892 // negative regulation of transcription, DNA-templated // inferred from electronic annotation
1435725_x_at[11]	0.005670	-1.47	-1.17	NM_174847//NM_006522974	<i>C2cd2</i>	C2 calcium-dependent domain containing 2	
1435946_at[143]	0.002981	-1.47	1.04	NM_152801//NM_006528313	<i>Arhgef6</i>	Rac/Cdc42 guanine nucleotide exchange factor (GEF) 6	0030032 // lamellipodium assembly // inferred from mutant phenotype//0032321 // positive regulation of Rho GTPase activity //
1436026_at[144]	0.004543	-1.47	-1.08	NM_021523//NM_006528933	<i>Huwei1</i>	HECT, UBA and WWE domain containing 1	0000209 // protein polyubiquitination // not recorded//0006281 // DNA repair // inferred from electronic annotation//0006284 // base-
1436032_at	0.009324	-1.48	-1.01	NM_001168304//NM_001291	<i>Cdk19</i>	cyclin-dependent kinase 19	0006468 // protein phosphorylation // inferred from electronic annotation//0007049 // cell cycle // inferred from electronic
1436172_at[145]	0.007312	-1.48	-1.15	NM_145359	<i>Ubold1</i>	UBA-like domain containing 1	
1436269_s_at[14]	0.006007	-1.48	-1.12	NM_001252313//NM_0011308	<i>Ncor1</i>	nuclear receptor co-repressor 1	0000122 // negative regulation of transcription from RNA polymerase II promoter // inferred from genetic interaction//0000122 //
1436277_at[144]	0.007613	-1.48	1.01	NM_011680//NM_006539733	<i>Usf2</i>	upstream transcription factor 2	0000432 // positive regulation of transcription from RNA polymerase II promoter by glucose // inferred from mutant
1436336_at[329]	0.003312	-1.48	1.13	NM_001029889//NM_006521	<i>Gm608</i>	predicted gene 608	0008152 // metabolic process // inferred from electronic annotation
1436339_at[144]	0.009796	-1.48	-1.24	NM_029436//NM_006522687	<i>Klhl24</i>	kelch-like 24	
1436344_at[143]	0.001640	-1.49	-1.10	NM_001160219//NM_001160	<i>Pum2</i>	pumilio RNA-binding family member 2	0006417 // regulation of translation // inferred from electronic annotation//0034063 // stress granule assembly // inferred from direct
1436542_at	0.006369	-1.49	-1.04	NM_028399	<i>Ccnt2</i>	cyclin T2	0000079 // regulation of cyclin-dependent protein serine/threonine kinase activity // inferred from electronic annotation//0006351 //
1436699_x_at[14]	0.004646	-1.49	-1.08	NM_016919//NM_006510487	<i>Col5a3</i>	collagen, type V, alpha 3	0007160 // cell-matrix adhesion // inferred from direct assay//0030198 // extracellular matrix organization // inferred from sequence or
1436736_x_at[14]	0.000335	-1.49	-1.02	NM_175274//NM_006504768	<i>Ttyh3</i>	twenty homolog 3 (Drosophila)	0006810 // transport // inferred from electronic annotation//0006811 // ion transport // inferred from electronic annotation//0006821
1436790_x_at[14]	0.004849	-1.49	-1.30	NM_013868	<i>Hspb7</i>	heat shock protein family, member 7 (cardiovascular)	0006950 // response to stress // inferred from electronic annotation//0009408 // response to heat // not recorded
1436955_at[144]	0.007856	-1.50	-1.18	NM_009547//NM_006524212	<i>Zbtb14</i>	zinc finger and BTB domain containing 14	0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 // regulation of transcription, DNA-templated
1436956_at	0.008819	-1.50	-1.04	NM_010585//NM_006505623	<i>Itpr</i>	inositol 1,4,5-trisphosphate receptor 1	0001666 // response to hypoxia // inferred from direct assay//0001666 // response to hypoxia // not recorded//0006810 // transport //
1437044_x_at[14]	0.007926	-1.50	-1.15	NM_001002764	<i>Smpg6</i>	Smp-6 homolog, nonsense mediated mRNA decay factor (C. elegans)	0000184 // nuclear-transcribed mRNA catabolic process, nonsense-mediated decay // not recorded//0000723 // telomere maintenance
1437082_at[145]	0.008014	-1.50	-1.77	NM_144828	<i>Ppp1r1b</i>	protein phosphatase 1, regulatory (inhibitor) subunit 1B	0001975 // response to amphetamine // inferred from genetic interaction//0006351 // transcription, DNA-templated // inferred from
1437103_at[143]	0.001404	-1.51	1.20	NM_008250	<i>Hlx</i>	H2.0-like homeobox	0001889 // liver development // inferred from mutant phenotype//0006351 // transcription, DNA-templated // inferred from electronic
1437111_at	0.008829	-1.51	-1.15	NM_007790	<i>Smc3</i>	structural maintenance of chromosomes 3	0006275 // regulation of DNA replication // not recorded//0006281 // DNA repair // inferred from electronic annotation//0006974 //
1437195_x_at[14]	0.004199	-1.51	-1.07	NM_027342	<i>Fam162a</i>	family with sequence similarity 162, member A	0006915 // apoptotic process // inferred from electronic annotation//0006919 // activation of cysteine-type endopeptidase activity //
1437288_at[143]	0.006015	-1.51	-1.14	NM_013889//NM_006537977	<i>Zfp292</i>	zinc finger protein 292	0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 // regulation of transcription, DNA-templated
1437423_a_at[2]	0.004235	-1.51	-1.11	NM_001290414//NM_001290	<i>Fgf13</i>	fibroblast growth factor 13	0000165 // MAPK cascade // not recorded//0001764 // neuron migration // inferred from mutant phenotype//0006915 // apoptotic
1437510_x_at[14]	0.000939	-1.52	-1.31	NM_032008//NM_006519724	<i>Slmap</i>	scarlemma associated protein	
1437510_x_at[14]	0.001575	-1.52	-1.25	NM_001164572//NM_133741	<i>Snrk</i>	SNF related kinase	0006468 // protein phosphorylation // not recorded//0016310 // phosphorylation // inferred from electronic annotation
1437667_a_at[14]	0.009766	-1.52	2.23	NM_009828	<i>Ccna2</i>	cyclin A2	0000079 // regulation of cyclin-dependent protein serine/threonine kinase activity // inferred from electronic annotation//0007049 //
1437709_x_at[14]	0.009788	-1.52	-1.21	NR_024329	<i>2900097C17Rik</i>	RIKEN cDNA 2900097C17 gene	0006629 // lipid metabolic process // inferred from electronic annotation//0016042 // lipid catabolic process // inferred from electronic
1437917_at[968]	0.000939	-1.52	-1.03	NM_001165954//NM_001165	<i>Phc3</i>	polyhomoeitic-like 3 (Drosophila)	0007275 // multicellular organismal development // inferred from electronic annotation
1438070_at[145]	0.001715	-1.52	-1.18	NM_001164159//NM_028999	<i>Ppp6r3</i>	protein phosphatase 6, regulatory subunit 3	0043666 // regulation of phosphoprotein phosphatase activity // not recorded
1438097_at[193]	0.005884	-1.52	-1.28	NM_019827//NM_006522425	<i>Gsk3b</i>	glycogen synthase kinase 3 beta	0000320 // re-entry into mitotic cell cycle // inferred from direct assay//0001837 // epithelial to mesenchymal transition // not
1438115_x_at[14]	0.004335	-1.53	-1.04	NM_133674//NM_006506387	<i>Arhgef5</i>	Rho guanine nucleotide exchange factor (GEF) 5	0002408 // myeloid dendritic cell chemotaxis // inferred from mutant phenotype//0030036 // actin cytoskeleton organization //
1438245_at	0.000412	-1.53	1.08	NM_181421//NM_006530351	<i>Gm15800</i>	predicted gene 15800	0008152 // metabolic process // inferred from electronic annotation//0016567 // protein ubiquitination // inferred from electronic
1438527_at[144]	0.001823	-1.53	-1.25	NM_001037155//NM_001185	<i>Wnk1</i>	WNK lysine deficient protein kinase 1	0003084 // positive regulation of systemic arterial blood pressure // inferred from mutant phenotype//0006468 // protein
1438527_at[144]	0.001823	-1.53	-1.01	NM_001012518//NM_001109	<i>Ehmt1</i>	ehmt1 homolog, nonsense mediated mRNA decay factor (C. elegans)	0000122 // negative regulation of transcription from RNA polymerase II promoter // inferred from mutant phenotype//0006306 // DNA
1438676_at[144]	0.000285	-1.53	1.09	NM_001159392//NM_009395	<i>Tnfrsf1p</i>	tumor necrosis factor, alpha-induced protein 1 (endothelial)	0006260 // DNA replication // not recorded//0006955 // immune response // inferred from sequence or structural similarity//0006955
1438712_at[145]	0.005225	-1.54	1.06	NM_001083891//NM_030087	<i>Ndufb3</i>	NADH dehydrogenase (ubiquinone) flavoprotein 3	0006810 // transport // inferred from electronic annotation//0055114 // oxidation-reduction process // inferred from electronic
1438716_at[145]	0.001024	-1.54	1.41	NM_025951//NM_028744//Xp	<i>PI4K2b</i>	phosphatidylinositol 4-kinase type 2 beta	0016310 // phosphorylation // inferred from electronic annotation//0046854 // phosphatidylinositol phosphorylation // inferred from
1438717_a_at[14]	0.003281	-1.54	1.20	NM_010806//NM_006523752	<i>MLL4</i>	myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, 5-adenosylmethionine decarboxylase 1	0007155 // cell adhesion // inferred from electronic annotation//0007156 // signal transduction // inferred from electronic annotation
1438758_at[143]	0.000952	-1.54	-1.10	NM_033574//NM_033575//Xp	<i>Pcdhga1</i>	protocadherin gamma subfamily A, 1//protocadherin gamma subfamily A, archaelysin family metalloproteinase 1	0007155 // cell adhesion // inferred from electronic annotation//0007156 // homophilic cell adhesion // traceable author
1438984_x_at[14]	0.002680	-1.54	1.88	NM_173405	<i>Ama1</i>	ama1 homolog, nonsense mediated mRNA decay factor (C. elegans)	0006508 // proteolysis // inferred from electronic annotation
1439018_at[144]	0.005367	-1.54	-1.04	NM_001081071//NM_001177	<i>Lcat1</i>	lysocardiolipin acyltransferase 1	0006629 // lipid metabolic process // inferred from electronic annotation//0007275 // multicellular organismal development // inferred
1439030_at[331]	0.005524	-1.54	-1.50	NM_021477//NM_183188//Xp	<i>Rbfox1</i>	RNA binding protein, fox-1 homolog (C. elegans) 1	0006397 // mRNA processing // inferred from electronic annotation//0008380 // RNA splicing // inferred from electronic
1439049_at[145]	0.005005	-1.54	-1.50	NM_177047	<i>Auts2</i>	autism susceptibility candidate 2	
1439121_at[144]	0.000296	-1.54	-1.01	NM_026598	<i>Ebp1</i>	emopamil binding protein-like	0016125 // sterol metabolic process // inferred from electronic annotation
1439121_at[144]	0.000296	-1.54	-1.22	NM_001205336//NM_139206	<i>Arap3</i>	ArfGAP with RhoGAP domain, ankyrin repeat and PH domain 3	0007165 // signal transduction // inferred from electronic annotation//0008360 // regulation of cell shape // inferred from direct
1439121_at[144]	0.000296	-1.54	1.18	NM_001159529//NM_009187	<i>Cox7a2l</i>	cytochrome c oxidase subunit VIIa polypeptide 2-like	1902600 // hydrogen ion transmembrane transport // inferred from electronic annotation
1439144_at[143]	0.002862	-1.55	-1.12	NM_011221	<i>Purb</i>	purine rich element binding protein B	0006268 // DNA unwinding involved in DNA replication // inferred from sequence or structural similarity//0006351 // transcription, DNA-
1439443_x_at[14]	0.001807	-1.55	-1.08	NM_001077696//NM_001284	<i>Hdca5</i>	histone deacetylase 5	0000122 // negative regulation of transcription from RNA polymerase II promoter // inferred from direct assay//0000122 // negative

Table S6

Gene_ID	p (Corr)	FC-RSV 1 d	FC-RSV 5 d	RefSeq Transcript ID	Gene Symbol	Gene Title	Gene Ontology Biological Process
1439771_s_at[5]	0.005669	-1.55	1.01	NM_145398//XM_006505029	<i>Casd1</i>	CAS1 domain containing 1	
1439771_s_at[11]	0.005669	-1.55	-1.42	NM_027722//XM_006514116	<i>Nudt4</i>	nudix (nucleoside diphosphate linked moiety X)-type motif 4	0008152 // metabolic process // inferred from electronic annotation//0008152 // metabolic process // inferred from sequence or
1440865_at[213]	0.001221	-1.55	-1.31	NM_001167983//NM_172579	<i>Sipa1l1</i>	signal-induced proliferation-associated 1 like 1	0031532 // actin cytoskeleton reorganization // not recorded//0032317 // regulation of Rap GTPase activity // inferred from mutant
1441013_at	0.009319	-1.55	1.05	NM_028839//XM_006519496	<i>Tmem110</i>	transmembrane protein 110	
1441134_at[145]	0.001001	-1.55	-1.04	NM_001037726//NM_009952	<i>Creb1</i>	cAMP responsive element binding protein 1	0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 // regulation of transcription, DNA-templated
14422025_a_at	0.000230	-1.56	-1.22	NM_007405//XM_006520303	<i>Adcy6</i>	adenylate cyclase 6	0006171 // cAMP biosynthetic process // inferred from direct assay//0006171 // cAMP biosynthetic process // not recorded//0006171
1445535_at[101]	0.004060	-1.56	-1.21	NM_028419	<i>Glrx5</i>	glutaredoxin 5 homolog (S. cerevisiae)	0030097 // hemopoiesis // inferred from sequence or structural similarity//0045454 // cell redox homeostasis // inferred from
1445689_at	0.004366	-1.56	-1.12	NM_019864//XM_006511184	<i>Atr</i>	ataxia telangiectasia and Rad3 related	0000077 // DNA damage checkpoint // inferred from mutant phenotype//0000077 // DNA damage checkpoint // not
1446086_s_at[14]	0.008012	-1.56	-1.13	NM_144892//XM_006499368	<i>Ncoa5</i>	nuclear receptor coactivator 5	0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 // regulation of transcription, DNA-templated
1448060_at[144]	0.002826	-1.56	-1.07	NM_001037842//NM_001201	<i>Cmlb3</i>	camello-like 3//predicted gene 11128//predicted gene 4477	0001702 // gastrulation with mouth forming second // non-traceable author statement//0007162 // negative regulation of cell adhesion
1448106_at[676]	0.008943	-1.56	-1.14	NM_022656//XM_006519353	<i>Nisch</i>	nischarin	0006006 // glucose metabolic process // inferred from electronic annotation//0006915 // apoptotic process // inferred from electronic
1448131_at[145]	0.007635	-1.56	-1.16	NM_019739	<i>Foxo1</i>	forkhead box O1	0000122 // negative regulation of transcription from RNA polymerase II promoter // inferred from direct assay//0001568 // blood vessel
1448188_at[145]	0.009998	-1.56	-1.49	NM_011892//XM_006519012	<i>Sqcg</i>	sarcoglycan, gamma (dystrophin-associated glycoprotein)	0061024 // membrane organization // traceable author statement
1448201_at[203]	0.006826	-1.57	-1.29	NM_024200//XM_006535525	<i>Mfn1</i>	mitofusin 1	0006184 // GTP catabolic process // inferred from electronic annotation//0007275 // multicellular organismal development // inferred
1448239_at[153]	0.006015	-1.57	-1.26	NM_018748//XM_006512187	<i>Golga4</i>	golgi autoantigen, golgin subfamily a, 4	0000042 // protein targeting to Golgi // inferred from electronic annotation//0006355 // regulation of transcription, DNA-templated //
1448244_at[143]	0.006835	-1.57	-1.36	NM_026542//XM_006534034	<i>Slc25a39</i>	solute carrier family 25, member 39	0006783 // heme biosynthetic process // inferred from electronic annotation//0006810 // transport // inferred from electronic
1448250_at[144]	0.001669	-1.57	-1.11	NM_001114328//NM_001286	<i>Ccpg1</i>	cell cycle progression 1	0007049 // cell cycle // inferred from electronic annotation//0008284 // positive regulation of cell proliferation // not
1448270_at[144]	0.008667	-1.57	1.01	NM_024236	<i>Qdpr</i>	quinoid dihydropteridine reductase	0001889 // liver development // inferred from electronic annotation//0006559 // L-phenylalanine catabolic process // inferred from
1448273_at[144]	0.003263	-1.57	-1.38	NM_134007	<i>Cisd1</i>	FK506 iron sulfur domain 1	0043457 // regulation of cellular respiration // inferred from mutant phenotype
1448287_at[145]	0.003408	-1.57	1.98	NM_023223	<i>Cdc20</i>	cell division cycle 20	0007049 // cell cycle // inferred from electronic annotation//0007067 // mitotic nuclear division // inferred from electronic
1448297_s_at[14]	0.003991	-1.58	-1.33	NM_016778	<i>Bok</i>	BCL2-related ovarian killer	0006915 // apoptotic process // not recorded//0006919 // activation of cysteine-type endopeptidase activity involved in apoptotic
1448303_at[143]	0.005720	-1.58	1.07	NM_009919//XM_006518505	<i>Cnih1</i>	cornichon homolog 1 (Drosophila)	0006810 // transport // inferred from electronic annotation//0016192 // vesicle-mediated transport // inferred from electronic
1448314_at[125]	0.001024	-1.58	-1.24	NM_001081122//XM_006511	<i>Cep63</i>	centrosomal protein 63	0000077 // DNA damage checkpoint // inferred from sequence or structural similarity//0006974 // cellular response to DNA damage
1448318_at[115]	0.005121	-1.59	-5.43	NM_001083934//NM_010867	<i>Myom1</i>	myomesin 1	0006936 // muscle contraction // inferred from direct assay
1448325_at[178]	0.002999	-1.59	-1.51	NM_011057//XM_006520590	<i>Pdgfrb</i>	platelet derived growth factor, B polypeptide	0001568 // blood vessel development // inferred from expression pattern//0001666 // response to hypoxia // inferred from electronic
1448377_at[205]	0.000533	-1.59	-1.05	NM_001033432//XM_006512	<i>Heca</i>	headcase homolog (Drosophila)	
1448388_a_at[1]	0.006710	-1.59	-1.17	NM_001286260//NM_018823	<i>Nfat5</i>	nuclear factor of activated T cells 5	0001816 // cytokine production // inferred from direct assay//0006351 // transcription, DNA-templated // inferred from sequence or
1448390_a_at[2]	0.009610	-1.59	-1.04	NM_010219//XR_406251	<i>Fkbp4</i>	FK506 binding protein 4//uncharacterized LOC102642559	0000413 // protein peptidyl-prolyl isomerization // not recorded//0006457 // protein folding // inferred from electronic
1448450_at[144]	0.009552	-1.59	-1.11	NM_007631//XM_006508466	<i>Ccnd1</i>	cyclin D1	0000079 // regulation of cyclin-dependent protein serine/threonine kinase activity // inferred from electronic annotation//0000082 //
1448492_s_at[6]	0.000285	-1.60	-1.42	NM_001109975//NM_177340	<i>Synpo</i>	synaptopodin	0030865 // cortical cytoskeleton organization // non-traceable author statement//0032235 // positive regulation of actin filament
1448495_at[221]	0.003716	-1.60	-1.47	NM_008243//XM_006511638	<i>Mst1</i>	macrophage stimulating 1 (hepatocyte growth factor-like)	0006508 // proteolysis // inferred from electronic annotation//0007283 // spermatogenesis // inferred from electronic
1448499_s_at[1]	0.003260	-1.60	-1.06	NM_177909	<i>Slc9a9</i>	solute carrier family 9 (sodium/hydrogen exchanger), member 9	0006810 // transport // inferred from electronic annotation//0006811 // ion transport // inferred from electronic annotation//0006812
1448508_at[103]	0.002566	-1.60	-1.12	NM_001033474	<i>Atxn7l3b</i>	ataxin 7-like 3B	
1448520_at[144]	0.003352	-1.60	-1.06	NM_175483//XM_006511091	<i>Snx33</i>	sorting nexin 33	0000281 // mitotic cytokinesis // not recorded//0006810 // transport // inferred from electronic annotation//0006886 // intracellular
1448521_at[143]	0.002161	-1.60	-1.05	NM_009125//XM_006530228	<i>Atxn2</i>	ataxin 2	0002091 // negative regulation of receptor internalization // not recorded//0002102 // cerebellar Purkinje cell differentiation // inferred
1448550_at[144]	0.000583	-1.60	-1.15	NM_019405	<i>Cctn2</i>	centrin 2	0006200 // ATP catabolic process // inferred from electronic annotation//0006281 // DNA repair // inferred from electronic
1448553_at[144]	0.000240	-1.60	-1.03	NM_175465//XM_006499200	<i>Sestd1</i>	SEC14 and spectrin domains 1	
1448561_at[179]	0.007926	-1.61	1.07	NM_213733//XM_006499443	<i>Npepl1</i>	aminopeptidase-like 1	0006508 // proteolysis // inferred from electronic annotation//0019538 // protein metabolic process // inferred from electronic
1448590_at[128]	0.002379	-1.61	-1.38	NM_018867//XM_006508033	<i>Cpxm2</i>	carboxypeptidase X 2 (M14 family)	0006508 // proteolysis // inferred from direct assay//0007155 // cell adhesion // inferred from electronic annotation
1448591_at[130]	0.001153	-1.61	-1.18	NM_001166552//NM_001276	<i>Zbed6</i>	zinc finger, BED domain containing 6//zinc finger CCCH type containing 11A	0000122 // negative regulation of transcription from RNA polymerase II promoter // inferred from direct assay//0006351 //
1448592_at[566]	0.009687	-1.61	-1.28	NM_138679//XM_006501141	<i>Ash1l</i>	ash1 (absent, small, or homeotic)-like (Drosophila)	0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 // regulation of transcription, DNA-templated
1448602_at[193]	0.000939	-1.61	-1.15	NM_001166552//NM_001276	<i>Zbed6</i>	zinc finger, BED domain containing 6//zinc finger CCCH type containing 11A	0000122 // negative regulation of transcription from RNA polymerase II promoter // inferred from direct assay//0006351 //
1448609_at[221]	0.004921	-1.61	-1.20	NM_027707//NM_201232//X	<i>Nipbl</i>	Nipped-B homolog (Drosophila)	0000122 // negative regulation of transcription from RNA polymerase II promoter // not recorded//0003007 // heart morphogenesis //
1448612_at[559]	0.004749	-1.61	-1.12	NM_001289617//NM_001289	<i>Zyx</i>	zyxin	0007155 // cell adhesion // inferred from electronic annotation//0050727 // regulation of inflammatory response // inferred from
1448617_at[145]	0.005663	-1.62	-1.11	NM_133697//XM_006504083	<i>Snim14</i>	small integral membrane protein 14	
1448620_at[141]	0.002566	-1.62	-1.03	NM_001101502//NM_001110	<i>Zfp703</i>	zinc finger protein 703	0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 // regulation of transcription, DNA-templated
1448627_s_at[5]	0.005434	-1.62	1.07	NM_001033298//XM_006499	<i>Kiz</i>	kizuna centrosomal protein	0007051 // spindle organization // not recorded
1448632_at[191]	0.003631	-1.62	-1.37	NM_153088	<i>Ctdsp1</i>	CTD (carboxy-terminal domain, RNA polymerase II, polypeptide A) small	0006357 // regulation of transcription from RNA polymerase II promoter // not recorded//0006470 // protein dephosphorylation // not
1448635_at[142]	0.002358	-1.62	-1.36	NM_001101478	<i>D3Erd254e</i>	DNA segment, Chr 3, ERATO Doi 254, expressed	0006355 // regulation of transcription, DNA-templated // not recorded
1448647_at[171]	0.002591	-1.62	1.00	NM_001009949//XM_006537	<i>Slc25a51</i>	solute carrier family 25, member 51	0006810 // transport // inferred from electronic annotation
1448649_at[138]	0.007584	-1.62	-1.07	NM_001166364//NM_175273	<i>Fam219b</i>	family with sequence similarity 219, member B	
1448655_at[144]	0.007909	-1.62	-1.08	NM_026388//XM_006539129	<i>Tprgl</i>	transformation related protein 63 regulated like	
1448657_s_at[5]	0.001646	-1.62	-1.12	NM_007885	<i>Slc26a2</i>	solute carrier family 26 (sulfate transporter), member 2	
1448703_at[143]	0.003408	-1.63	1.02	NM_019580	<i>Gde1</i>	glycerolphosphodiester phosphodiesterase 1	
1448752_at[123]	0.000296	-1.63	1.16	NM_009933	<i>Col6a1</i>	collagen, type VI, alpha 1	0001649 // osteoblast differentiation // not recorded//0007155 // cell adhesion // inferred from electronic annotation//00070208 //
1448756_at[202]	0.000412	-1.63	-1.51	NR_002847	<i>Malat1</i>	metastasis associated lung adenocarcinoma transcript 1 (non-coding RNA)	0000381 // regulation of alternative mRNA splicing, via spliceosome // inferred from mutant phenotype//0035063 // nuclear speck
1448757_at[145]	0.001119	-1.63	-1.11	NM_026984//XM_006535805	<i>Kmt2e</i>	lysine (K)-specific methyltransferase 2E	0002446 // neutrophil mediated immunity // inferred from mutant phenotype//0006306 // DNA methylation // inferred from mutant
1448786_at[668]	0.002333	-1.64	-1.48	NM_001033531//NM_001163	<i>Klhl32</i>	kelch-like 32	
1448792_s_at[1]	0.008611	-1.64	-1.23	NM_001122889//NM_001290	<i>Epha7</i>	Eph receptor A7	0006468 // protein phosphorylation // inferred from electronic annotation//0006915 // apoptotic process // inferred from electronic
1448830_at[192]	0.003436	-1.64	-1.14	NM_001010928//NM_201637	<i>Chd8</i>	chromodomain helicase DNA binding protein 8	0001701 // in utero embryonic development // inferred from mutant phenotype//0006200 // ATP catabolic process // not
1448855_at[144]	0.009324	-1.64	1.06	NM_001077403//NM_001077	<i>Nirp2</i>	neuropilin 2	0001525 // angiogenesis // inferred from electronic annotation//0001755 // neural crest cell migration // inferred from mutant
1448870_at[141]	0.009788	-1.64	-1.02	NM_001285463//NM_001285	<i>Nirp2</i>	calcium response factor	0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 // regulation of transcription, DNA-templated
1448891_at[808]	0.005796	-1.65	-1.11	NM_145492//XM_006525818	<i>Zfp521</i>	zinc finger protein 521	0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 // regulation of transcription, DNA-templated
1448893_at[145]	0.009097	-1.65	-1.23	NM_025613	<i>Eid1</i>	EP300 interacting inhibitor of differentiation 1	0000122 // negative regulation of transcription from RNA polymerase II promoter // not recorded//0006351 // transcription, DNA-
1448894_at[141]	0.005884	-1.65	-1.53	NM_001039094//NM_177274	<i>Nesr1</i>	neuronal growth regulator 1	0007155 // cell adhesion // inferred from electronic annotation//0007626 // locomotory behavior // inferred from mutant
1448919_at[145]	0.000614	-1.65	-1.30	NM_001290659//NM_198294	<i>Tanc1</i>	tetratricopeptide repeat, ankyrin repeat and coiled-coil containing 1	0007520 // myoblast fusion // inferred from mutant phenotype//0008542 // visual learning // inferred from mutant
1448923_at[239]	0.003312	-1.65	-1.28	NM_001012396//NM_013935	<i>Ptpla</i>	protein tyrosine phosphatase-like (proline instead of catalytic arginine),	0006629 // lipid metabolic process // inferred from electronic annotation//0006631 // fatty acid metabolic process // inferred from
1448926_at[144]	0.006265	-1.65	1.04	NM_134117	<i>Pkdcx</i>	protein kinase domain containing, cytoplasmic	0001501 // skeletal system development // inferred from mutant phenotype//0001503 // ossification // inferred from electronic
1448939_at[144]	0.006764	-1.65	-1.08	NM_001013380//XM_006530	<i>Dync1l1</i>	dynein, cytoplasmic 1 light intermediate chain 2	0000226 // microtubule cytoskeleton organization // inferred from mutant phenotype//0006810 // transport // inferred from electronic
1448942_at[660]	0.003335	-1.66	-1.03	NM_001113573//NM_001113	<i>Brd3</i>	bromodomain containing 3	0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 // regulation of transcription, DNA-templated
1448954_at[785]	0.002351	-1.66	-1.43	NM_001159883//NM_001159	<i>Dnajb2</i>	DnaJ (Hsp40) homolog, subfamily B, member 2	0008285 // negative regulation of cell proliferation // not recorded//0030308 // negative regulation of cell growth // not
1448987_at[144]	0.003821	-1.66	-1.47	NM_177760//XM_006530515	<i>Wdr66</i>	WD repeat domain 66	
1449000_at[282]	0.005094	-1.66	-3.00	NM_011443	<i>Sox2</i>	SRY (sex determining region Y)-box 2	0000122 // negative regulation of transcription from RNA polymerase II promoter // inferred from genetic interaction//0001649 //
1449003_s_at[5]	0.000321	-1.66	-1.08	NM_001081378//XM_006515	<i>Kidins220</i>	kinase D-interacting substrate 220	0001701 // in utero embryonic development // inferred from mutant phenotype//0010976 // positive regulation of neuron projection
1449009_at[218]	0.000457	-1.66	-1.27	NM_001081298//XM_006502	<i>Lphn2</i>	latrophilin 2	0007165 // signal transduction // inferred from electronic annotation//0007166 // cell surface receptor signaling pathway // inferred
1449009_at[100]	0.000457	-1.66	-1.24	NM_008714	<i>Notch1</i>	notch 1	0000122 // negative regulation of transcription from RNA polymerase II promoter // inferred from direct assay//0000122 // negative
1449015_at[572]	0.000573	-1.66	-1.17	NM_009261//NM_176932//X	<i>Strbp</i>	spermatid perinuclear RNA binding protein	0006928 // cellular component movement // inferred from mutant phenotype//0007275 // multicellular organismal development //
1449024_s_at[1]	0.009959	-1.66	-1.08	NM_133947//XM_006507169	<i>Numa1</i>	nuclear mitotic apparatus protein 1	0000132 // establishment of mitotic spindle orientation // inferred from mutant phenotype//0051321 // meiotic cell cycle // inferred

Table S6

Gene_ID	p (Corr)	FC-RSV 1 d	FC-RSV 5 d	RefSeq Transcript ID	Gene Symbol	Gene Title	Gene Ontology Biological Process
1449025_at 159	0.000103	-1.66	-1.24	NM_001290315//NM_020043	<i>Igdc4c</i>	immunoglobulin superfamily, DCC subclass, member 4	
1449049_at 218	0.006178	-1.66	1.07	NM_134012//NM_006531884	<i>Mbtb1</i>	mbt domain containing 1	0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 // regulation of transcription, DNA-templated
1449127_at 203	0.007841	-1.66	-1.19	NM_001076789//NM_001110	<i>Cbx5</i>	chromobox 5	0045892 // negative regulation of transcription, DNA-templated // inferred from direct assay//0045892 // negative regulation of
1449130_at 144c	0.003127	-1.67	-1.08	NM_001037764//NM_009021	<i>Rai1</i>	retinoic acid induced 1	0001501 // skeletal system development // inferred from mutant phenotype//0006357 // regulation of transcription from RNA
1449164_at 125	0.001295	-1.67	-1.24	NM_025790	<i>Acat13</i>	acyl-CoA thioesterase 13	0008152 // metabolic process // not recorded//0051289 // protein homotetramerization // not recorded
1449174_at 109	0.002347	-1.67	1.00	NM_011101	<i>Prkca</i>	protein kinase C, alpha	0000188 // inactivation of MAPK activity // inferred from mutant phenotype//0000302 // response to reactive oxygen species // not
1449175_at 147	0.003269	-1.67	-1.11	NM_009388	<i>Tkt</i>	transketolase	0006098 // pentose-phosphate shunt // not recorded//0008152 // metabolic process // inferred from electronic annotation//0009052
1449178_at 533	0.003925	-1.67	-1.07	NM_001190401//NM_006514	<i>Usp34</i>	ubiquitin specific peptidase 34	0006508 // proteolysis // not recorded//0006511 // ubiquitin-dependent protein catabolic process // inferred from electronic
1449203_at 108	0.002072	-1.67	1.00	NM_008033	<i>Fnta</i>	farnesyltransferase, CAAX box, alpha	0007528 // neuromuscular junction development // inferred from mutant phenotype//0008284 // positive regulation of cell
1449218_at 128	0.000750	-1.68	1.01	NM_008584	<i>Meox2</i>	mesenchyme homeobox 2	0001525 // angiogenesis // inferred from mutant phenotype//0001757 // somite specification // inferred from genetic
1449220_at 834	0.008226	-1.68	-1.21	NM_181395//NM_006515205	<i>Pxdn</i>	peroxidasin homolog (Drosophila)	0006979 // response to oxidative stress // inferred from electronic annotation//0030198 // extracellular matrix organization // inferred
1449222_at 504	0.004914	-1.68	1.07	NM_030707//NM_006502369	<i>Fcrls</i>	Fc receptor-like 5, scavenger receptor	0006898 // receptor-mediated endocytosis // inferred from electronic annotation//0009967 // positive regulation of signal transduction
1449227_at 126	0.000671	-1.68	-1.20	NM_001253752//NM_001253	<i>Zmym5</i>	zinc finger, MYM-type 5	
1449254_at 207	0.002689	-1.68	-1.08	NM_029332//NM_006541250	<i>Akap13</i>	A kinase (PRKA) anchor protein 13	0006468 // protein phosphorylation // inferred from electronic annotation//0010611 // regulation of cardiac muscle hypertrophy // not
1449265_at 123	0.003018	-1.68	-1.24	NM_001081103//NM_054083	<i>Stim2</i>	stromal interaction molecule 2	0006810 // transport // inferred from electronic annotation//0006811 // ion transport // inferred from electronic annotation//0006816
1449266_at 146c	0.001037	-1.68	1.12	NM_172490//NM_006503827	<i>Sepsec5</i>	Sep (O-phosphoserine) tRNA:Sec (selenocysteine) tRNA synthase	0001514 // selenocysteine incorporation // inferred from direct assay//0006412 // translation // inferred from electronic
1449277_at 240	0.002163	-1.68	-1.16	NM_001081279//NM_006509	<i>Mfas1</i>	malignant fibrous histiocytoma amplified sequence 1	
1449277_at 100	0.002163	-1.68	1.09	NM_001199357//NM_001199	<i>Tmem164</i>	transmembrane protein 164	
1449277_at 100	0.002163	-1.69	1.06	NM_026641//NM_006501966	<i>Ift80</i>	intraflagellar transport 80	0001649 // osteoblast differentiation // inferred from genetic interaction//0001649 // osteoblast differentiation // inferred from mutant
1449277_at 100	0.002163	-1.69	-1.37	NM_001290995//NM_008441	<i>Kif1b</i>	kinesin family member 1B	0006200 // ATP catabolic process // inferred from direct assay//0007018 // microtubule-based movement // inferred from direct
1449277_at 100	0.002163	-1.69	-1.05	NM_025611	<i>Cul7</i>	cullin 7	0000226 // microtubule cytoskeleton organization // inferred from sequence or structural similarity//0000281 // mitotic cytokinesis //
1449277_at 100	0.002163	-1.69	-1.10	NM_001004362	<i>2610008E11Rik</i>	RIKEN cDNA 2610008E11 gene	0006355 // regulation of transcription, DNA-templated // inferred from electronic annotation
1449277_at 100	0.002163	-1.69	1.01	NM_001039581//NM_013855	<i>Abca3</i>	ATP-binding cassette, sub-family A (ABC1), member 3	0006200 // ATP catabolic process // inferred from electronic annotation//0006810 // transport // not recorded//0008152 // metabolic
1449289_at_a_t 14	0.000694	-1.69	-1.27	NM_175266	<i>Epm2a1p1</i>	EPM2A (laforin) interacting protein 1	0032868 // response to insulin // inferred from mutant phenotype//0045725 // positive regulation of glycogen biosynthetic process //
1449308_at 122	0.007141	-1.69	-1.66	NM_001025379//NM_006518	<i>Sema3g</i>	sema domain, immunoglobulin domain (lg), short basic domain, secreted,	0007275 // multicellular organismal development // inferred from electronic annotation
1449326_x_at 2i	0.000160	-1.69	-1.96	NM_001081326//NM_006502	<i>Ag1</i>	amylol-1,6-glucosidase, 4-alpha-glucanotransferase	0005975 // carbohydrate metabolic process // inferred from electronic annotation//0005977 // glycogen metabolic process // inferred
1449329_at 142c	0.007369	-1.70	-1.21	NM_011743//NM_006499039	<i>Zfp106</i>	zinc finger protein 106	0008286 // insulin receptor signaling pathway // inferred from direct assay
1449353_at 224	0.006215	-1.70	-1.24	NM_172924//NM_006511167	<i>Peak1</i>	pseudopodium-enriched atypical kinase 1	0006468 // protein phosphorylation // inferred from electronic annotation//0016310 // phosphorylation // inferred from electronic
1449360_at 145c	0.001490	-1.70	1.10	NM_026844//NM_006531282	<i>Cmc2</i>	COD assembly mitochondrial protein 2	
1449363_at 119	0.005181	-1.70	-1.24	NM_001291046//NM_019837	<i>Nudt3</i>	nucleotide diphosphate linked moiety X)-type motif 3	0008152 // metabolic process // inferred from electronic annotation//0071544 // diphosphoinositol polyphosphate catabolic process //
1449366_at 173	0.000099	-1.70	-1.23	NM_030719	<i>Gatsl2</i>	GATS protein-like 2	
1449379_at 165	0.009555	-1.70	-1.43	NM_001285920//NM_001285	<i>Mfn2</i>	mitofusin 2	0001825 // blastocyst formation // inferred from mutant phenotype//0006184 // GTP catabolic process // not recorded//0006626 //
1449396_at 117	0.003675	-1.70	-1.63	NM_008898//NM_006504398	<i>Por</i>	P450 (cytochrome) oxidoreductase	0003420 // regulation of growth plate cartilage chondrocyte proliferation // not recorded//0007584 // response to nutrient // inferred
1449399_a_at 1i	0.001575	-1.71	-1.05	NM_001045536//NM_006532	<i>Zzf1</i>	zinc finger, ZZ-type with EF hand domain 1	
1449432_a_at 2	0.002566	-1.71	2.04	NM_009696//NM_006539484	<i>Apoe</i>	apolipoprotein E	0001937 // negative regulation of endothelial cell proliferation // not recorded//0002021 // response to dietary excess // inferred from
1449434_at 146c	0.001248	-1.71	-1.16	NM_022980//NM_006539042	<i>Rcan3</i>	regulator of calcineurin 3	0019722 // calcium-mediated signaling // inferred from electronic annotation
1449449_at 144c	0.004256	-1.71	-1.20	NM_008139	<i>Gnaq</i>	guanine nucleotide binding protein, alpha q polypeptide	0001501 // skeletal system development // inferred from mutant phenotype//0001508 // action potential // inferred from mutant
1449465_at 196	0.006710	-1.72	-1.18	NM_008478//NM_006527857	<i>L1cam</i>	L1 cell adhesion molecule	0007155 // cell adhesion // inferred from electronic annotation//0007156 // homophilic cell adhesion // inferred from mutant
1449486_at 126	0.004493	-1.72	-1.07	NM_001081144//NM_001177	<i>Zfp518b</i>	zinc finger protein 518B	0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 // regulation of transcription, DNA-templated
1449498_at 145c	0.009747	-1.72	-1.75	NM_001033777//NM_029122	<i>Iqca</i>	IQ motif containing with AAA domain	0008152 // metabolic process // inferred from electronic annotation
1449525_at 142	0.001297	-1.73	-1.12	NM_001252094//NM_001252	<i>Mett120</i>	methyltransferase like 20	0006479 // protein methylation // inferred from electronic annotation//0032259 // methylation // inferred from electronic annotation
1449544_a_at 1i	0.005256	-1.73	-1.15	NM_172627//NM_006525866	<i>Pggt1b</i>	protein geranylpyrophosphate transferase type I, beta subunit	0008152 // metabolic process // inferred from electronic annotation//0008284 // positive regulation of cell proliferation // not
1449583_at 938	0.008771	-1.73	1.08	NM_016704//NM_006519957	<i>C6</i>	complement component 6	0001701 // in utero embryonic development // inferred from genetic interaction//0001970 // positive regulation of activation of
1449591_at 123	0.003081	-1.73	-1.00	NM_138650//NM_006521708	<i>Dgkq</i>	diacylglycerol kinase, gamma	0007205 // protein kinase C-activating G-protein coupled receptor signaling pathway // inferred from electronic annotation//0008152 //
1449622_at 5	0.003804	-1.73	1.03	NM_177351	<i>Hykk</i>	hydroxylase kinase 1	0016310 // phosphorylation // inferred from electronic annotation
1449678_at 146c	0.007761	-1.73	-1.12	NM_001081383//NM_006535	<i>Kmt2c</i>	lysine (K)-specific methyltransferase 2C	0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 // regulation of transcription, DNA-templated
1449698_at 144c	0.001709	-1.73	-1.13	NM_001291111//NM_008180	<i>Gss</i>	glutathione synthetase	0006750 // glutathione biosynthetic process // inferred from direct assay//0006750 // glutathione biosynthetic process // not
1449815_a_at 14	0.006540	-1.73	1.00	NM_207212//NM_006539445	<i>Wtip</i>	WT1-interacting protein	0001666 // response to hypoxia // not recorded//0006351 // transcription, DNA-templated // inferred from electronic
1449855_s_at 5i	0.008313	-1.74	1.01	NM_001282992//NM_008787	<i>Pcnt</i>	pericentrin (kendrin)	0000226 // microtubule cytoskeleton organization // inferred from sequence or structural similarity//0000226 // microtubule
1449855_s_at 9i	0.008313	-1.74	-1.28	NM_026482//NM_006514015	<i>Atp2b1</i>	ATPase, Ca++ transporting, plasma membrane 1	0006812 // cation transport // inferred from electronic annotation//0006816 // calcium ion transport // traceable author
1449874_at 170	0.005661	-1.74	1.21	NM_025866//NM_006500053	<i>Cdc47</i>	cell division cycle associated 7	0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 // regulation of transcription, DNA-templated
1449901_a_at 5i	0.002665	-1.74	-1.30	NM_025359	<i>Tspan13</i>	tetraspanin 13	
1449946_a_at 14	0.003354	-1.75	-1.22	NM_028493//NM_006517410	<i>Rhabtb3</i>	Rho-related BTB domain containing 3	0006200 // ATP catabolic process // not recorded//0006810 // transport // inferred from electronic annotation//0007264 // small
1449976_a_at 6	0.005866	-1.75	-2.16	NM_018824//NM_006499906	<i>Slc23a2</i>	solute carrier family 23 (nucleobase transporters), member 2	0006810 // transport // inferred from electronic annotation//0006811 // ion transport // inferred from electronic annotation//0006814
1449984_at 203	0.000590	-1.75	-1.12	NM_029979	<i>Trim35</i>	tripartite motif-containing 35	0006915 // apoptotic process // inferred from electronic annotation//0008285 // negative regulation of cell proliferation // inferred
1450009_at 170	0.003273	-1.75	1.19	NM_175460//NM_006529455	<i>Nmnat2</i>	nicotinamide nucleotide adenyltransferase 2	0009058 // biosynthetic process // inferred from electronic annotation//0009435 // NAD biosynthetic process // inferred from
1450019_at 145c	0.005097	-1.75	-1.30	NM_001290805//NM_001290	<i>Kif3a</i>	kinesin family member 3A	0001701 // in utero embryonic development // inferred from genetic interaction//0001822 // kidney development // inferred from
1450115_at 142f	0.007377	-1.75	-1.17	NM_012017//NM_006517259	<i>Zfp346</i>	zinc finger protein 346	0043065 // positive regulation of apoptotic process // inferred from mutant phenotype
1450150_a_at 14	0.007047	-1.75	-1.07	NM_001081056//NM_006514	<i>Xpot</i>	exportin, tRNA (nuclear export receptor for tRNAs)	0006409 // tRNA export from nucleus // not recorded//0006810 // transport // inferred from electronic annotation//0006886 //
1450165_at 205	0.001570	-1.75	-1.47	NM_011838	<i>Lynx1</i>	Ly6b, neurotoxin 1	0007271 // synaptic transmission, cholinergic // inferred by curator//0002072 // negative regulation of receptor activity // inferred from
1450234_at 736	0.001693	-1.75	1.02	NM_011213//NM_006502864	<i>Ptprf</i>	protein tyrosine phosphatase, receptor type, F	0001960 // negative regulation of cytokine-mediated signaling pathway // not recorded//0006470 // protein dephosphorylation // not
1450297_at 161	0.007076	-1.75	-1.14	NM_009320//NM_006505868	<i>Slc6a6</i>	solute carrier family 6 (neurotransmitter transporter, taurine), member 6	0001762 // beta-alanine transport // inferred from direct assay//0003333 // amino acid transmembrane transport // inferred from
1450318_a_at 1i	0.008675	-1.75	-1.31	NM_194462//NM_006503518	<i>Akap9</i>	A kinase (PRKA) anchor protein (ytotiao) 9	0007165 // signal transduction // inferred from electronic annotation//0007283 // spermatogenesis // inferred from mutant
1450355_s_at 14	0.002566	-1.76	-1.18	NM_177899	<i>Zfp866</i>	zinc finger protein 866	0006355 // regulation of transcription, DNA-templated // inferred from electronic annotation
1450357_s_at 1i	0.002251	-1.76	-1.52	NM_010636//NM_006518623	<i>Klf12</i>	Kruppel-like factor 12	0000122 // negative regulation of transcription from RNA polymerase II promoter // inferred from direct assay//0000122 // negative
1450413_at 145c	0.008054	-1.76	-2.68	NM_022029	<i>Nrgn</i>	neurogranin	0035556 // intracellular signal transduction // traceable author statement
1450473_at 143i	0.006927	-1.77	-1.24	NM_175229//NM_006525076	<i>Srm2</i>	serine/arginine repetitive matrix 2	0006397 // mRNA processing // inferred from electronic annotation//0008380 // RNA splicing // inferred from electronic annotation
1450492_at 309	0.001889	-1.77	-1.39	NM_026648	<i>Dnaaf1</i>	dynein, axonemal assembly factor 1	0001947 // heart looping // not recorded//0003341 // cilium movement // not recorded//0003356 // regulation of cilium beat
1450495_at 2	0.004990	-1.77	-1.06	NM_134126//NM_006523402	<i>Ift140</i>	intraflagellar transport 140	0035721 // intracellular retrograde transport // inferred by curator//0042384 // cilium assembly // inferred from mutant
1450499_at 143	0.004130	-1.77	1.19	NM_024264//NM_006495607	<i>Cyp27a1</i>	cytochrome P450, family 27, subfamily a, polypeptide 1	0008203 // cholesterol metabolic process // not recorded//0036378 // catriol biosynthetic process from cald // not
1450502_at 143i	0.002198	-1.77	1.00	NM_031397//NM_006514341	<i>Bic1c</i>	bicaudal Chromolug 1 (Drosophila)	0007275 // multicellular organismal development // inferred from electronic annotation//0009090 // negative regulation of canonical
1450513_at 124	0.000127	-1.77	-1.27	NM_029770//NM_006513028	<i>Unc5b</i>	unc-5 homolog B (C. elegans)	0006915 // apoptotic process // inferred from electronic annotation//0007165 // signal transduction // inferred from electronic
1450562_at 170	0.008536	-1.77	-1.44	NM_021422//NM_006511325	<i>Dnao4</i>	Dna1 (Hsp40) homolog, subfamily A, member 4	0006457 // protein folding // inferred from electronic annotation//0009408 // response to heat // inferred from electronic
1450582_at 145i	0.000412	-1.77	-1.84	NM_008592	<i>Foxc1</i>	forkhead box C1	0000122 // negative regulation of transcription from RNA polymerase II promoter // not recorded//0001501 // skeletal system
1450586_at 120	0.004130	-1.77	-1.91	NM_001286552//NM_008733	<i>Nrap</i>	nebulin-related anchoring protein	0030036 // actin cytoskeleton organization // traceable author statement
1450611_at 184	0.007782	-1.78	-1.03	NM_001253822//NM_008393	<i>Irx3</i>	irxois related homeobox 3	0001656 // metanephros development // inferred from expression pattern//0001822 // kidney development // not recorded//0006351
1450626_at 110	0.008675	-1.78	-1.46	NM_009697//NM_183261//X	<i>Nr2f2</i>	nuclear receptor subfamily 2, group F, member 2	0000122 // negative regulation of transcription from RNA polymerase II promoter // inferred from direct assay//0000122 // negative
1450639_at 269	0.006903	-1.78	-1.13	NM_172145//NM_006503036	<i>Eva1b</i>	eva-1 homolog B (C. elegans)	

Table S6

Gene_ID	p (Corr)	FC-RSV 1 d	FC-RSV 5 d	RefSeq Transcript ID	Gene Symbol	Gene Title	Gene Ontology Biological Process
1450639_at[381]	0.006903	-1.78	1.03	NM_207213//XM_006509242	<i>Snx25</i>	sorting nexin 25	0006810 // transport // inferred from electronic annotation//0007154 // cell communication // inferred from electronic
1450672_a_at[2]	0.000345	-1.78	-1.13	NM_001253904//NM_001253	<i>Ncor2</i>	nuclear receptor co-repressor 2	0000122 // negative regulation of transcription from RNA polymerase II promoter // inferred from direct assay//0000122 // negative
1450672_a_at[14]	0.000380	-1.78	-1.22	NM_198625//XM_006531011	<i>Mts1</i>	metastasis suppressor 1-like	0007165 // signal transduction // inferred from electronic annotation//0046847 // filopodium assembly // inferred from electronic
1450678_at[164]	0.008852	-1.78	-1.06	NM_001291104//NM_010198	<i>Fgf11</i>	fibroblast growth factor 11	
1450696_at[169]	0.004383	-1.78	-1.12	NM_199446//XM_006530528	<i>Phkb</i>	phosphorylase kinase beta	0005975 // carbohydrate metabolic process // inferred from electronic annotation//0005976 // polysaccharide metabolic process //
1450724_at[1846]	0.002517	-1.78	1.11	NM_011941//XM_006499587	<i>Mapkbp1</i>	mitogen-activated protein kinase binding protein 1	0007256 // activation of JNKK activity // inferred from direct assay
1450729_at[145]	0.008431	-1.79	-1.13	NM_001033228	<i>Igta1</i>	integrin alpha 1	0000187 // activation of MAPK activity // not recorded//0007155 // cell adhesion // inferred from mutant phenotype//0007229 //
1450738_at[1447]	0.001511	-1.79	-1.17	NM_018858//NM_008021//	<i>Pebp1</i>	phosphatidylethanolamine binding protein 1//RIKEN cDNA 4933413G19	0000165 // MAPK cascade // not recorded//0001505 // regulation of neurotransmitter levels // not recorded//0001933 // negative
1450783_at[159]	0.000103	-1.80	-1.69	NM_027402//XM_006503212	<i>Fndc5</i>	fibronectin type III domain containing 5	0014850 // response to muscle activity // inferred from direct assay//0090336 // positive regulation of brown fat cell differentiation //
1450792_at[221]	0.003304	-1.80	-1.07	NM_001080832//NM_176850	<i>Bptf</i>	bromodomain PHD finger transcription factor	0000122 // negative regulation of transcription from RNA polymerase II promoter // not recorded//0001892 // embryonic placenta
1450798_at[818]	0.003635	-1.80	-1.65	NM_021391//XM_006521219	<i>Ppp1r1a</i>	protein phosphatase 1, regulatory (inhibitor) subunit 1A	0005975 // carbohydrate metabolic process // inferred from electronic annotation//0005977 // glycogen metabolic process // inferred
1450808_at[142]	0.002620	-1.80	-1.11	NM_001159361//NM_172819	<i>Dip2b</i>	DIP2 disco-interacting protein 2 homolog B (Drosophila)	0008152 // metabolic process // inferred from electronic annotation
1450828_at[143]	0.000126	-1.80	-1.02	NM_145570//XM_006505960	<i>Eva1a</i>	eva-1 homolog A (C. elegans)	0006914 // autophagy // inferred from electronic annotation//0006915 // apoptotic process // inferred from electronic annotation
1450829_at[143]	0.001490	-1.80	-1.33	NM_001145952//NM_001145	<i>Lpp</i>	LIM domain containing preferred translocation partner in lipoma	0007155 // cell adhesion // inferred from electronic annotation
1450834_at[145]	0.003555	-1.80	-1.15	NM_009149	<i>Glg1</i>	golgi apparatus protein 1	0010955 // negative regulation of protein processing // inferred from genetic interaction//0010955 // negative regulation of protein
1450842_a_at[14]	0.007332	-1.80	-1.28	NM_001083945//NM_025789	<i>Rsph3a</i>	radial spoke 3A homolog (Chlamydomonas)//radial spoke 3B homolog	
1450920_at[124]	0.001877	-1.80	-1.24	NM_138601	<i>D10ihu81e</i>	DNA segment, Chr 10, Johns Hopkins University 81 expressed	
1450950_at[145]	0.003790	-1.80	-1.24	NM_001276764//NM_010081	<i>Dst</i>	dystonin	0000226 // microtubule cytoskeleton organization // inferred from electronic annotation//0007010 // cytoskeleton organization //
1450981_at[127]	0.006895	-1.80	1.01	NM_133214//XM_006510043	<i>Smc4a</i>	single-pass membrane protein with coiled-coil domains 4	
1450992_a_at[14]	0.003563	-1.81	-1.25	NM_001038621//NM_013862	<i>Rabgap1l</i>	RAB GTPase activating protein 1-like	0032313 // regulation of Rab GTPase activity // inferred from electronic annotation//0032851 // positive regulation of Rab GTPase
1451006_at[224]	0.000420	-1.81	1.01	NM_028130//XM_006504625	<i>Zfp157</i>	zinc finger protein 157	0006355 // regulation of transcription, DNA-templated // inferred from electronic annotation//0010453 // regulation of cell fate
1451020_at[143]	0.003694	-1.81	-1.39	NM_029057//XM_006514253	<i>Tbc1d30</i>	TBC1 domain family, member 30	0032313 // regulation of Rab GTPase activity // inferred from electronic annotation//0032851 // positive regulation of Rab GTPase
1451026_at[560]	0.006716	-1.81	-1.04	NM_028283//XM_006511480	<i>Uaca</i>	uveal autoantigen with coiled-coil domains and ankyrin repeats	0008630 // intrinsic apoptotic signaling pathway in response to DNA damage // inferred from mutant phenotype//0008631 // intrinsic
1451050_at[107]	0.001652	-1.82	-1.27	NM_023662//XM_006509298	<i>Pcm1</i>	pericentriolar material 1	0020207 // interkinetic nuclear migration // inferred from mutant phenotype//0030030 // cell projection organization // inferred from
1451054_at[184]	0.000100	-1.82	-1.62	NM_007976	<i>F5</i>	coagulation factor V	0006508 // proteolysis // not recorded//0007155 // cell adhesion // inferred from electronic annotation//0007596 // blood coagulation
1451064_a_at[14]	0.001698	-1.82	1.13	NM_001168392//NM_016894	<i>Ramp1</i>	receptor (calcitonin) activity modifying protein 1	0001525 // angiogenesis // not recorded//0006810 // transport // inferred from electronic annotation//0006816 // calcium ion
1451099_at[1446]	0.008254	-1.82	1.16	NM_001081125//XM_006529	<i>Gli2</i>	GLI-Kruppel family member GLI2	0000122 // negative regulation of transcription from RNA polymerase II promoter // inferred from genetic interaction//0000122 //
1451132_at[146]	0.001757	-1.83	1.36	NM_011077	<i>Phex</i>	phosphate regulating endonucleidase homolog, X-linked	0006508 // proteolysis // not recorded//0019637 // organophosphate metabolic process // inferred from mutant phenotype//0030282
1451139_at[720]	0.003442	-1.83	-1.08	NM_181072//XM_006511445	<i>Myo1e</i>	myosin IE	0001570 // vasculogenesis // inferred from mutant phenotype//0001701 // in utero embryonic development // inferred from mutant
1451145_a_at[6]	0.006133	-1.83	-1.30	NM_144812//NM_177124	<i>Tnrc6b</i>	trinucleotide repeat containing 6b	0006417 // regulation of translation // inferred from electronic annotation//0031047 // gene silencing by RNA // not
1451161_a_at[1]	0.001404	-1.83	-1.12	NM_008861//XM_006534815	<i>Pkd2</i>	polycystic kidney disease 2	0001658 // branching involved in uterine bud morphogenesis // inferred from electronic annotation//0001822 // kidney development
1451163_at[143]	0.000626	-1.83	-2.10	NM_010362	<i>Gsto1</i>	glutathione S-transferase omega 1	0008152 // metabolic process // inferred from electronic annotation//0010880 // regulation of release of sequestered calcium ion into
1451171_at[224]	0.003312	-1.83	-1.19	NM_007462//XM_006525529	<i>Apc</i>	adenomatosis polyposis coli	0000281 // mitotic cytokinesis // inferred from mutant phenotype//0000281 // mitotic cytokinesis // not recorded//0001822 // kidney
1451172_at[678]	0.004621	-1.83	1.00	NM_175268//NM_212473//X	<i>Fam53b</i>	family with sequence similarity 53, member B	
1451187_at[660]	0.009319	-1.83	-1.96	NM_001277903//NM_001277	<i>Tnnt1</i>	troponin T1, skeletal, slow	0003009 // skeletal muscle contraction // not recorded//0006937 // regulation of muscle contraction // not recorded//0031444 // slow-
1451227_a_at[2]	0.004794	-1.84	-1.05	NM_053145	<i>Pcdhb20</i>	protodanherin beta 20	0007155 // cell adhesion // inferred from electronic annotation//0007156 // homophilic cell adhesion // inferred from electronic
1451229_at[145]	0.004130	-1.84	1.07	NM_001276452//NM_172773	<i>Sclt7a5</i>	solute carrier family 17 (anion/sugar transporter), member 5	0006810 // transport // inferred from electronic annotation//0006865 // amino acid transport // inferred from electronic
1451233_at[220]	0.008784	-1.84	1.49	NM_018815//XM_006506400	<i>Nup210</i>	nucleoporin 210	0006810 // transport // inferred from electronic annotation//0015031 // protein transport // inferred from electronic
1451253_at[218]	0.002163	-1.84	-1.00	NM_001293641//NM_146141	<i>Ppo2</i>	pyrophosphatase (inorganic) 2	0006796 // phosphate-containing compound metabolic process // inferred from electronic annotation//0016311 // dephosphorylation
1451277_at[225]	0.004716	-1.84	-1.04	NM_001005341	<i>Ype1c</i>	Ympep-like 2 (Drosophila)	
1451290_at[144]	0.003985	-1.85	-1.32	NM_001008542//NM_001008	<i>Mxi1</i>	Max interacting protein 1	0000122 // negative regulation of transcription from RNA polymerase II promoter // inferred from direct assay//0006351 //
1451320_at[731]	0.002714	-1.85	-1.23	NM_001164041//NM_001164	<i>Smao5</i>	SMAD family member 5	0001503 // ossification // inferred from electronic annotation//0001525 // angiogenesis // inferred from electronic
1451331_at[190]	0.007959	-1.85	-1.33	NM_012026//XM_006517518	<i>Arhgef28</i>	Rho guanine nucleotide exchange factor (GEF) 28	0021955 // central nervous system neuron axonogenesis // inferred from mutant phenotype//0030154 // cell differentiation // inferred
1451332_at[143]	0.006266	-1.85	-1.11	NM_146090//XM_006526460	<i>Zadh2</i>	zinc binding alcohol dehydrogenase, domain containing 2	0055114 // oxidation-reduction process // inferred from electronic annotation
1451335_at[231]	0.001054	-1.85	-1.05	NM_138756//XM_006510870	<i>Slc25a36</i>	solute carrier family 25, member 36	0006810 // transport // inferred from electronic annotation//0032355 // response to estradiol // not recorded//0055085 //
1451340_at[214]	0.004377	-1.85	-1.27	NM_001205330//NM_001205	<i>Map4</i>	microtubule-associated protein 4	0007052 // mitotic spindle organization // inferred from direct assay//0007052 // mitotic spindle organization // not
1451344_at[231]	0.006323	-1.85	-2.33	NM_001271533//NM_025728	<i>Spag16</i>	sperm associated antigen 16	0007283 // spermatogenesis // inferred from mutant phenotype//0030030 // cell projection organization // inferred from electronic
1451362_at[226]	0.004067	-1.85	-1.19	NM_001290817//NM_009242	<i>Sporc</i>	secreted acidic cysteine rich glycoprotein	0001503 // ossification // inferred from electronic annotation//0007165 // signal transduction // inferred from electronic
1451385_at[144]	0.004759	-1.86	-1.16	NM_001014390//XM_006514	<i>Dyrk2</i>	dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 2	0006468 // protein phosphorylation // not recorded//0006915 // apoptotic process // inferred from electronic annotation//0006974 //
1451416_a_at[2]	0.002233	-1.86	-1.34	NM_008710//NR_003544	<i>Nnt</i>	nicotinamide nucleotide transhydrogenase	0015992 // proton transport // inferred from electronic annotation//0055114 // oxidation-reduction process // inferred from electronic
1451439_at[212]	0.006249	-1.86	-1.07	NM_024288//XM_006506539	<i>Rmnd5a</i>	required for meiotic nuclear division 5 homolog A (S. cerevisiae)	
1451498_at[227]	0.001408	-1.86	-1.09	NM_019517//XM_006523068	<i>Bace2</i>	beta-site APP-cleaving enzyme 2	0006508 // proteolysis // inferred from electronic annotation//0006509 // membrane protein ectodomain proteolysis // not
1451523_a_at[6]	0.004235	-1.86	-1.12	NM_001160400//XR_931069	<i>Megf8</i>	multiple EGF-like domains 8	0003143 // embryonic heart tube morphogenesis // inferred from mutant phenotype//0007275 // multicellular organismal
1451527_at[764]	0.005097	-1.86	-1.20	NM_019472//XM_006520024	<i>Myo10</i>	myosin X	0006200 // ATP catabolic process // inferred from sequence or structural similarity//0006810 // transport // inferred from electronic
1451537_at[126]	0.000099	-1.86	-1.09	NM_029007	<i>Fam84a</i>	family with sequence similarity 84, member A	
1451550_at[138]	0.006871	-1.86	-1.15	NM_026878	<i>Ras11b</i>	RAS-like, family 11, member B	0006184 // GTP catabolic process // inferred from electronic annotation//0007165 // signal transduction // inferred from electronic
1451564_at[143]	0.001304	-1.86	-1.26	NM_008305//XM_006538571	<i>Hspg2</i>	heparan (heparan sulfate) proteoglycan 2	0001525 // angiogenesis // inferred from electronic annotation//0001958 // endochondral ossification // inferred from mutant
1451567_a_at[1]	0.002679	-1.86	-1.06	NM_001159965//NM_001159	<i>Ralaps2</i>	Ral GEF with PH domain and SH3 binding motif 2	0007264 // small GTPase mediated signal transduction // inferred from electronic annotation//0043547 // positive regulation of GTPase
1451575_a_at[5]	0.004199	-1.87	1.03	NM_001159543//NM_010074	<i>Dpp4</i>	dipeptidylpeptidase 4	0001666 // response to hypoxia // not recorded//0002709 // regulation of T cell mediated immunity // not recorded//0006508 //
1451576_at[190]	0.002620	-1.87	-1.31	NM_021423//XM_006521220	<i>Shank3</i>	SH3/ankyrin domain gene 3	0000615 // MAPK cascade // inferred from genetic interaction//0001838 // embryonic epithelial tube formation // inferred from genetic
1451601_a_at[2]	0.001049	-1.87	-1.81	NM_172904	<i>Fsd2</i>	fibronectin type III and SPRY domain containing 2	
1451610_at[232]	0.005452	-1.88	-1.13	NM_133949//XM_006541323	<i>Ptqv1</i>	prostate tumor over expressed gene 1	0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 // regulation of transcription, DNA-templated
1451643_a_at[1]	0.003821	-1.88	-1.42	NM_146224//XM_006511118	<i>Zfp280d</i>	zinc finger protein 280D	0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 // regulation of transcription, DNA-templated
1451650_at[143]	0.007227	-1.88	-1.03	NM_019922	<i>Crtap</i>	cartilage associated protein	0007283 // spermatogenesis // inferred from expression pattern//0018400 // peptidyl-proline hydroxylation to 3-hydroxy-L-proline //
1451655_at[276]	0.002971	-1.88	-1.63	NM_001081307//NR_015606/	<i>Ppp1r12b</i>	protein phosphatase 1, regulatory (inhibitor) subunit 12B	
1451693_a_at[14]	0.001511	-1.88	1.03	NM_009012	<i>Rad50</i>	RAD50 homolog (S. cerevisiae)	0000019 // regulation of mitotic recombination // not recorded//0000737 // DNA catabolic process, endonucleolytic // not
1451755_a_at[1]	0.006413	-1.88	-1.49	NM_009879//XM_006530127	<i>Iftr1</i>	intraflagellar transport 81	0007275 // multicellular organismal development // inferred from electronic annotation//0007283 // spermatogenesis // inferred from
1451764_at[144]	0.002826	-1.88	-1.22	NM_008739//XM_006517134	<i>Nsd1</i>	nuclear receptor-binding SET-domain protein 1	0000122 // negative regulation of transcription from RNA polymerase II promoter // inferred from direct assay//0001702 // gastrulation
1451777_at[143]	0.001152	-1.88	1.12	NM_028135	<i>Tmem163</i>	transmembrane protein 163	
1451793_at[142]	0.000296	-1.89	-1.24	NM_182997//XM_006500840	<i>Prkab2</i>	protein kinase, AMP-activated, beta 2 non-catalytic subunit	0006468 // protein phosphorylation // not recorded//0006468 // protein phosphorylation // traceable author statement//0006629 //
1451858_at[235]	0.002430	-1.90	-2.04	NM_019697	<i>Kcnd2</i>	potassium voltage-gated channel, Shal-related family, member 2	0001508 // action potential // inferred from mutant phenotype//0001508 // action potential // not recorded//0006810 // transport //
1451858_at[668]	0.002430	-1.90	1.03	NM_144916	<i>Tmem150a</i>	transmembrane protein 150A	0009056 // catabolic process // inferred from electronic annotation
1451890_at[143]	0.008038	-1.90	-1.13	NM_178111//XM_006500112	<i>Trp53inp2</i>	transformation related protein 53 inducible nuclear protein 2	0000045 // autophagic vacuole assembly // not recorded//0001649 // osteoblast differentiation // inferred from mutant
1451905_a_at[1]	0.000176	-1.90	-1.82	NM_008634//XM_006517548	<i>Map1b</i>	microtubule-associated protein 1B	0000226 // microtubule cytoskeleton organization // inferred from electronic annotation//0001578 // microtubule bundle formation //
1451932_a_at[2]	0.002566	-1.90	-1.23	NM_134052	<i>Adi1</i>	aciredutone dioxygenase 1	0006355 // regulation of transcription, DNA-templated // inferred from electronic annotation//0008652 // cellular amino acid
1452013_at[144]	0.006553	-1.90	-1.01	NM_146193//XM_006541322	<i>Btbd1</i>	BTB (POZ) domain containing 1	0016567 // protein ubiquitination // inferred from electronic annotation
1452016_at[116]	0.006826	-1.91	-1.13	NM_023850//XM_006500388	<i>Cstt1</i>	carboxylate domain sulfate Gal-6) sulfotransferase 1	0005975 // carbohydrate metabolic process // inferred from electronic annotation//0006012 // galactose metabolic process // not
1452047_at[123]	0.009196	-1.91	-1.60	NM_001099633//XM_006533	<i>Dnao9</i>	dynein, axonemal, heavy chain 9	0006200 // ATP catabolic process // inferred from electronic annotation//0007018 // microtubule-based movement // inferred from

Table S6

Gene_ID	p (Corr)	FC-RSV 1 d	FC-RSV 5 d	RefSeq Transcript ID	Gene Symbol	Gene Title	Gene Ontology Biological Process
1452055_at 227	0.004235	-1.91	-1.82	NM_009626//XM_006500919	<i>Adh7</i>	alcohol dehydrogenase 7 (class IV), mu or sigma polypeptide	0001523 // retinoid metabolic process // not recorded//0006067 // ethanol metabolic process // not recorded//0006068 // ethanol
1452062_at 212	0.007430	-1.91	-1.06	NM_001286728//NM_001286	<i>Glcci1</i>	glucocorticoid induced transcript 1	
1452067_at 145	0.003419	-1.91	-1.11	NM_198298//XM_006534504	<i>Helz</i>	helicase with zinc finger domain	0008152 // metabolic process // inferred from electronic annotation
1452070_at 673	0.007480	-1.91	-1.14	NM_172448//XM_006532701	<i>Rnf43</i>	ring finger protein 43	0007165 // signal transduction // inferred from electronic annotation//0016055 // Wnt signaling pathway // inferred from electronic
1452170_at 145	0.007312	-1.91	1.11	NM_009255//XM_006496459	<i>Serpine2</i>	serine (or cysteine) peptidase inhibitor, clade E, member 2	0007275 // multicellular organismal development // inferred from electronic annotation//0007399 // nervous system development //
1452178_at 671	0.000555	-1.91	-1.38	NM_021568//XM_006513916	<i>Pcbp3</i>	poly(rC) binding protein 3	
1452218_at 146	0.005058	-1.91	1.01	NM_021345//XM_006511324	<i>Ptprd1</i>	protein tyrosine phosphatase-like A domain containing 1	0006629 // lipid metabolic process // inferred from electronic annotation//0006631 // fatty acid metabolic process // inferred from
1452242_at 145	0.000296	-1.92	1.08	NM_007731//XM_006513166	<i>Col13a1</i>	collagen, type XIII, alpha 1	0001503 // ossification // inferred from electronic annotation//0001763 // morphogenesis of a branching structure // inferred from
1452304_a_at 5	0.001304	-1.92	-1.49	NM_001079908//NM_001079	<i>Fgfr1</i>	fibroblast growth factor receptor 1	0000122 // negative regulation of transcription from RNA polymerase II promoter // inferred from mutant phenotype//0001525 //
1452313_at 724	0.004123	-1.92	-1.22	NM_001145947//NM_011792	<i>Bace1</i>	beta-site APP cleaving enzyme 1	0006508 // proteolysis // inferred from direct assay//0006508 // proteolysis // not recorded//00050435 // beta-amyloid metabolic
1452330_a_at 7	0.008314	-1.92	-1.15	NM_001135577	<i>Smim13</i>	small integral membrane protein 13	
1452345_at 936	0.000533	-1.92	-1.26	NM_207232//XM_006516921	<i>Ptpdc1</i>	protein tyrosine phosphatase domain containing 1	0006470 // protein dephosphorylation // inferred from electronic annotation//0007224 // smoothened signaling pathway // inferred
1452348_s_at 14	0.001511	-1.93	1.02	NM_001252453//NM_001252	<i>Ptprs</i>	protein tyrosine phosphatase, receptor type, S	0006470 // protein dephosphorylation // inferred from electronic annotation//0007155 // cell adhesion // inferred from electronic
1452348_s_at 14	0.001511	-1.93	-1.51	NM_001291508//NM_001291	<i>Pbx1</i>	pre B cell leukemia homeobox 1	0001655 // urogenital system development // inferred from mutant phenotype//0001658 // branching involved in ureteric bud
1452398_at 740	0.006305	-1.94	-1.11	AU015536		expressed sequence AU015536	
1452413_at 143	0.008329	-1.94	1.28	NM_001039175//NM_001039	<i>Elovl1</i>	elongation of very long chain fatty acids (FEN1/Elo2, SUR4/Elo3, yeast)-like 1	0006629 // lipid metabolic process // inferred from electronic annotation//0006631 // fatty acid metabolic process // inferred from
1452414_s_at 14	0.004334	-1.94	-1.35	NM_031185	<i>Akap12</i>	A kinase (PRKA) anchor protein (gravin) 12	0005975 // protein targeting // inferred from electronic annotation//0007165 // signal transduction // not recorded//0007165 // signal
1452472_at 235	0.005720	-1.94	-2.04	NM_144534//XM_006509771	<i>Tmem38a</i>	transmembrane protein 38A	0006810 // transport // inferred from electronic annotation//0006811 // ion transport // inferred from electronic annotation//0006813
1452492_a_at 5i	0.009685	-1.94	-1.25	NM_001162926//NM_207269	<i>Fam84b</i>	family with sequence similarity 84, member B	
1452496_at 144	0.004895	-1.95	-1.07	NM_172588	<i>Serinc5</i>	serine incorporator 5	0006629 // lipid metabolic process // inferred from electronic annotation//0006658 // phosphatidylserine metabolic process // not
1452500_at	0.009980	-1.95	-1.07	NM_153127	<i>Mmrn2</i>	multimerin 2	0001525 // angiogenesis // inferred from electronic annotation//0030948 // negative regulation of vascular endothelial growth factor
1452519_a_at 2	0.009131	-1.95	-1.05	NM_172780//XM_006527979	<i>Slc9a6</i>	solute carrier family 9 (sodium/hydrogen exchanger), member 6	0006810 // transport // inferred from electronic annotation//0006811 // ion transport // inferred from electronic annotation//0006812
1452595_at 145	0.001490	-1.95	-1.04	NM_207239	<i>Gtf3c1</i>	general transcription factor III C 1	0006351 // transcription, DNA-templated // inferred from electronic annotation
1452598_at 145	0.003166	-1.95	-1.05	NM_001136227//NM_009106	<i>Rtkn</i>	receptor tyrosine kinase 1	0006915 // apoptotic process // inferred from electronic annotation//0007165 // signal transduction // not recorded//0007266 // Rho
1452603_at 226	0.007922	-1.95	-1.10	NM_001159634//NM_172661	<i>Prrc2b</i>	proline-rich coiled-coil 2B	
1452639_at 1434	0.001042	-1.96	-1.02	NM_001103177//NM_001103	<i>Abilim1</i>	actin-binding LIM protein 1	0007010 // cytoskeleton organization // inferred from electronic annotation//0007411 // axon guidance // inferred from direct
1452646_at 1444	0.003998	-1.96	-1.38	NM_170779	<i>Wwv1</i>	WW, C2 and coiled-coil domain containing 1	0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 // regulation of transcription, DNA-templated
1452648_at 213	0.007782	-1.96	-1.63	NM_153781	<i>Pgylb</i>	brain glycogen phosphorylase	0005975 // carbohydrate metabolic process // inferred from electronic annotation//0005977 // glycogen metabolic process // not
1452676_a_at 14	0.002248	-1.96	-1.04	NM_001085549//XM_006503	<i>Trab2b</i>	Trab domain containing 2B	0006508 // proteolysis // not recorded//0008152 // metabolic process // not recorded//0016055 // Wnt signaling pathway // inferred
1452714_at 1444	0.008089	-1.96	-1.86	NM_001081025//NM_177104	<i>Maats1</i>	MYCB-associated, testis expressed 1	0008295 // spermidine biosynthetic process // inferred from electronic annotation
1452718_at 1444	0.005137	-1.96	-1.74	NM_007450	<i>Slc25a4</i>	solute carrier family 25 (mitochondrial carrier, adenine nucleotide	0006810 // transport // inferred from electronic annotation//0008637 // apoptotic mitochondrial changes // inferred from genetic
1452732_at 678	0.009827	-1.96	-1.10	NM_177699	<i>Fhod1</i>	formin homology 2 domain containing 1	0007015 // actin filament organization // inferred from electronic annotation//0045944 // positive regulation of transcription from RNA
1452769_at 743	0.003922	-1.96	-1.59	NM_010111//XM_006508694	<i>Efnb2</i>	ephrin B2	0001525 // angiogenesis // inferred from electronic annotation//0001945 // lymph vessel development // inferred from mutant
1452917_at 721	0.005121	-1.97	-1.28	NM_001081006//NM_001177	<i>Etla</i>	enhancer trap locus 4	0007275 // multicellular organismal development // inferred from electronic annotation//0048706 // embryonic skeletal system
1453076_at 381	0.001987	-1.97	1.18	NM_198170//XM_006503012	<i>Szt2</i>	seizure threshold 2	0007417 // central nervous system development // inferred from mutant phenotype//0009790 // embryo development // inferred from
1453196_a_at 2	0.000380	-1.97	-1.29	NM_001036684//NM_009723	<i>Atp2b2</i>	ATPase, Ca++ transporting, plasma membrane 2	0009902 // cell morphogenesis // inferred from mutant phenotype//0006200 // ATP catabolic process // inferred from mutant
1453238_s_at 7	0.003763	-1.97	-1.12	NM_010826//NM_194464//X	<i>Mrvn1</i>	MRV integration site 1	0019934 // cGMP-mediated signaling // inferred from mutant phenotype//0045986 // negative regulation of smooth muscle contraction
1453299_a_at 6i	0.000240	-1.98	-1.39	NM_153100//XM_006512112	<i>Rtp3</i>	receptor transporter protein 3	0001580 // detection of chemical stimulus involved in sensory perception of bitter taste // inferred from electronic
1453486_a_at 5i	0.006692	-1.98	-1.07	NM_001172424//NM_011303	<i>Dhrs3</i>	dehydrogenase/reductase (SDR family) member 3	0001523 // retinoid metabolic process // inferred from mutant phenotype//0003151 // outflow tract morphogenesis // inferred from
1453576_at 143	0.006857	-1.98	-1.11	D7Wsu130e		DNA segment, Chr 7, Wayne State University 130, expressed	
1453748_a_at 14	0.001032	-1.98	-1.31	NM_001290997//NM_001291	<i>Sema6d</i>	sema domain, transmembrane domain (TM), and cytoplasmic domain,	0007275 // multicellular organismal development // inferred from electronic annotation//0007399 // nervous system development //
1454622_at 209	0.003294	-1.99	-1.03	NM_009655//XM_006521714	<i>Alcam</i>	activated leukocyte cell adhesion molecule	0007155 // cell adhesion // inferred from electronic annotation//0007411 // axon guidance // inferred from mutant
1454648_s_at 14	0.008905	-1.99	1.07	NM_030018//XM_006523110	<i>Tmem50b</i>	transmembrane protein 50B	
1454670_at 1435	0.002923	-1.99	-1.06	NM_001291065//NM_001291	<i>Foxa2</i>	forkhead box A2	0000122 // negative regulation of transcription from RNA polymerase II promoter // --//0000432 // positive regulation of transcription
1454708_at 1444	0.001274	-1.99	-1.16	NM_144919//XM_006505995	<i>Hdac11</i>	histone deacetylase 11	0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 // regulation of transcription, DNA-templated
1454771_at 102	0.001995	-1.99	-1.04	NM_053090//XM_006535820	<i>Fam126a</i>	family with sequence similarity 126, member A	
1454838_s_at 14	0.008187	-1.99	-1.25	NM_013835//XM_006529294	<i>Trove2</i>	TROVE domain family, member 2	0002520 // immune system development // inferred from mutant phenotype//0007224 // smoothened signaling pathway // inferred
1455006_at 101	0.005483	-1.99	-1.22	NM_001177751//NM_009366	<i>Tsc2d1</i>	TSC2 domain family, member 1	0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 // regulation of transcription, DNA-templated
1455134_at 242	0.004540	-1.99	-1.07	NM_001159354//NM_133853	<i>Magi3</i>	membrane associated guanylate kinase, WW and PDZ domain containing 3	0016310 // phosphorylation // inferred from electronic annotation//0043507 // positive regulation of JUN kinase activity // inferred
1455271_at 145	0.001127	-1.99	-1.44	NM_029851//XM_006509826	<i>Dync2h1</i>	dynein cytoplasmic 2 heavy chain 1	0001539 // cilium or flagellum-dependent cell motility // inferred from electronic annotation//0006200 // ATP catabolic process //
1455279_at 381	0.005978	-2.00	-1.72	NM_175138//XR_390339//X	<i>Dnaic1</i>	dynein, axonemal, intermediate chain 1	0003351 // epithelial cilium movement // inferred from mutant phenotype//0008152 // metabolic process // inferred from electronic
1455562_at 143	0.007392	-2.00	-1.28	NM_011952	<i>Mapk3</i>	mitogen-activated protein kinase 3	0000165 // MAPK cascade // inferred from mutant phenotype//0000165 // MAPK cascade // not recorded//0000189 // MAPK import
1455615_a_at 14	0.005199	-2.00	-1.03	NM_001110147//NM_001289	<i>Tnk2</i>	tyrosine kinase, non-receptor, 2	0006468 // protein phosphorylation // inferred from electronic annotation//0006897 // endocytosis // inferred from electronic
1456383_at 664	0.008544	-2.00	-1.13	NM_022563//XM_006496696	<i>Ddr2</i>	discoidin domain receptor family, member 2	0001503 // ossification // inferred from electronic annotation//0003416 // endochondral bone growth // inferred from mutant
1456694_s_at 14	0.009361	-2.01	-1.85	NM_016762//XM_006520023	<i>Matn2</i>	matrilin 2	0001764 // neuron migration // inferred from direct assay//0007411 // axon guidance // inferred from genetic interaction//0008347 //
1456706_at	0.005524	-2.01	-2.02	NM_001122603//NM_175444	<i>Fcgbp</i>	Fc fragment of IgG binding protein	
1459817_at	0.001161	-2.01	-1.08	NM_001199304//NM_001199	<i>Atxn1</i>	ataxin 1	0000122 // negative regulation of transcription from RNA polymerase II promoter // inferred from genetic interaction//0006351 //
1459900_at 972	0.002179	-2.01	-1.84	NM_025769//XM_006522474	<i>Efcab1</i>	EF hand calcium binding domain 1	
1460042_at 226	0.005483	-2.01	-1.26	NM_026361//NM_175464//X	<i>Pkp4</i>	plakophilin 4	0007043 // cell-cell junction assembly // inferred from mutant phenotype//0007155 // cell adhesion // inferred from electronic
1460168_at 143	0.003991	-2.01	-1.29	NM_009260//NM_175836//X	<i>Sptbn1</i>	spectrin beta, non-erythrocytic 1	0000281 // mitotic cytokinesis // not recorded//0007009 // plasma membrane organization // not recorded//0007182 // common-
1460194_at 169	0.006053	-2.01	-1.50	NM_001102563//NM_030240	<i>Pagp1a//Prrt2</i>	PAXP1 associated glutamate rich protein 1A//proline-rich transmembrane	0009607 // response to biotic stimulus // inferred from electronic annotation//00050884 // neuromuscular process controlling posture //
1460210_at 187	0.001511	-2.01	-1.55	NM_001081157//XM_006506	<i>Lmod3</i>	leiomodin 3 (fetal)	
1460218_at 238	0.007244	-2.01	-1.13	NM_172903//XM_006540598	<i>Mann2a2</i>	mannosidase 2, alpha 2	0005975 // carbohydrate metabolic process // inferred from electronic annotation//0006013 // mannose metabolic process // inferred
1460224_at 678	0.004895	-2.02	-1.22	NM_175171//XM_006517693	<i>Mast4</i>	microtubule associated serine/threonine kinase family member 4	0006468 // protein phosphorylation // inferred from electronic annotation//0016310 // phosphorylation // inferred from electronic
1460251_at 141	0.000939	-2.02	-1.30	NM_145743//XM_006512697	<i>Loce1</i>	lactation elevated 1	
1460257_a_at 14	0.004922	-2.02	-1.34	NM_027144//XM_006510586	<i>Arhgef12</i>	Rho guanine nucleotide exchange factor (GEF) 12	0007186 // G-protein coupled receptor signaling pathway // not recorded//0032321 // positive regulation of Rho GTPase activity //
1460257_s_at 1i	0.007918	-2.02	-1.16	NM_001083587//XM_006514	<i>Tns3</i>	tensin 3	0008284 // positive regulation of cell proliferation // inferred from mutant phenotype//0016477 // cell migration // inferred from
1460271_at 582	0.005005	-2.02	-1.39	NM_027972	<i>Ccdc19</i>	coiled-coil domain containing 19	
1460273_s_at 1	0.002933	-2.02	-1.13	NM_021310	<i>Jmy</i>	junction-mediating and regulatory protein	0006281 // DNA repair // inferred from electronic annotation//0006357 // regulation of transcription from RNA polymerase II promoter
1460282_at 144	0.004321	-2.02	-1.35	NM_177730	<i>Impad1</i>	inositol monophosphatase domain containing 1	0001501 // skeletal system development // inferred from mutant phenotype//0001958 // endochondral ossification // inferred from
1460283_at 544	0.007612	-2.02	-1.05	NM_001081049//XM_006510	<i>Kmt2a</i>	lysine (K)-specific methyltransferase 2A	0006306 // DNA methylation // inferred from mutant phenotype//0006351 // transcription, DNA-templated // inferred from electronic
1460318_at 130	0.004130	-2.02	-2.44	NM_009063	<i>Rgs5</i>	regulator of G-protein signaling 5	0007165 // signal transduction // not recorded//0007186 // G-protein coupled receptor signaling pathway // traceable author
1460334_at 131	0.003818	-2.02	-1.49	NM_001002267	<i>Tmem158</i>	transmembrane protein 158	
1460348_at 718	0.004659	-2.03	1.09	NM_028266//XM_006502639	<i>Col16a1</i>	collagen, type XVI, alpha 1	
1460361_at 677	0.003708	-2.03	-1.10	NM_001206335//NM_207217	<i>Ifg3</i>	integrin alpha FG-GAP repeat containing 3	0007155 // cell adhesion // not recorded//0071230 // cellular response to amino acid stimulus // inferred from direct assay
1460416_s_at 1i	0.002562	-2.03	-1.08	NM_177368//XM_006513715	<i>Tmtc2</i>	transmembrane and tetrapeptide repeat containing 2	
1460428_at 684	0.007100	-2.03	1.15	NM_029519	<i>Rap2a</i>	RAS related protein 2A	0006184 // GTP catabolic process // not recorded//0007165 // signal transduction // inferred from electronic annotation//0007264 //
1460722_at 223	0.007227	-2.03	-1.24	NM_080456	<i>Mrp6</i>	mitochondrial ribosomal protein S6	0006020 // inositol metabolic process // inferred from mutant phenotype//0006412 // translation // inferred from electronic

Table S6

Gene_ID	p (Corr)	FC-RSV 1 d	FC-RSV 5 d	RefSeq Transcript ID	Gene Symbol	Gene Title	Gene Ontology Biological Process
1428278_at 145:	0.006146	-2.03	-1.30	NM_010453	<i>Hoxa5</i>	homeobox A5	0001501 // skeletal system development // inferred from mutant phenotype//0002009 // morphogenesis of an epithelium // inferred
1428352_at 708:	0.002333	-2.04	-1.33	NM_001081241//XM_006531	<i>Fam65a</i>	family with sequence similarity 65, member A	0007165 // signal transduction // inferred from electronic annotation
1428447_at 757:	0.008810	-2.04	-1.28	NM_001197321//NM_001197	<i>Foxp1</i>	forkhead box P1	0000122 // negative regulation of transcription from RNA polymerase II promoter // inferred from direct assay//0000122 // negative
1428457_at 1425:	0.009629	-2.04	1.05	NM_011159//XM_006521857	<i>Prkdc</i>	protein kinase, DNA activated, catalytic polypeptide	0000773 // telomere maintenance // inferred from mutant phenotype//00001756 // somitogenesis // inferred from genetic
1428480_at 1425:	0.000613	-2.05	-1.14	NM_001033445	<i>Garem</i>	GRB2 associated, regulator of MAPK1	0007173 // epidermal growth factor receptor signaling pathway // not recorded//0008284 // positive regulation of cell proliferation //
1428553_at 730:	0.005986	-2.05	1.11	NM_007934	<i>Enpep</i>	glutamyl aminopeptidase	0001525 // angiogenesis // inferred from mutant phenotype//0003081 // regulation of systemic arterial blood pressure by renin-
1428579_at 714:	0.003137	-2.05	-1.38	NM_019427//XM_006538087	<i>Eppa4.114b</i>	erythrocyte protein band 4.1-like 4b	0031032 // actomyosin structure organization // not recorded
1428598_at 145:	0.008505	-2.05	-1.04	NM_153578//XM_006540836	<i>Nlpa1</i>	not imprinted in Prader-Willi/Angelman syndrome 1 homolog (human)	0006810 // transport // inferred from electronic annotation//0006811 // ion transport // inferred from electronic annotation//0015693
1428613_at 1425:	0.003923	-2.06	-1.23	NM_025943//XM_006519383	<i>Dzip1</i>	DAZ interacting protein 1	0007275 // multicellular organismal development // inferred from electronic annotation//0007283 // spermatogenesis // inferred from
1428636_at 1435:	0.000849	-2.06	-1.48	NM_013701//NM_145079//	<i>Ugt1a1//Ugt1a10//Ugt1a2//L</i>	UDP glucuronosyltransferase 1 family, polypeptide A1//UDP	0001889 // liver development // inferred from electronic annotation//0005975 // carbohydrate metabolic process // inferred from
1428705_at 693:	0.004976	-2.06	-2.89	NM_007702	<i>Cidea</i>	cell death-inducing DNA fragmentation factor, alpha subunit-like effector A	0001659 // temperature homeostasis // inferred from mutant phenotype//0006309 // apoptotic DNA fragmentation // inferred from
1428713_s_at 14:	0.005114	-2.06	1.08	NM_146019//XM_006532879	<i>Chd3</i>	chromodomain helicase DNA binding protein 3	0006200 // ATP catabolic process // inferred from electronic annotation//0006325 // chromatin organization // inferred from electronic
1428733_at 147:	0.002018	-2.06	-1.21	NM_027373//XM_006504097	<i>Afpap1</i>	actin filament associated protein 1	0009966 // regulation of signal transduction // not recorded
1428767_at 691:	0.002787	-2.07	-1.23	NM_177814//XM_006518930	<i>Erc2</i>	ELKS/RAB6-interacting/CAST family member 2	
1428805_at 215:	0.002289	-2.07	1.10	NM_012022//XR_035714//X	<i>Ppnr</i>	per-pentamer repeat gene	
1428808_at 243:	0.005795	-2.08	-1.34	NM_178726//XM_006501470	<i>Ppm1l</i>	protein phosphatase 1 (formerly 2C)-like	0000165 // MAPK cascade // inferred from physical interaction//0006470 // protein dephosphorylation // inferred from electronic
1428812_at 732:	0.009319	-2.08	-1.97	NM_001122758//NM_018764	<i>Pcdh7</i>	protodactherin 7	0007155 // cell adhesion // inferred from electronic annotation//0007156 // homophilic cell adhesion // inferred from electronic
1428827_at 1435:	0.004658	-2.08	-2.08	NM_001039376//NM_001110	<i>Pde4dip</i>	phosphodiesterase 4D interacting protein (myomegalin)	0043623 // cellular protein complex assembly // not recorded//0043623 // cellular protein complex assembly // inferred from sequence
1428859_at 212:	0.009950	-2.08	-1.95	NM_053106	<i>Lmod1</i>	leiomodin 1 (smooth muscle)	
1428887_at 145:	0.003294	-2.08	-1.70	NM_025735//NR_046364	<i>Map1lc3a</i>	microtubule-associated protein 1 light chain 3 alpha	0000045 // autophagic vacuole assembly // not recorded//0000422 // mitochondrion degradation // not recorded//0006914 //
1428899_at 381:	0.006369	-2.08	-1.06	NM_009441//XM_006522984	<i>Tnc3</i>	tetratricopeptide repeat domain 3	0006511 // ubiquitin-dependent protein catabolic process // not recorded//0001771 // negative regulation of cell morphogenesis
1428936_at 1425:	0.007637	-2.09	-1.26	NM_001081242//NM_027458	<i>Tln2</i>	talin 2	0007016 // cytoskeletal anchoring at plasma membrane // inferred from electronic annotation//0007155 // cell adhesion // inferred
1428972_at 1425:	0.005308	-2.09	-1.00	NM_001174107//NM_177395	<i>Map3k9</i>	mitogen-activated protein kinase kinase kinase 9	0000165 // MAPK cascade // inferred from electronic annotation//0000186 // activation of MAPK activity // inferred from electronic
1429008_at 674:	0.002145	-2.09	1.04	NM_172870//XM_006537929	<i>Bnc2</i>	basonuclin 2	0003416 // endochondral bone growth // inferred from mutant phenotype//0006351 // transcription, DNA-templated // inferred from
1429012_at 144:	0.004823	-2.10	-1.23	NM_019806	<i>Vapb</i>	vesicle-associated membrane protein, associated protein B and C	0006874 // cellular calcium ion homeostasis // not recorded//0006986 // response to unfolded protein // inferred from electronic
1429049_at 741:	0.008329	-2.10	-1.33	NM_001081364//NM_001128	<i>Arhgap21</i>	Rho GTPase activating protein 21	0007030 // Golgi organization // not recorded//0007165 // signal transduction // inferred from electronic annotation//0043547 //
1429071_at 109:	0.006369	-2.10	-1.33	NM_007620	<i>Cbr1</i>	carbonyl reductase 1	0008152 // metabolic process // inferred from electronic annotation//0017144 // drug metabolic process // not recorded//0042373 //
1429082_at 1434:	0.003908	-2.10	-1.00	NM_001289588//NM_178702	<i>Radil</i>	Ras association and DIL domains	0007155 // cell adhesion // inferred from electronic annotation//0007165 // signal transduction // inferred from electronic
1429089_s_at 14:	0.000583	-2.10	-1.28	NM_027526//XM_006506594	<i>Rasgef1a</i>	RasGEF domain family, member 1A	0007264 // small GTPase mediated signal transduction // inferred from electronic annotation//0016477 // cell migration // not
1429096_at 728:	0.001489	-2.10	-1.20	NM_001145830//NM_019677	<i>Pclb1</i>	phospholipase C, beta 1	0000086 // G2/M transition of mitotic cell cycle // inferred from direct assay//0000086 // G2/M transition of mitotic cell cycle // non-
1429111_at 1425:	0.002139	-2.11	-1.30	NM_153103//XM_006532320	<i>Kif1c</i>	kinasin family member 1C	0006890 // retrograde vesicle-mediated transport, Golgi to ER // inferred from direct assay//0007018 // microtubule-based movement
1429113_at 690:	0.001297	-2.11	-2.32	NM_001013390	<i>Scn4b</i>	sodium channel, type IV, beta	0006810 // transport // inferred from electronic annotation//0006811 // ion transport // inferred from electronic annotation//0006814
1429114_at 145:	0.005025	-2.11	-1.47	NM_011921	<i>Aldh1a7</i>	aldehyde dehydrogenase family 1, subfamily A7	0006068 // ethanol catabolic process // inferred from electronic annotation//0008152 // metabolic process // inferred from electronic
1429116_at 235:	0.002198	-2.11	-1.44	NM_008688//NM_026756//Xf	<i>Nfic</i>	nuclear factor I/c	0000122 // negative regulation of transcription from RNA polymerase II promoter // inferred from direct assay//0000122 // negative
1429163_at 233:	0.002863	-2.11	-1.27	NM_001170555//NM_001170	<i>Prkag2</i>	protein kinase, AMP-activated, gamma 2 non-catalytic subunit	0005977 // glycogen metabolic process // not recorded//0006110 // regulation of glycolytic process // not recorded//0006468 //
1429175_at 680:	0.007612	-2.11	-1.21	NM_001172121//NM_001172	<i>Rbms3</i>	RNA binding motif, single stranded interacting protein	0045727 // positive regulation of translation // inferred from direct assay
1429184_at 745:	0.001233	-2.11	-1.07	NM_007743	<i>Col1a2</i>	collagen, type I, alpha 2	0001501 // skeletal system development // not recorded//0001568 // blood vessel development // not recorded//0007179 //
1429184_at 100:	0.001233	-2.11	-1.55	NM_007382	<i>Acadm</i>	acyl-Coenzyme A dehydrogenase, medium chain	0001889 // liver development // inferred from mutant phenotype//0005978 // glycogen biosynthetic process // inferred from mutant
1429195_at 719:	0.004017	-2.11	-2.54	NM_001081306//NM_011219	<i>Ptpn22</i>	protein tyrosine phosphatase, receptor type Z, polypeptide 1	0002244 // hematopoietic progenitor cell differentiation // inferred from mutant phenotype//0006470 // protein dephosphorylation //
1429201_at 1425:	0.006175	-2.12	-1.67	NM_001165957//NR_028123	<i>160002914Rik//Nme9</i>	RIKEN CDNA 160002914 gene//NME/NM23 family member 9	0006165 // nucleoside diphosphate phosphorylation // inferred from electronic annotation//0006183 // GTP biosynthetic process //
1429235_at 1425:	0.002196	-2.12	-1.22	NM_008989//XM_006525724	<i>Pura//Ilgp</i>	purine rich element binding protein A//IgA inducing protein	0006268 // DNA unwinding involved in DNA replication // not recorded//0006270 // DNA replication initiation // traceable author
1429237_at 228:	0.003084	-2.12	1.10	NM_001164612//NM_001164	<i>Atp13a4</i>	ATPase type 13A4	0006200 // ATP catabolic process // inferred from electronic annotation//0006812 // cation transport // inferred from electronic
1429250_at 110:	0.008587	-2.13	1.09	NM_013755//XM_006535481	<i>Gyg</i>	glycogenin	0005978 // glycogen biosynthetic process // not recorded//0008152 // metabolic process // inferred from electronic annotation
1429272_s_at 14:	0.005181	-2.13	-1.22	NM_001170537//NM_025282	<i>Mef2c</i>	myocyte enhancer factor 2C	0000122 // negative regulation of transcription from RNA polymerase II promoter // inferred from genetic interaction//0000122 //
1429281_at 721:	0.008816	-2.13	-1.15	NM_001081146//NM_001134	<i>Prickle2</i>	prickle homolog 2 (Drosophila)	0031175 // neuron projection development // inferred from mutant phenotype//0045197 // establishment or maintenance of epithelial
1429298_at 1425:	0.004957	-2.13	-1.04	NM_015734//XM_006497644	<i>Col5a1</i>	collagen, type V, alpha 1	0001568 // blood vessel development // inferred from mutant phenotype//0003007 // heart morphogenesis // inferred from genetic
1429316_at 1435:	0.006103	-2.13	-1.11	NM_010143//XM_006521788	<i>Ephb3</i>	Eph receptor B3	0001525 // angiogenesis // inferred from mutant phenotype//0001655 // urogenital system development // inferred from mutant
1429338_s_at 14:	0.009159	-2.14	-1.07	NM_009517//XM_006535441	<i>Zmat3</i>	zinc finger matrix type 3	0006810 // transport // inferred from electronic annotation//0006915 // apoptotic process // inferred from electronic
1429344_at 745:	0.001561	-2.14	-1.46	NM_001037221//NM_001163	<i>Samd4</i>	sterile alpha motif domain containing 4	0006417 // regulation of translation // inferred from electronic annotation//0017148 // negative regulation of translation // not
1429413_at 145:	0.004217	-2.14	-1.04	NM_153582	<i>Cmtm4</i>	CKLF-like MARVEL transmembrane domain containing 4	0006935 // chemotaxis // inferred from electronic annotation
1429468_at 685:	0.001757	-2.15	-4.06	NM_001012401//XM_006539	<i>Hspb6</i>	heat shock protein, alpha-crystallin-related, B6	0006937 // regulation of muscle contraction // inferred from electronic annotation//0006950 // response to stress // inferred from
1429471_at 737:	0.009117	-2.15	-1.54	NM_001163638//NM_001163	<i>Ttrcl8</i>	tetratricopeptide repeat domain 18	
1429502_at 143:	0.006175	-2.15	-1.21	NM_0011436	<i>Sorl1</i>	soritin-related receptor, LDLR class A repeats-containing	0000042 // protein targeting to Golgi // not recorded//0006605 // protein targeting // not recorded//0006622 // protein targeting to
1429543_at 144:	0.001533	-2.15	-1.14	NM_001170745//NM_001170	<i>Magi2</i>	membrane associated guanylate kinase, WW and PDZ domain containing 2	0002092 // positive regulation of receptor internalization // not recorded//0007165 // signal transduction // inferred from physical
1429564_at 1434:	0.003222	-2.15	-1.24	NM_001270475//NM_153396	<i>Mical3</i>	microtubule associated monooxygenase, calponin and LIM domain containing	0006887 // exocytosis // inferred from electronic annotation//0007010 // cytoskeleton organization // not recorded//0008152 //
1429570_at 745:	0.000353	-2.15	-1.17	NM_010629//XM_006496679	<i>Kifap3</i>	kinasin-associated protein 3	0007017 // microtubule-based process // inferred from physical interaction//0007266 // Rho protein signal transduction // traceable
1429769_at 1425:	0.002923	-2.16	-1.52	NM_001002012//NM_008301	<i>Hspa2</i>	heat shock protein 2	0000902 // cell morphogenesis // inferred from electronic annotation//0001934 // positive regulation of protein phosphorylation //
1429779_at 145:	0.000645	-2.16	-1.12	NM_001039546//NM_008662	<i>Myo6</i>	myosin VI	0006605 // protein targeting // inferred from physical interaction//0006810 // transport // inferred from electronic
1429822_at 708:	0.002787	-2.17	-1.23	NM_175473//XM_006534873	<i>Fras1</i>	Franer syndrome 1 homolog (human)	0002009 // morphogenesis of an epithelium // inferred from mutant phenotype//0003338 // metanephros morphogenesis // inferred
1429927_at 760:	0.003587	-2.17	-1.13	NM_001081150	<i>Lorrf1</i>	LOR peptidease N-terminal domain and ring finger 1	0002600 // ATP catabolic process // inferred from electronic annotation//0005008 // proteolysis // inferred from electronic annotation
1429930_at 718:	0.004130	-2.17	-1.17	NM_013464	<i>Ahr</i>	aryl-hydrocarbon receptor	0000122 // negative regulation of transcription from RNA polymerase II promoter // inferred from direct assay//0009092 // cell
1429977_at 745:	0.000320	-2.17	-1.18	NM_080793	<i>Setd7</i>	SET domain containing (lysine methyltransferase) 7	0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 // regulation of transcription, DNA-templated
1430030_at 681:	0.001023	-2.17	-1.00	NM_177561//XM_006504268	<i>Usp46</i>	ubiquitin specific peptidase 46	0001662 // behavioral fear response // inferred from mutant phenotype//0006508 // proteolysis // not recorded//0006511 // ubiquitin-
1430112_at 143:	0.002489	-2.17	-1.34	NM_173444//XM_006496028	<i>Nbeal1</i>	neurobeachin like 1	
1430135_at 100:	0.000837	-2.18	1.11	NM_021344//XR_387574	<i>Tesc</i>	tescalcin	0006469 // negative regulation of protein kinase activity // inferred from electronic annotation//0006810 // transport // inferred from
1430137_at 100:	0.006291	-2.18	-1.11	NM_001085492//XM_006537	<i>Rere</i>	arginine glutamic acid dipeptide (RE) repeats	0006338 // chromatin remodeling // inferred from physical interaction//0006351 // transcription, DNA-templated // inferred from
1430183_at	0.001757	-2.18	-1.56	NM_029556//XM_006519497	<i>Clybl</i>	citrate lyase beta like	0006725 // cellular aromatic compound metabolic process // inferred from electronic annotation
1430185_at 143:	0.001012	-2.18	-1.04	NM_183186//XM_006516232	<i>Foxn3</i>	forkhead box N3	0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 // regulation of transcription, DNA-templated
1430196_at 688:	0.009319	-2.19	-1.13	NM_001007220//NM_001007	<i>Adam22</i>	a disintegrin and metalloproteinase domain 22	0006508 // proteolysis // inferred from electronic annotation//0007229 // integrin-mediated signaling pathway // inferred from
1430269_at 687:	0.004444	-2.19	-1.42	NM_001081276//NM_001293	<i>Clasp1</i>	CLIP associating protein 1	0000226 // microtubule cytoskeleton organization // not recorded//0001578 // microtubule bundle formation // not
1430343_at 145:	0.002665	-2.19	-1.00	NM_001008501	<i>Zfp760</i>	zinc finger protein 760	0006355 // regulation of transcription, DNA-templated // inferred from electronic annotation
1430404_at 757:	0.003013	-2.19	-1.02	NM_001190374//XM_006507	<i>Adamsl3</i>	ADAMTS-like 3	0006508 // proteolysis // inferred from electronic annotation
1430449_at 143:	0.003312	-2.19	-1.33	NM_001162943//XM_006507	<i>Dchs1</i>	dachsous 1 (Drosophila)	0001658 // branching involved in ureteric bud morphogenesis // inferred from mutant phenotype//0001736 // establishment of planar
1430530_s_at 14:	0.000669	-2.19	-1.04	NM_001290679//NM_029398	<i>Tmem14a</i>	transmembrane protein 14A	
1430607_at 1435:	0.006140	-2.20	-1.13	NM_001040459//XM_006527	<i>Shroom4</i>	shroom family member 4	0000902 // cell morphogenesis // inferred from sequence or structural similarity//0007015 // actin filament organization // inferred
1430612_at 691:	0.005881	-2.20	-1.39	NM_027629//XM_006508204	<i>Pgm2l1</i>	phosphoglucomutase 2-like 1	0005975 // carbohydrate metabolic process // inferred from electronic annotation//0006006 // glucose metabolic process // not
1430637_at 701:	0.006265	-2.20	-1.59	NM_001101535	<i>Ccdc8</i>	coiled-coil domain containing 8	0000226 // microtubule cytoskeleton organization // inferred from sequence or structural similarity//0007088 // regulation of mitosis //
1430642_at 769:	0.004709	-2.20	1.04	NM_026514//XM_006524295	<i>Cdc42ep3</i>	CDC42 effector protein (Rho GTPase binding) 3	0008360 // regulation of cell shape // inferred from electronic annotation

Table S6

Gene_ID	p (Corr)	FC-RSV 1 d	FC-RSV 5 d	RefSeq Transcript ID	Gene Symbol	Gene Title	Gene Ontology Biological Process
1430646_at,1435	0.004267	-2.21	-1.19	NM_013476	<i>Ar</i>	androgen receptor	0001701 // in utero embryonic development // inferred from mutant phenotype//0003073 // regulation of systemic arterial blood
1430704_at,1435	0.004017	-2.21	-2.39	NM_001081425//XR_382235	<i>Rbm24</i>	RNA binding motif protein 24	0010830 // regulation of myotube differentiation // inferred from mutant phenotype//00030154 // cell differentiation // inferred from
1430781_at,1788	0.002258	-2.21	-1.55	NM_011340	<i>Serpinf1</i>	serine (or cysteine) peptidase inhibitor, clade F, member 1	0001822 // kidney development // inferred from electronic annotation//0007568 // aging // inferred from electronic
1430796_at,1435	0.001763	-2.22	-2.43	NM_001289533//NM_010212	<i>Fhl2</i>	four and a half UIM domains 2	0000122 // negative regulation of transcription from RNA polymerase II promoter // not recorded//0001649 // osteoblast
1430852_at,1697	0.006636	-2.22	-2.17	NM_029920//XM_006504890	<i>Mtus2</i>	microtubule associated tumor suppressor candidate 2	
1430852_at,1623	0.006636	-2.22	-1.85	NM_001159487//NM_011255	<i>Rbp4</i>	retinol binding protein 4, plasma	0001654 // eye development // inferred from mutant phenotype//0001654 // eye development // not recorded//0006094 //
1430886_at,1435	0.003594	-2.23	-1.21	NM_001039959//NM_001286	<i>Ahnak</i>	AHNAK nucleoprotein (desmoyokin)	0043484 // regulation of RNA splicing // inferred from direct assay//0051259 // protein oligomerization // inferred from mutant
1431079_at,1691	0.002520	-2.23	-1.05	NM_133710//XM_006512262	<i>Ctdsp1</i>	CTD (carboxy-terminal domain, RNA polymerase II, polypeptide A) small	0008152 // metabolic process // inferred from electronic annotation//0016311 // dephosphorylation // inferred from electronic
1431095_a_at,14	0.000240	-2.23	-1.21	NM_178214	<i>Hist2h2be</i>	histone cluster 2, H2be	0002227 // innate immune response in mucosa // not recorded//0006334 // nucleosome assembly // inferred from electronic
1431114_at,1435	0.001858	-2.23	-1.47	NM_010617//XM_006516861	<i>Kif13a</i>	kinesin family member 13A	0000910 // cytokinesis // not recorded//0006810 // transport // inferred from electronic annotation//0006886 // intracellular protein
1431173_at,1455	0.002138	-2.23	-1.47	NM_139300//XM_006521702	<i>Myk1</i>	myosin, light polypeptide kinase	0006468 // protein phosphorylation // not recorded//0006939 // smooth muscle contraction // inferred from mutant
1431192_at,1435	0.002747	-2.23	-1.06	NM_146234	<i>Mmg1</i>	membrane magnesium transporter 1	0006810 // transport // inferred from electronic annotation//0006812 // cation transport // inferred from direct assay//0006824 //
1431248_at,1681	0.008494	-2.23	-1.27		<i>E130014H10rik</i>	RIKEN cDNA E130014H10 gene	0006536 // glutamate metabolic process // inferred from mutant phenotype//0006537 // glutamate biosynthetic process // inferred
1431358_at,1435	0.009324	-2.24	-1.29	NM_001097621//XM_006516	<i>Kif26a</i>	kinesin family member 26A	0001560 // regulation of cell growth by extracellular stimulus // inferred from mutant phenotype//0007018 // microtubule-based
1431462_at,1434	0.005072	-2.24	-3.87	NM_146117	<i>Lrrc26</i>	leucine rich repeat containing 26	0006810 // transport // inferred from electronic annotation//0006811 // ion transport // inferred from electronic annotation
1431471_at,1770	0.005972	-2.25	-2.37	NM_182992	<i>Mypp</i>	myopalladin	0045214 // sarcomere organization // not recorded
1431528_at,1760	0.003059	-2.25	1.23	NM_001277305//NM_175643	<i>Adams2</i>	a disintegrin-like and metalloproteinase (prolysin type) with	000508 // proteolysis // inferred from direct assay//0007283 // spermatogenesis // inferred from mutant phenotype//0016485 //
1431733_at,1714	0.008617	-2.25	-1.25	NM_001033198//NM_001167	<i>Ankrd50</i>	ankyrin repeat domain 50	0003143 // embryonic heart tube morphogenesis // inferred from genetic interaction//0006351 // transcription, DNA-templated //
1431799_at,1435	0.004080	-2.25	-1.40	NM_001166584//NM_001166	<i>Tea1</i>	TEA domain family member 1	0000281 // mitotic cytokinesis // not recorded//0007009 // plasma membrane organization // not recorded//0007165 // signal
1432037_at,1444	0.001604	-2.26	-1.14	NM_009670//NM_146005//	<i>Ank3</i>	ankyrin 3, epithelial	0006810 // transport // inferred from electronic annotation//0006869 // lipid transport // inferred from electronic
1432049_at,1746	0.006808	-2.26	-1.42	NM_145823//XM_006534262	<i>Pitpnc1</i>	phosphatidylinositol transfer protein, cytoplasmic 1	0001525 // angiogenesis // inferred from mutant phenotype//0001569 // patterning of blood vessels // inferred from mutant
1432060_at,1435	0.004263	-2.26	-1.16	NM_008737//XM_006530766	<i>Nrp1</i>	neuropilin 1	0001574 // ganglioside biosynthetic process // not recorded//0006486 // protein glycosylation // not recorded//0006491 // N-glycan
1432205_a_at,14	0.004513	-2.26	-1.03	NM_001159745//NM_009183	<i>St8sia4</i>	ST8 alpha-N-acetyl-neuraminidase alpha-2,8-sialyltransferase 4	0008206 // insulin receptor signaling pathway // inferred from direct assay//0016310 // phosphorylation // inferred from electronic
1432476_at,1770	0.006015	-2.27	-1.22	NM_181585//XM_006502859	<i>Plk3r3</i>	platelet-derived growth factor receptor subunit, polypeptide 3 (p55)	0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 // regulation of transcription, DNA-templated
1432757_at,1435	0.003455	-2.27	1.18	NM_033327//XM_006531534	<i>Zfp423</i>	zinc finger protein 423	0000122 // negative regulation of transcription from RNA polymerase II promoter // inferred from direct assay//0000122 // negative
1432861_at,1454	0.001640	-2.27	-1.62	NM_009234	<i>Sox11</i>	SRF (sex determining region Y)-box 11	0030030 // cell projection organization // inferred from electronic annotation//0042073 // intracellular transport // inferred by curator
1433000_at,1434	0.000919	-2.28	-2.08	NM_028235	<i>Tcc30b</i>	tetratricopeptide repeat domain 30B	0010629 // negative regulation of gene expression // not recorded//0035356 // cellular triglyceride homeostasis // not
1433093_at,1454	0.002184	-2.29	1.15	NM_001204134//NM_030888	<i>C1qtnf3</i>	C1q and tumor necrosis factor related protein 3	0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 // regulation of transcription, DNA-templated
1433184_at,1777	0.002537	-2.29	-1.20	NM_001111026//NM_001111	<i>Runx1t1</i>	runt-related transcription factor 1; translocated to, 1 (cyclin D-related)	0060857 // establishment of glial blood-brain barrier // inferred from expression pattern
1433266_at,1702	0.000927	-2.29	-1.10	NM_024263//XM_006539325	<i>Mxra8</i>	membrane-remodelling associated 8	0006810 // transport // inferred from electronic annotation//0006811 // ion transport // inferred from electronic annotation//0006813
1433481_at,1455	0.004858	-2.30	-2.44	NM_008426//XM_006497728	<i>Kcnj3</i>	potassium inwardly-rectifying channel, subfamily J, member 3	
1433523_at,1231	0.003001	-2.30	-1.47	NM_173038//XM_006510390	<i>Tbce1</i>	tubulin folding cofactor E-like	
1433529_at,1210	0.000524	-2.31	-1.31	NM_029875//XR_380382	<i>Slc35e3</i>	solute carrier family 35, member E3	0055085 // transmembrane transport // inferred from electronic annotation
1433566_at,1276	0.004493	-2.31	-1.06	NM_031392	<i>Wdr6</i>	WD repeat domain 6	0007049 // cell cycle // inferred from electronic annotation//0007050 // cell cycle arrest // not recorded//0008285 // negative
1433624_at,1435	0.001478	-2.31	-1.74	NM_001033478//NM_001170	<i>Fam47e</i>	family with sequence similarity 47, member E	
1433647_s_at,14	0.007141	-2.31	-1.59	NM_145983	<i>Kcna5</i>	potassium voltage-gated channel, shaker-related subfamily, member 5	0001666 // response to hypoxia // inferred from electronic annotation//0006810 // transport // inferred from electronic
1433651_at,1011	0.008627	-2.32	-1.47	NM_001109661//NM_007521	<i>Bach2</i>	B7H and CNC homology 2	0000122 // negative regulation of transcription from RNA polymerase II promoter // inferred from direct assay//0006351 //
1433790_at,1455	0.006379	-2.32	-1.51	NM_177566//XM_006533664	<i>Arhgef15</i>	Rho guanine nucleotide exchange factor (GEF) 15	0032319 // regulation of Rho GTPase activity // inferred from direct assay//0032319 // regulation of Rho GTPase activity // not
1433812_at,1280	0.009088	-2.32	-1.62	NM_152915	<i>Dner</i>	delta/notch-like EGF-related receptor	0007219 // Notch signaling pathway // inferred from electronic annotation//0007220 // Notch receptor processing // inferred from
1433823_at,1435	0.001742	-2.32	-2.04	NM_138628	<i>Txnib</i>	taxilin beta	
1433854_at,1454	0.007322	-2.32	-1.65	NM_027491	<i>Rragd</i>	Ras-related GTP binding D	
1433857_at,1411	0.001071	-2.32	-1.33	NM_001082414//NM_012059	<i>Sh3d19</i>	SH3 domain protein D19	0007010 // cytoskeleton organization // not recorded//0022604 // regulation of cell morphogenesis // not recorded//0051044 //
1433861_at,1455	0.003558	-2.33	1.05	NM_011828//XM_006501449	<i>Hs2st1</i>	heparan sulfate 2-O-sulfotransferase 1	0015014 // heparan sulfate proteoglycan biosynthetic process, polysaccharide chain biosynthetic process // inferred from mutant
1433864_at,1239	0.008301	-2.33	-1.15	NM_011261//XM_006535644	<i>Reln</i>	reelin	0000904 // cell morphogenesis involved in differentiation // inferred from mutant phenotype//0001764 // neuron migration // inferred
1433873_s_at,14	0.001958	-2.33	-1.56	NM_138956//XM_006513379	<i>Rassf3</i>	Ras association (RalGDS/AF-6) domain family member 3	0007165 // signal transduction // inferred from electronic annotation
1433877_at,100	0.004383	-2.33	-1.00	NM_010062//NR_103491	<i>Dnase2a</i> //LOC100503676	deoxyribonuclease II alpha//uncharacterized LOC100503676	0000737 // DNA catabolic process, endonucleolytic // inferred from direct assay//0006259 // DNA metabolic process // inferred from
1433920_at,1203	0.004839	-2.33	1.10	NM_001291227//NM_001291	<i>Slit2</i>	slit homolog 2 (Drosophila)	0001656 // metanephros development // inferred from mutant phenotype//0001657 // ureteric bud development // not
1433937_at,1435	0.005121	-2.33	-2.10	NM_011382//XM_006515632	<i>Six4</i>	sine oculis-related homeobox 4	0006355 // regulation of transcription, DNA-templated // inferred from electronic annotation//0007275 // multicellular organismal
1433986_at,108	0.001166	-2.34	1.03	NM_026239	<i>Tmem35</i>	transmembrane protein 35	
1433992_at,1444	0.005031	-2.34	-2.03	NM_001122683//NM_175177	<i>Bdh1</i>	3-hydroxybutyrate dehydrogenase, type 1	0001889 // liver development // inferred from electronic annotation//0007420 // brain development // inferred from electronic
1434015_at,1227	0.009610	-2.35	1.21	NM_147220//XM_006533064	<i>Abca9</i>	ATP-binding cassette, sub-family A (ABC1), member 9	0006200 // ATP catabolic process // inferred from electronic annotation//0006810 // transport // inferred from electronic
1434046_at,1433	0.003594	-2.36	-3.03	NM_009204//XM_006532653	<i>Slc2a4</i>	solute carrier family 2 (facilitated glucose transporter), member 4	0006810 // transport // inferred from electronic annotation//0008643 // carbohydrate transport // inferred from electronic
1434067_at,1434	0.003576	-2.36	-1.15	NM_001290733//NM_001290	<i>Osp4l6</i>	oxysterol binding protein-like 6	0006810 // transport // inferred from electronic annotation//0006869 // lipid transport // inferred from electronic annotation
1434086_at,1444	0.005346	-2.36	-1.60	NM_010608	<i>Kcnk3</i>	potassium channel, subfamily K, member 3	0006810 // transport // inferred from electronic annotation//0006811 // ion transport // inferred from electronic annotation//0006813
1434111_at,1434	0.003984	-2.36	-1.21	NM_053128	<i>Pcdhb3</i>	protocadherin beta 3	0007155 // cell adhesion // inferred from electronic annotation//0007156 // homophilic cell adhesion // inferred from electronic
1434139_at,1444	0.003042	-2.36	1.87	NM_009144//XM_006501183	<i>Sfrp2</i>	secreted frizzled-related protein 2	0001569 // patterning of blood vessels // inferred from direct assay//0001756 // somitogenesis // inferred from genetic
1434202_a_at,14	0.009827	-2.37	1.03	NM_019641	<i>Stmn1</i>	stathmin 1	0007019 // microtubule depolymerization // not recorded//0007052 // mitotic spindle organization // not recorded//0007275 //
1434301_at,1399	0.002111	-2.38	-1.35	NM_001042615//NM_030127	<i>Htra3</i>	HtrA serine peptidase 3	0001525 // regulation of cell growth // inferred from electronic annotation//0006508 // proteolysis // inferred from direct
1434338_at,1242	0.004133	-2.38	-1.31	NM_001081390//NM_001293	<i>Pallid</i>	palladin, cytoskeletal associated protein	0031175 // neuron projection development // not recorded//0031529 // ruffle organization // not recorded//0071803 // positive
1434377_at,106	0.006440	-2.39	-1.40	NM_001122952//NM_001122	<i>Nfia</i>	nuclear factor I- α	0006260 // DNA replication // inferred from electronic annotation//0006351 // transcription, DNA-templated // inferred from electronic
1434477_at,1434	0.004460	-2.39	-1.17	NM_001033281//XM_006525	<i>Pdr1m6</i>	PR domain containing 6	0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 // regulation of transcription, DNA-templated
1434815_a_at,14	0.003832	-2.40	-1.33	NM_001161763//NM_001161	<i>Fmo5</i>	flavin containing monooxygenase 5	0055114 // oxidation-reduction process // not recorded
1434909_at,1444	0.004948	-2.42	-1.04	NM_001159533//NM_001159	<i>Cacna1c</i>	calcium channel, voltage-dependent, L type, alpha 1C subunit	0006810 // transport // inferred from electronic annotation//0006811 // ion transport // inferred from electronic annotation//0006816
1434945_at,1444	0.004348	-2.42	1.06	NM_145376//XM_006517188	<i>Lpcat1</i>	lysophosphatidylcholine acyltransferase 1	0006629 // lipid metabolic process // inferred from electronic annotation//0006644 // phospholipid metabolic process // inferred from
1434991_at,109	0.001646	-2.42	1.13	NR_028574//NR_028573	<i>Shnlg8</i> // <i>Snora24</i>	small nucleolar RNA host gene 8//small nucleolar RNA, H/ACA box 24	
1434997_at,1455	0.000738	-2.42	-1.01	NM_175549//XM_006523035	<i>Robo2</i>	roundabout homolog 2 (Drosophila)	0001656 // metanephros development // inferred from mutant phenotype//0001657 // ureteric bud development // inferred from
1435078_at,1435	0.005986	-2.43	-1.18	NM_001146180//NM_144800	<i>Mts1</i>	metastasis suppressor 1	0001701 // in utero embryonic development // inferred from genetic interaction//0007015 // actin filament organization // inferred
1435208_at,1435	0.001489	-2.43	-1.27	NM_001166493//NM_207246	<i>Rasgrp3</i>	RAS, guanyl releasing protein 3	0007264 // small GTPase mediated signal transduction // inferred from electronic annotation//0007265 // Ras protein signal
1435264_at,1246	0.005500	-2.44	-1.27	NM_025877//XM_006524806	<i>Slc25a23</i>	solute carrier family 25 (mitochondrial carrier; phosphate carrier), member	0002082 // regulation of oxidative phosphorylation // inferred from mutant phenotype//0006810 // transport // inferred from
1435279_at,1444	0.006015	-2.44	-2.20	NM_029044//XM_006534382	<i>Lrrc48</i>	leucine rich repeat containing 48	
1435280_at,1455	0.005139	-2.44	-1.62	NM_027442//XM_006512842	<i>Ddo</i>	D-aspartate oxidase	0006531 // aspartate metabolic process // inferred from mutant phenotype//0006533 // aspartate catabolic process // not
1435313_at,1239	0.005334	-2.44	-1.28	NM_172867//XM_006537915	<i>Zfp462</i>	zinc finger protein 462	0006325 // chromatin organization // inferred from mutant phenotype//0007010 // cytoskeleton organization // inferred from
1435325_at,1435	0.006175	-2.45	1.02	NM_001034863//XM_006510	<i>Tmem136</i>	transmembrane protein 136	
1435359_at,1244	0.004990	-2.46	-1.25	NM_010621//XM_006500509	<i>Startd9</i>	START domain containing 9	0007018 // microtubule-based movement // inferred from electronic annotation//0008152 // metabolic process // inferred from
1435361_at,1218	0.006485	-2.47	-1.22	NM_008808//XM_006504658	<i>Pdgra</i>	platelet derived growth factor, alpha	0001525 // angiogenesis // inferred from direct assay//0001666 // response to hypoxia // inferred from electronic
1435490_at,1444	0.008460	-2.47	-1.01	NM_019759	<i>Dpt</i>	dermatopontin	0007155 // cell adhesion // inferred from electronic annotation//0008285 // negative regulation of cell proliferation // inferred from
1435529_at,1667	0.000815	-2.47	-1.19	NM_177756//XR_387172	<i>Colgalt2</i>	collagen beta(1-O)galactosyltransferase 2	0009103 // lipopolysaccharide biosynthetic process // inferred from electronic annotation
1435553_at,1444	0.004201	-2.47	-2.43	NM_001109040//NM_001109	<i>Kif21a</i>	kinesin family member 21A	0007018 // microtubule-based movement // inferred from electronic annotation//0008152 // metabolic process // inferred from

Table S6

Gene_ID	p (Corr)	FC-RSV 1 d	FC-RSV 5 d	RefSeq Transcript ID	Gene Symbol	Gene Title	Gene Ontology Biological Process
1435557_at 234	0.001720	-2.47	-1.03	NM_170778//XM_006502422	<i>Dpyd</i>	dihydropyrimidine dehydrogenase	0006145 // purine nucleobase catabolic process // not recorded//0006208 // pyrimidine nucleobase catabolic process // inferred from
1435582_at 144	0.008085	-2.48	-1.44	NM_001081337//XM_006531	<i>Sipa1l2</i>	signal-induced proliferation-associated 1 like 2	0043547 // positive regulation of GTPase activity // inferred from electronic annotation//00051056 // regulation of small GTPase
1435642_at 145	0.001309	-2.49	1.05	NM_029522//XM_006502526	<i>Gpsm2</i>	G-protein signalling modulator 2 (AGS3-like, C. elegans)	0000132 // establishment of mitotic spindle orientation // inferred from mutant phenotype//0008277 // regulation of G-protein coupled
1435649_at 688	0.006144	-2.49	1.12	NR_028573//NR_028574	<i>Shhg8//Snora24</i>	small nucleolar RNA host gene 8//small nucleolar RNA, H/ACA box 24	
1435691_at 144	0.004283	-2.49	-1.20	NM_025331	<i>Gng11</i>	guanine nucleotide binding protein (G protein), gamma 11	0007165 // signal transduction // inferred from electronic annotation//0007186 // G-protein coupled receptor signaling pathway //
1435699_at 143	0.004990	-2.49	-1.38		<i>A1448984</i>	expressed sequence A1448984	0006260 // DNA replication // inferred from electronic annotation//0006260 // DNA replication // traceable author
1435719_at 100	0.002779	-2.49	-1.16	NM_001287514//NM_001287	<i>Cebpa</i>	CCAAT/enhancer binding protein (C/EBP), alpha	0000050 // urea cycle // inferred from direct assay//0000122 // negative regulation of transcription from RNA polymerase II promoter //
1435813_at 144	0.006794	-2.50	-1.23	NM_009955//XM_006518508	<i>Dpyl2</i>	dihydropyrimidinase-like 2	0001975 // response to amphetamine // inferred from electronic annotation//0006208 // pyrimidine nucleobase catabolic process //
1435874_at 143	0.007663	-2.50	-1.11	NM_172619//NR_037707//NM	<i>Adams10</i>	a disintegrin-like and metalloproteinase (repolysin type) with	0006508 // proteolysis // inferred from electronic annotation
1435880_at 996	0.004958	-2.50	-1.57	NM_011020//XM_006500766	<i>Hspa4l//4921509117rik</i>	heat shock protein 4 like//RIKEN cDNA 4921509117 gene	0000902 // cell morphogenesis // inferred from electronic annotation//0006457 // protein folding // not recorded//0006950 //
1435917_at 145	0.009213	-2.51	-1.68	NM_172859//XM_006499511	<i>Dzank1</i>	double zinc ribbon and ankryrin repeat domains 1	
1435938_at 145	0.009474	-2.51	-1.33	NM_001271725//NM_001271	<i>Trim2</i>	tripartite motif-containing 2	0016567 // protein ubiquitination // inferred from direct assay//0043523 // regulation of neuron apoptotic process // inferred from
1435947_at	0.009588	-2.51	-1.29	NM_001164717//NM_008018	<i>Sh3pxd2a</i>	SH3 and PX domains 2A	0006801 // superoxide metabolic process // not recorded//0007154 // cell communication // inferred from electronic
1435948_at 547	0.008726	-2.52	-1.93	NM_178774//NR_028280	<i>Prr18</i>	proline rich 18	
1435948_at 100	0.008726	-2.52	-3.21	NM_001168318//NM_028903	<i>Scara5</i>	scavenger receptor class A, member 5 (putative)	0006810 // transport // inferred from electronic annotation//0006811 // ion transport // inferred from electronic annotation//0006879
1435990_at 145	0.007140	-2.52	-1.59	NM_001198790//NM_001198	<i>Ak1</i>	adenylylate kinase 1	0006139 // nucleobase-containing compound metabolic process // inferred from electronic annotation//0006165 // nucleoside
1436035_at 217	0.005452	-2.52	-2.43	NM_178689//XM_006527054	<i>Eno4</i>	enolase 4	0006096 // glycolytic process // inferred from mutant phenotype//0030317 // sperm motility // inferred from mutant
1436074_at 243	0.008839	-2.52	-2.50	NM_009694	<i>Apobec2</i>	apolipoprotein B mRNA editing enzyme, catalytic polypeptide 2	0006397 // mRNA processing // inferred from electronic annotation//0016556 // mRNA modification // inferred from mutant
1436080_at 144	0.002665	-2.52	-1.21	NM_001081175//XM_006496	<i>itpkb</i>	inositol 1,4,5-trisphosphate 3-kinase B	0001665 // MAPK cascade // inferred from mutant phenotype//0007166 // cell surface receptor signaling pathway // inferred from
1436120_at 239	0.001136	-2.52	-1.37	NM_001291910//NM_009624	<i>Adcy9</i>	adenylylate cyclase 9	0006171 // cAMP biosynthetic process // inferred from direct assay//0006171 // cAMP biosynthetic process // not recorded//0006171
1436126_at 145	0.008505	-2.52	-1.31	NM_001115130//NM_172765	<i>Zbtb44</i>	zinc finger and BTB domain containing 44	0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 // regulation of transcription, DNA-templated
1436155_at 226	0.006097	-2.53	-1.30	NM_026793	<i>Myct1</i>	myc target 1	
1436281_at 144	0.005199	-2.53	-1.34	NM_011125//XM_006498952	<i>Pltp</i>	phospholipid transfer protein	0006810 // transport // inferred from electronic annotation//0006869 // lipid transport // inferred from electronic
1436332_at 243	0.001963	-2.54	-1.41	NM_001289645//NM_001289	<i>Pxylp1</i>	2-phosphoxyleose phosphatase 1	0008152 // metabolic process // inferred from electronic annotation//0016311 // dephosphorylation // inferred from electronic
1436492_x_at 14	0.006697	-2.54	-1.33	NM_025451	<i>Camk2n1</i>	calcium/calmodulin-dependent protein kinase II inhibitor 1	0006469 // negative regulation of protein kinase activity // not recorded
1436503_at 232	0.002853	-2.55	-2.35	NM_172469	<i>Clic6</i>	chloride intracellular channel 6	0006810 // transport // inferred from electronic annotation//0006811 // ion transport // inferred from electronic annotation//0006821
1436576_at 215	0.001680	-2.56	-1.88	NM_029993	<i>Mlana</i>	melan-A	
1436612_at 697	0.009518	-2.56	1.09	NM_001163155//NM_007736	<i>Col4a5</i>	collagen, type IV, alpha 5	0007528 // neuromuscular junction development // inferred from mutant phenotype
1436633_at	0.000467	-2.56	-1.98	NM_178143//XM_006502651	<i>Pknox2</i>	protein kinase, AMP-activated, alpha 2 catalytic subunit	0006281 // DNA repair // inferred from electronic annotation//0006310 // DNA recombination // inferred from electronic
1436673_at 143	0.001241	-2.56	-1.19	NM_052994//XM_006514347	<i>Spock2</i>	sparc/osteonectin, cwc and kazal-like domains proteoglycan 2	0007165 // signal transduction // inferred from electronic annotation//0010811 // positive regulation of cell-substrate adhesion //
1436675_at 242	0.009993	-2.56	-1.96	NM_001079844//NM_011821	<i>Gpc6</i>	glypican 6	0016477 // cell migration // not recorded
1436705_at 143	0.002724	-2.57	-1.98	NM_028030//XM_001477422	<i>Gm3470//Rbpm25</i>	predicted gene 3470//RNA binding protein with multiple splicing 2	
1436735_at 143	0.004815	-2.58	-1.24	NM_019933//XM_006529253	<i>Ptpn4</i>	protein tyrosine phosphatase, non-receptor type 4	0006470 // protein dephosphorylation // inferred from electronic annotation//0016311 // dephosphorylation // inferred from electronic
1436785_x_at 14	0.008948	-2.59	-1.18	NM_007496//XM_006530585	<i>Zfhx3</i>	zinc finger homeobox 3	0000122 // negative regulation of transcription from RNA polymerase II promoter // not recorded//0006351 // transcription, DNA-
1436814_at 143	0.000935	-2.59	-1.10	NM_026639	<i>Art4</i>	ADP-ribosyltransferase 4	0006471 // protein ADP-ribosylation // inferred from electronic annotation
1436827_at 145	0.006917	-2.59	-1.32	NM_001004468//NM_021314	<i>Tacc2</i>	transforming, acidic coiled-coil containing protein 2	0000226 // microtubule cytoskeleton organization // inferred from mutant phenotype//0008283 // cell proliferation // inferred from
1436907_at 143	0.000239	-2.60	-1.41	NM_173437//XM_006529369	<i>Nav1</i>	neuron navigator 1	0001578 // microtubule bundle formation // inferred from direct assay//0001764 // neuron migration // inferred from mutant
1436962_at 225	0.006710	-2.61	-2.14	NM_021456	<i>Ces1g</i>	carboxylesterase 1G	0008152 // metabolic process // inferred from electronic annotation
1437060_at 380	0.001877	-2.61	-1.25	NM_007963//NM_021442//X	<i>Mecom</i>	MDS1 and EVI1 complex locus	0001701 // in utero embryonic development // inferred from mutant phenotype//0001780 // neutrophil homeostasis // inferred from
1437087_at	0.007721	-2.61	-1.10	NM_001166635//NM_026524	<i>Mid1p1</i>	Mid1 interacting protein 1 (gastrulation specific G12-like (zebrafish))	0006629 // lipid metabolic process // inferred from electronic annotation//0007026 // negative regulation of microtubule
1437093_at 143	0.006485	-2.61	-1.29	NM_001029937	<i>Sec14l3</i>	SEC14-like 3 (S. cerevisiae)	0006810 // transport // inferred from electronic annotation
1437176_at 434	0.001297	-2.61	-1.20	NM_011682//XM_006512706	<i>Utrn</i>	utrophin	0001954 // positive regulation of cell-matrix adhesion // not recorded//0007527 // adult somatic muscle development // traceable
1437400_at 143	0.001570	-2.62	-1.07	NM_007735	<i>Col4a4</i>	collagen, type IV, alpha 4	0032836 // glomerular basement membrane development // inferred from mutant phenotype//0032836 // glomerular basement
1437442_at	0.004067	-2.62	-1.17	NM_028763	<i>Cbx6</i>	chromobox 6	0000122 // negative regulation of transcription from RNA polymerase II promoter // not recorded//0006351 // transcription, DNA-
1437482_at 243	0.005546	-2.62	-1.84	NM_001024474//XM_006516	<i>Diras2</i>	DIRAS family, GTP-binding RAS-like 2	0006184 // GTP catabolic process // inferred from electronic annotation//0007165 // signal transduction // inferred from electronic
1437514_at 320	0.001877	-2.62	1.05	NM_001042752//NM_008684	<i>Neo1</i>	neogenin	0006355 // regulation of transcription, DNA-templated // inferred from direct assay//0007155 // cell adhesion // inferred from
1437577_at	0.004864	-2.63	-1.07	NM_015775//XM_006523064	<i>Tmprss2</i>	transmembrane protease, serine 2	0006508 // proteolysis // inferred from direct assay//0006508 // proteolysis // not recorded//0006898 // receptor-mediated
1437595_at 226	0.002163	-2.63	-1.38	NM_172665//XM_006499197	<i>Pdk1</i>	pyruvate dehydrogenase kinase, isoenzyme 1	0005975 // carbohydrate metabolic process // inferred from electronic annotation//0006006 // glucose metabolic process // inferred
1437798_at 999	0.006265	-2.63	-1.34	NM_001193271//NM_010789	<i>Meis1</i>	Meis homeobox 1	0001525 // angiogenesis // inferred from mutant phenotype//0002089 // lens morphogenesis in camera-type eye // inferred from
1437871_at 226	0.009730	-2.64	-1.96	NM_001033460	<i>Drc1</i>	dynein regulatory complex subunit 1	0006285 // cilium-dependent cell motility // not recorded//0007286 // axonemal dynein complex assembly // not recorded//0007193
1437930_at 269	0.002562	-2.64	-1.01	NM_198171//XM_006530885	<i>Ces2b</i>	carboxylesterase 2B	0006508 // proteolysis // inferred from electronic annotation//0008152 // metabolic process // inferred from electronic annotation
1438003_at 143	0.000320	-2.64	-2.59	NM_001110140//NM_009722	<i>Atp2a2</i>	ATPase, Ca++ transporting, cardiac muscle, slow twitch 2	0002026 // regulation of the force of heart contraction // inferred from genetic interaction//0006200 // ATP catabolic process //
1438027_at	0.003019	-2.65	-1.20	NM_008306//XM_006525667	<i>Ndst1</i>	N-deacetylase-N-sulfotransferase (heparan glucosaminyl) 1	0000165 // MAPK cascade // inferred from mutant phenotype//0000271 // polysaccharide biosynthetic process // inferred from mutant
1438072_at	0.000939	-2.65	-1.79	NM_001033301//NM_001205	<i>Fhdc1</i>	FH2 domain containing 1	
1438308_at 145	0.008943	-2.66	-1.20	NM_173378	<i>Trp53bp2</i>	transformation related protein 53 binding protein 2	0006915 // apoptotic process // inferred from electronic annotation//0007049 // cell cycle // inferred from electronic
1438311_at 145	0.003587	-2.66	-2.80	NM_001001179//XM_006506	<i>BC048546</i>	cDNA sequence BC048546	0010466 // negative regulation of peptidase activity // inferred from electronic annotation//0010951 // negative regulation of
1438350_at 143	0.004983	-2.66	-2.43	NM_007392//XM_006526606	<i>Acta2</i>	actin, alpha 2, smooth muscle, aorta	0006936 // muscle contraction // not recorded//0008217 // regulation of blood pressure // inferred from mutant phenotype//0009615
1438409_at 281	0.007015	-2.66	-2.15	NM_001164248//NM_001164	<i>Tpm1</i>	tropomyosin 1, alpha	0001701 // in utero embryonic development // inferred from mutant phenotype//0003065 // positive regulation of heart rate by
1438439_at 229	0.008882	-2.67	-1.60	NM_013630//XM_006523834	<i>Pkd1</i>	polycystic kidney disease 1 homolog	0001502 // cartilage condensation // inferred from mutant phenotype//0001568 // blood vessel development // inferred from mutant
1438466_at 227	0.006881	-2.67	-1.09	NM_001271599//NM_019972	<i>Sort1</i>	sortilin 1	0001503 // ossification // inferred from electronic annotation//0006810 // transport // inferred from electronic annotation//0006895
1438466_at 100	0.006881	-2.67	-1.02	NM_001193666//NM_001193	<i>Ccl21a//Ccl21b//Ccl21c//Gm1</i>	chemokine (C-C motif) ligand 21A (serine)////chemokine (C-C motif) ligand 21B	0001768 // establishment of T cell polarity // inferred from sequence or structural similarity//0000171 // immunological synapse
1438762_at	0.002863	-2.67	-1.10	NM_026950//XM_006504014	<i>Ocid2</i>	OC1A domain containing 2	
1438861_at 144	0.003307	-2.67	-1.22	NM_008514//XM_006505657	<i>Lrp6</i>	low density lipoprotein receptor-related protein 6	0001702 // gastrulation with mouth forming second // inferred from genetic interaction//0001756 // somitogenesis // inferred from
1438868_at 219	0.000297	-2.68	-2.03	NM_028775	<i>Cyp2s1</i>	cytochrome P450, family 2, subfamily s, polypeptide 1	0055114 // oxidation-reduction process // inferred from electronic annotation
1438879_at	0.003414	-2.68	-1.11	NM_153403//XM_006503067	<i>Ago1</i>	argonaute RISC catalytic subunit 1	0000956 // nuclear-transcribed mRNA catabolic process // not recorded//0006351 // transcription, DNA-templated // inferred from
1438891_at	0.009250	-2.68	-2.16	NM_175223	<i>Dnal1</i>	dynein, axonemal, light intermediate polypeptide 1	0003341 // cilium movement // inferred by curator//0008152 // metabolic process // inferred from electronic annotation
1438895_at 109	0.001858	-2.68	-1.55	NM_001113283//NM_153584	<i>Fam214a</i>	family with sequence similarity 214, member A	
1438906_at	0.007926	-2.68	-1.11	NM_133738	<i>Antrp2</i>	anthrax toxin receptor 2	0022414 // reproductive process // inferred from mutant phenotype
1439019_at 144	0.005382	-2.68	-1.29	NM_001114311//NM_001286	<i>Stox2</i>	storkhead box 2	0001893 // maternal placenta development // inferred from electronic annotation//0001893 // maternal placenta development //
1439101_at 213	0.001144	-2.69	-1.54	NM_178118//XM_006510450	<i>Dixd1</i>	DIX domain containing 1	0007049 // cell cycle // inferred from mutant phenotype//0007275 // multicellular organismal development // inferred from electronic
1439106_at 145	0.000048	-2.69	-1.36	NM_007742	<i>Col1a1</i>	collagen, type I, alpha 1	0001501 // skeletal system development // inferred from mutant phenotype//0001501 // skeletal system development // not
1439125_at	0.003084	-2.69	-1.53	NM_011416//NM_026003//X	<i>Smorac2</i>	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, involved in	0006325 // chromatin organization // traceable author statement//0006334 // nucleosome assembly // traceable author
1439156_at 381	0.004133	-2.71	-1.82	NM_009208//XM_006496449	<i>Sic4a3</i>	solute carrier family 4 (anion exchanger), member 3	0006810 // transport // inferred from electronic annotation//0006811 // ion transport // inferred from electronic annotation//0006820
1439204_at 202	0.000738	-2.71	-2.99	NM_001205219//NM_127552	<i>Sorbs2</i>	sorbin and SH3 domain containing 2	0007015 // actin filament organization // inferred from electronic annotation//0007155 // cell adhesion // inferred from electronic
1439219_at 101	0.006237	-2.72	-1.23	NM_022319//XM_006511334	<i>Clnn2</i>	calyxin 2	0007155 // cell adhesion // inferred from electronic annotation//0007156 // homophilic cell adhesion // inferred from electronic
1439220_at	0.005936	-2.72	-2.23	NM_001276419//NM_001276	<i>Fgf12//B230343J05rik</i>	fibroblast growth factor 12//RIKEN cDNA B230343J05	0003254 // regulation of membrane depolarization // not recorded//0007254 // JNK cascade // not recorded//0007268 // synaptic
1439330_at 320	0.001582	-2.73	-1.06	NM_177784//XM_006499677	<i>Klhl23</i>	kelch-like 23	
1439347_at 144	0.006835	-2.73	-1.30	NM_001271538//NM_001271	<i>Myh14</i>	myosin, heavy polypeptide 14	0003009 // skeletal muscle contraction // not recorded//0006200 // ATP catabolic process // inferred from direct assay//0006200 //

Table S6

Gene ID	p (Corr)	FC-RSV 1 d	FC-RSV 5 d	RefSeq Transcript ID	Gene Symbol	Gene Title	Gene Ontology Biological Process
1439492_at,1446	0.003900	-2.73	-1.11	NM_054041//XM_006506564	<i>Antrx1</i>	anthrax toxin receptor 1	0007165 // signal transduction // not recorded//00022414 // reproductive process // inferred from mutant phenotype//00031532 // actin
1439586_at,1548	0.000583	-2.74	-1.61	NM_001163154//NM_007960	<i>Etv1//Gm5454</i>	ets variant 1//predicted gene 5454	0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 // regulation of transcription, DNA-templated
1439644_at,1441	0.005820	-2.74	-1.42	NM_181039//XM_006531117	<i>Lphn1</i>	latrophilin 1	0007157 // heterophilic cell-cell adhesion // not recorded//0007165 // signal transduction // inferred from electronic
1439652_at,1445	0.005812	-2.74	-1.29	NM_145853//XR_387565//Xc	<i>Tpcn1</i>	two pore channel 1	0006810 // transcription // inferred from electronic annotation//0006811 // ion transport // inferred from electronic annotation//0006816
1439658_at,1320	0.006127	-2.74	-2.23	NM_008904//NR_027710//Xc	<i>Pparγc1α</i>	peroxisome proliferative activated receptor, gamma, coactivator 1 alpha	0001666 // response to hypoxia // inferred from electronic annotation//0006012 // galactose metabolic process // inferred from
1439705_at,1444	0.004944	-2.74	1.04	NM_146007//XM_006513177	<i>Colga2</i>	collagen, type VI, alpha 2	0007155 // cell adhesion // inferred from electronic annotation//0009749 // response to glucose // inferred from electronic
1439713_at,1455	0.003765	-2.75	-1.33	NR_001461	<i>Kcna1ot1</i>	KCNQ1 overlapping transcript 1	0006349 // regulation of gene expression by genetic imprinting // inferred from direct assay//0006349 // regulation of gene expression
1439716_at,1447	0.003058	-2.75	-1.35	NM_001013753//XM_006518	<i>Pcdh17</i>	protocadherin 17	0007155 // cell adhesion // inferred from electronic annotation//0007156 // homophilic cell adhesion // inferred from electronic
1439773_at,1455	0.001165	-2.75	-1.23	NM_001081286//XM_006509	<i>Fat1</i>	FAT tumor suppressor homolog 1 (Drosophila)	0007015 // actin filament organization // inferred from mutant phenotype//0007155 // cell adhesion // inferred from electronic
1439784_at,1783	0.000835	-2.75	-1.72	NM_011056//XM_006517643	<i>Pde4d</i>	phosphodiesterase 4D, cAMP specific	0002027 // regulation of heart rate // inferred from mutant phenotype//0006198 // cAMP catabolic process // inferred from direct
1439814_at,1445	0.005661	-2.76	-1.50	NM_001113209//NM_001113	<i>Nfib</i>	nuclear factor I/b	0000122 // negative regulation of transcription from RNA polymerase II promoter // not recorded//0002062 // chondrocyte
1439819_at,101	0.002198	-2.76	-1.32	NM_175492//NM_181071//Xc	<i>Tanc2</i>	tetratricopeptide repeat, ankyrin repeat and coiled-coil containing 2	0001701 // in utero embryonic development // inferred from mutant phenotype
1439839_at,1319	0.005318	-2.77	-2.11	NM_006519758//XM_006519	<i>Dnah12</i>	dynein, axonemal, heavy chain 12	0006200 // ATP catabolic process // inferred from electronic annotation//0007018 // microtubule-based movement // inferred from
1439849_at,1445	0.009022	-2.78	-1.38	NM_017378	<i>Pcdh12</i>	protocadherin 12	0005977 // glycogen metabolic process // inferred from mutant phenotype//0007155 // cell adhesion // inferred from electronic
1439901_at,1445	0.005683	-2.79	-1.58	NM_008492//XM_006506920	<i>Ldhd</i>	lactate dehydrogenase B	0005975 // carbohydrate metabolic process // inferred from electronic annotation//0006089 // lactate metabolic process // not
1439906_at,1445	0.005467	-2.80	-1.29	NM_001286607//NM_053242	<i>Foxp2</i>	forkhead box P2	0000122 // negative regulation of transcription from RNA polymerase II promoter // inferred from direct assay//0002053 // positive
1439915_at,1445	0.008721	-2.80	-1.62	NM_172532	<i>Aldh5a1</i>	aldehyde dehydrogenase family 5, subfamily A1	0006006 // glucose metabolic process // inferred from mutant phenotype//0006083 // acetate metabolic process // inferred from
1439929_at,1445	0.009324	-2.80	-1.09	NM_178929//XM_006526566	<i>Kazal1</i>	Kazal-type serine peptidase inhibitor domain 1	0001503 // ossification // inferred from electronic annotation//0001558 // regulation of cell growth // inferred from electronic
1439930_at,1445	0.001365	-2.81	-1.29	NM_012037	<i>Vat1</i>	vesicle amine transport protein 1 homolog (T californica)	0010637 // negative regulation of mitochondrial fusion // not recorded//005114 // oxidation-reduction process // inferred from
1439933_at,1402	0.004887	-2.81	-1.01	NM_013811//XM_006523588	<i>Dnah8</i>	dynein, axonemal, heavy chain 8	0006200 // ATP catabolic process // inferred from electronic annotation//0007018 // microtubule-based movement // inferred from
1440051_at,1445	0.005114	-2.84	-1.11	NM_175518//XM_006537925	<i>Tmem245</i>	transmembrane protein 245	0000160 // phosphorelay signal transduction system // inferred from electronic annotation//0006355 // regulation of transcription, DNA
1440084_at,1445	0.008758	-2.84	-1.54	NM_001294162//NM_013569	<i>Kcnh2</i>	potassium voltage-gated channel, subfamily H (eag-related), member 2	0008333 // endosome to lysosome transport // not recorded//1990172 // G-protein coupled receptor catabolic process // not recorded
1440092_at,1445	0.007926	-2.84	-1.28	NM_001004359//NM_001005	<i>Gsprs1</i>	G protein-coupled receptor associated sorting protein 1	0006402 // mRNA catabolic process // not recorded//0006417 // regulation of translation // inferred from electronic
1440317_at,1402	0.005114	-2.85	-1.16	NM_153177//XM_006503481	<i>Ago4</i>	argonaute RISC catalytic subunit 4	0007015 // actin filament organization // inferred from physical interaction//0019722 // calcium-mediated signaling // inferred from
1440372_at,1445	0.000705	-2.86	1.04	NM_181595//XM_006505070	<i>Ppp1r9a</i>	protein phosphatase 1, regulatory (inhibitor) subunit 9A	
1440431_at,1445	0.005019	-2.87	-1.20	NM_133218//XM_006530055	<i>Zfp704</i>	zinc finger protein 704	
1440462_at,1441	0.008588	-2.87	-1.32	NM_001110843//NM_001110	<i>Cacna2d1</i>	calcium channel, voltage-dependent, alpha2/delta subunit 1	0006810 // transport // inferred from electronic annotation//0006811 // ion transport // inferred from electronic annotation//0006816
1440579_at,1445	0.001468	-2.88	-1.51	NM_001190490//NM_001190	<i>Dmpk</i>	dystrophin myotonia-protein kinase	0002028 // regulation of sodium ion transport // inferred from mutant phenotype//0006468 // protein phosphorylation // not
1440637_at,1445	0.005546	-2.89	-1.10	NM_144942//XM_006520997	<i>Csad</i>	cysteine sulfonic acid decarboxylase	0008152 // metabolic process // inferred from electronic annotation//0019452 // L-cysteine catabolic process to taurine // traceable
1440643_at,1445	0.004595	-2.90	-1.74	NM_007817	<i>Cyp2f2</i>	cytochrome P450, family 2, subfamily f, polypeptide 2	0009636 // response to toxic substance // inferred from mutant phenotype//0018931 // naphthalene metabolic process // inferred
1440660_at,1445	0.002558	-2.90	-1.13	NM_008520//XM_006531668	<i>Ltbp3</i>	latent transforming growth factor beta binding protein 3	0001501 // skeletal system development // inferred from mutant phenotype//0007179 // transforming growth factor beta receptor
1440879_at,1455	0.004728	-2.91	-4.05	NM_009363	<i>Tjtf2</i>	trefoil factor 2 (spasmolytic protein 1)	0008284 // positive regulation of cell proliferation // inferred from genetic interaction//0008284 // positive regulation of cell
1440907_at,1381	0.006586	-2.93	-1.33	NM_024188	<i>Oxct1</i>	3-oxoacid CoA transferase 1	0007420 // brain development // inferred from electronic annotation//0007507 // heart development // inferred from electronic
1440969_at,1407	0.000461	-2.93	-1.29	NM_011526	<i>Tagln</i>	transglutinin	0007010 // cytoskeleton organization // inferred from mutant phenotype//0030855 // epithelial cell differentiation // not recorded
1440977_at,1445	0.006381	-2.93	-2.63	NM_010043	<i>Des</i>	desmin	0007517 // muscle organ development // traceable author statement
1440990_at,1269	0.000457	-2.93	-1.45	NM_008716	<i>Notch3</i>	notch 3	0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 // regulation of transcription, DNA-templated
1441032_at,1791	0.009788	-2.93	-1.22	NM_001159410//NM_008193	<i>Guk1</i>	guanylate kinase 1	0006163 // purine nucleotide metabolic process // inferred from direct assay//0006163 // purine nucleotide metabolic process // not
1441114_at,1455	0.006173	-2.94	-1.81	NM_010612	<i>Kdr</i>	kinase insert domain protein receptor	0001525 // angiogenesis // inferred from electronic annotation//0001541 // ovarian follicle development // inferred from mutant
1441177_at,1445	0.009429	-2.95	-1.36	NM_001005510	<i>Syne2</i>	spectrin repeat containing, nuclear envelope 2	0006998 // nuclear envelope organization // inferred from mutant phenotype//0007097 // nuclear migration // not recorded//0007163
1441231_at,1445	0.001453	-2.96	-1.47	NM_001161420//NM_013703	<i>Vldlr</i>	very low density lipoprotein receptor	0000122 // negative regulation of transcription from RNA polymerase II promoter // inferred from mutant phenotype//0006629 // lipid
1441334_at,1445	0.003991	-2.97	1.32	NM_010680//XM_006525685	<i>Lama3</i>	laminin, alpha 3	0007155 // cell adhesion // inferred from electronic annotation//0016337 // single organismal cell-cell adhesion // not
1441386_at,1445	0.001998	-2.97	-1.43	NM_172803//XM_006515085	<i>Dock4</i>	dedicator of cytokinesis 4	0007264 // small GTPase mediated signal transduction // inferred from electronic annotation//0032855 // positive regulation of Rac
1441415_at,1445	0.008839	-2.98	-2.03	NM_001163487//NM_001163	<i>Pfkfb</i>	phosphofructokinase, muscle	0006002 // fructose 6-phosphate metabolic process // not recorded//0006096 // glycolytic process // inferred from direct
1441437_at,1445	0.000572	-2.98	-1.19	NM_001276383//NM_153060	<i>Spsn2</i>	spinster homolog 2	0001782 // B cell homeostasis // inferred from mutant phenotype//0002260 // lymphocyte homeostasis // inferred from mutant
1441539_at,1445	0.007672	-2.98	-1.26	NM_175013	<i>Pgm5</i>	phosphoglucomutase 5	0005975 // carbohydrate metabolic process // inferred from electronic annotation//0006006 // glucose metabolic process // inferred
1441540_at,1454	0.004647	-2.98	-1.97	XR_379378//XR_379379//XR	<i>LOC102635638//2010007H06Rik</i>	uncharacterized LOC102635638//RIKEN cDNA 2010007H06 gene	0006085 // acetyl-CoA biosynthetic process // inferred from direct assay//0006085 // acetyl-CoA biosynthetic process // not
1441556_at,1445	0.009610	-2.99	-1.26	NM_080575	<i>Acsf1</i>	acyl-CoA synthetase short-chain family member 1	
1441567_at,1445	0.003408	-3.00	-1.81	NM_183315	<i>Ctxm1</i>	cortexin 1	
1441588_at,1447	0.005678	-3.01	-1.43	NM_001195268//NM_015761	<i>Dos</i>	downstream of Stk11	
1441769_at,1445	0.006144	-3.02	-1.08	NM_027468//XM_006514090	<i>Cpm</i>	carboxypeptidase M	
1442041_at,1552	0.001785	-3.03	-1.17	NM_001177881//NM_001177	<i>Mfap3l</i>	microfibrillar-associated protein 3-like	0006508 // proteolysis // inferred from electronic annotation//0008152 // metabolic process // inferred from electronic annotation
1442056_at,1445	0.001917	-3.03	-1.29	NM_026516	<i>Tmem178</i>	transmembrane protein 178	
1442118_at,1445	0.007856	-3.04	-1.25	NM_001114339//NM_023792	<i>Pank1</i>	panthothenate kinase 1	0015937 // coenzyme A biosynthetic process // inferred from direct assay//0015937 // coenzyme A biosynthetic process // inferred
1442181_at,1445	0.007260	-3.05	-1.21	NM_016719//XM_006499883	<i>Grib14</i>	growth factor receptor bound protein 14	0007165 // signal transduction // traceable author statement//0008286 // insulin receptor signaling pathway // not recorded//0009967
1442214_at,1445	0.001513	-3.05	-1.09	NM_009181//XM_006540731	<i>Sts1a2</i>	ST8 alpha-N-acetyl-neuraminidase alpha-2,8-sialyltransferase 2	0001574 // ganglioside biosynthetic process // not recorded//0006486 // protein glycosylation // not recorded//0006491 // N-glycan
1442218_at,1455	0.004538	-3.05	1.15	NM_031374//XM_006508975	<i>Tex15</i>	testis expressed gene 15	0007129 // synapsis // inferred from mutant phenotype//0007130 // synaptonemal complex assembly // inferred from mutant
1442270_at,1445	0.004017	-3.05	-1.00	NM_026979//XM_006534109	<i>C1qtnf2</i>	C1q and tumor necrosis factor related protein 2	0000187 // activation of MAPK activity // inferred from direct assay//0045725 // positive regulation of glycogen biosynthetic process //
1442412_at,1455	0.002999	-3.07	-1.11	NM_173788//XM_006537833	<i>Npr2</i>	atriuretic peptide receptor 2	0001503 // ossification // inferred from electronic annotation//0006182 // cGMP biosynthetic process // inferred from direct
1442435_at,1445	0.005610	-3.07	-1.68	NM_001039485//NM_172629	<i>Piezo2</i>	piezo-type mechanosensitive ion channel component 2	0006810 // transport // inferred from electronic annotation//0006811 // ion transport // inferred from electronic annotation//0006812
1442473_at,1445	0.000834	-3.07	-1.58	NM_027641//XM_006500174	<i>Spef1</i>	sperm flagellar 1	
1442593_at,1445	0.005005	-3.08	-1.01	NM_001029836//NM_001287	<i>Nprnt</i>	nephronectin	0001657 // ureteric bud development // inferred from mutant phenotype//0001658 // branching involved in ureteric bud
1442620_at,1445	0.001785	-3.08	-12.80	NM_024406//XM_006530048	<i>Fabp4</i>	fatty acid binding protein 4, adipocyte	0001816 // cytokine production // inferred from mutant phenotype//0006469 // negative regulation of protein kinase activity // inferred
1442640_at,1445	0.008786	-3.09	-1.93	NM_001159284//NM_001284	<i>Smtn</i>	smoothelin	
1442704_at,1445	0.007171	-3.09	-3.22	NM_009943	<i>Cox6a2</i>	cytochrome c oxidase subunit VIa polypeptide 2	1902600 // hydrogen ion transmembrane transport // inferred from electronic annotation
1442771_at,1445	0.005170	-3.09	-1.33	NR_002845	<i>Copg2os2</i>	coatamer protein complex, subunit gamma 2, opposite strand 2	
1442979_at,1445	0.008318	-3.10	-1.27	NM_001081064//XM_006520	<i>Pdsd2//LOC102642479</i>	PDZ domain containing 2//uncharacterized LOC102642479	
1442986_at,1445	0.004621	-3.11	1.10	NM_013589//XM_006515501	<i>Ltbp2</i>	latent transforming growth factor beta binding protein 2	
1442988_at,1020	0.007227	-3.11	-2.28	NM_145838//XM_006497477	<i>Sts1a6</i>	ST8 alpha-N-acetyl-neuraminidase alpha-2,8-sialyltransferase 6	0001574 // ganglioside biosynthetic process // inferred from direct assay//0006486 // protein glycosylation // inferred from electronic
1443075_at,1445	0.001116	-3.12	-3.37	NM_025557//XM_006496957	<i>Pcp4l1</i>	Parkin-like cell protein 4-like 1	
1443088_at,1319	0.008000	-3.12	-2.24	NM_001243092//NM_008181	<i>Gm3776//Gsta1//Gsta2</i>	predicted gene 3776//glutathione S-transferase, alpha 1 (Ya)//glutathione S-	0006749 // glutathione metabolic process // not recorded//0008152 // metabolic process // inferred from electronic
1443151_at,1445	0.004201	-3.13	-2.47	NM_001033409//XM_006529	<i>Lgr6</i>	leucine-rich repeat-containing G protein-coupled receptor 6	0007165 // signal transduction // inferred from electronic annotation//0007186 // G-protein coupled receptor signaling pathway //
1443163_at,1214	0.000297	-3.14	-2.79	NM_177406	<i>Cyp4a12a</i>	cytochrome P450, family 4, subfamily a, polypeptide 12a	0006631 // fatty acid metabolic process // inferred from sequence or structural similarity//0055114 // oxidation-reduction process //
1443201_at,1445	0.006992	-3.14	-1.44		<i>5930427L02Rik</i>	RIKEN cDNA 5930427L02 gene	
1443214_at,1445	0.008382	-3.15	-1.26	NM_175503	<i>Aard</i>	alanine and arginine rich domain containing protein	0030324 // lung development // inferred from electronic annotation
1443220_at,1445	0.001221	-3.15	-1.05	NM_011812//XM_006515864	<i>Fbln5</i>	fibulin 5	0001558 // regulation of cell growth // inferred from electronic annotation//0007155 // cell adhesion // inferred from electronic
1443231_at,1445	0.000208	-3.15	-3.95	NM_021447	<i>Trim54</i>	tripartite motif-containing 54	0007026 // negative regulation of microtubule depolymerization // inferred from direct assay//0007275 // multicellular organismal
1443233_at,1445	0.004235	-3.15	-1.24	NM_178899//XM_006504957	<i>Hepacam2</i>	HEPACAM family member 2	0000236 // mitotic prometaphase // inferred from sequence or structural similarity//0007049 // cell cycle // inferred from electronic
1443299_at,1445	0.002247	-3.16	1.11	NM_001252563//NM_013592	<i>Matn4</i>	matrilin 4	0048678 // response to axon injury // inferred from direct assay

Table S6

Gene_ID	p (Corr)	FC-RSV 1 d	FC-RSV 5 d	RefSeq Transcript ID	Gene Symbol	Gene Title	Gene Ontology Biological Process
1443338_at	0.005614	-3.17	-1.43	NM_199465//XM_006501990	Nexn	nexlin	0006468 // protein phosphorylation // not recorded//0003034 // regulation of cell migration // not recorded//0048739 // cardiac
1443363_at	0.006710	-3.17	-1.05	NM_001190448//NM_016672	Ddc	dopa decarboxylase	0006520 // cellular amino acid metabolic process // inferred from electronic annotation//0007623 // circadian rhythm // inferred from
1443393_at	0.004794	-3.18	-1.48	NM_016854	Ppp1r3c	protein phosphatase 1, regulatory (inhibitor) subunit 3C	0005975 // carbohydrate metabolic process // inferred from electronic annotation//0005977 // glycogen metabolic process // inferred
1443533_at	0.007767	-3.19	-1.09	NM_001163314//NM_175508	Pgap1	post-GPI attachment to proteins 1	0006505 // GPI anchor metabolic process // inferred from electronic annotation//0006506 // GPI anchor biosynthetic process // not
1443534_at	0.005610	-3.20	-1.91	NM_016798//XM_006509465	Pdlm3	PDZ and LIM domain 3	0007015 // actin filament organization // inferred from direct assay//0007507 // heart development // inferred from mutant
1443858_at 1445	0.000392	-3.21	-1.23	NM_008609	Mmp15	matrix metalloproteinase 15	0006508 // proteolysis // inferred from sequence or structural similarity//0032355 // response to estradiol // inferred from electronic
1443926_at	0.009097	-3.23	-3.42	NM_172604	Scara3	scavenger receptor class A, member 3	
1443977_at 319	0.002691	-3.23	-1.67	NM_011542//XM_006538710	Tcea3	transcription elongation factor A (SII), 3	0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 // regulation of transcription, DNA-templated
1444045_at	0.002242	-3.23	-2.59	NM_153801	Tecr1	trans-2,3-enoyl-CoA reductase-like	0006629 // lipid metabolic process // inferred from electronic annotation//0055114 // oxidation-reduction process // inferred from
1444077_at 1445	0.000771	-3.23	-3.08	NM_026056//XM_006516946	Cap2	CAP, adenylate cyclase-associated protein, 2 (yeast)	0000902 // cell morphogenesis // inferred from electronic annotation//0007010 // cytoskeleton organization // inferred from electronic
1444109_at 399	0.000412	-3.24	-1.33	NM_001002268//XM_006512	Gpr126	G protein-coupled receptor 126	0007165 // signal transduction // inferred from electronic annotation//0007166 // cell surface receptor signaling pathway // inferred
1444190_at	0.002018	-3.25	-1.73	NM_019707//XM_006530627	Cdh13	cadherin 13	0000278 // mitotic cell cycle // inferred from electronic annotation//0001558 // regulation of cell growth // not recorded//0001938 //
1444406_at	0.001468	-3.25	-1.43	NM_019588//XM_006527394	Plce1	phospholipase C, epsilon 1	0000187 // activation of MAPK activity // not recorded//0006629 // lipid metabolic process // inferred from electronic
1444445_at 976	0.007430	-3.25	-1.41	NM_001164791//NM_023057	Zak	sterile alpha motif and leucine zipper containing kinase AZK	0000075 // cell cycle checkpoint // not recorded//0000077 // DNA damage checkpoint // not recorded//0000165 // MAPK cascade //
1444494_at 228	0.001404	-3.26	-1.18	NM_176846//XM_006510425	Exph5	exophilin 5	0003334 // keratinocyte development // not recorded//0006886 // intracellular protein transport // inferred from electronic
1444515_at	0.009886	-3.27	-1.86	NM_023842//XM_006516532	Dsp	desmoplakin	0002934 // desmosome organization // inferred from mutant phenotype//0003223 // ventricular compact myocardium morphogenesis
1444609_at	0.002797	-3.29	1.01	NM_008481//XM_006512566	Lama2	laminin, alpha 2	0007155 // cell adhesion // inferred from electronic annotation//0007411 // axon guidance // inferred from genetic
1444693_at	0.000992	-3.30	-1.14	NM_001177794//NM_198247	Sertad4	SERTA domain containing 4	
1444728_at	0.003635	-3.32	-1.59	NM_001038609//NM_001285	Mapt	microtubule-associated protein tau	0000226 // microtubule cytoskeleton organization // inferred from mutant phenotype//0000226 // microtubule cytoskeleton
1444746_at	0.004728	-3.32	-1.17	NM_001162532	Fam174b	family with sequence similarity 174, member B	
1444749_at	0.000296	-3.33	-2.63	NM_022032	Perp	PERP, TP53 apoptosis effector	0002934 // desmosome organization // inferred from mutant phenotype//0006915 // apoptotic process // inferred from electronic
1444764_at	0.001877	-3.33	-1.07	NM_008011//XM_006517099	Fgf4	fibroblast growth factor receptor 4	0001759 // organ induction // inferred from mutant phenotype//0006468 // protein phosphorylation // inferred from electronic
1444765_at	0.005750	-3.33	-1.69	NM_009437	Tst	thiosulfate sulfurtransferase, mitochondrial	0008152 // metabolic process // inferred from electronic annotation//0030855 // epithelial cell differentiation // not
1444785_at	0.000866	-3.33	-2.47	NM_080451//XM_006500923	Synpo2	synaptodin 2	
1444890_at	0.001144	-3.34	-3.24	NM_009381	Thrsf	thyroid hormone responsive	0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 // regulation of transcription, DNA-templated
1444992_at 103	0.006541	-3.38	-1.69	NM_175329//XM_006512993	Chchd10	coiled-coil-helix-coiled-coil-helix domain containing 10	0006119 // oxidative phosphorylation // not recorded//0006754 // ATP biosynthetic process // not recorded//0000984 // negative
1445001_at	0.005936	-3.39	-1.29	NM_001136086//NM_001291	Dpps3	dihydropyrimidinase-like 3	0006208 // pyrimidine nucleobase catabolic process // inferred from electronic annotation//0007399 // nervous system development //
1445137_at	0.003307	-3.42	-1.23	NM_013462//XM_006508987	Adrb3	adrenergic receptor, beta 3	0002024 // diet induced thermogenesis // inferred from genetic interaction//0002025 // vasodilation by norepinephrine-epinephrine
1445398_at	0.008746	-3.44	-1.19	NM_001146299//NM_172966	Sh3rf2	SH3 domain containing ring finger 2	0010923 // negative regulation of phosphatase activity // not recorded//0016567 // protein ubiquitination // inferred from electronic
1445492_at	0.009454	-3.45	-1.49	NM_031166	Id4	inhibitor of DNA binding 4	0000082 // G1/S transition of mitotic cell cycle // inferred from mutant phenotype//0000122 // negative regulation of transcription from
1445550_at 145f	0.006389	-3.45	-1.28	NM_001142916//NM_011961	Plod2	procollagen lysine, 2-oxoglutarate 5-dioxygenase 2	0001666 // response to hypoxia // inferred from electronic annotation//0055114 // oxidation-reduction process // inferred from
1445687_at 380	0.005199	-3.48	-1.18	NM_001267796//NM_008989	Igip1/Pura	IgA inducing protein//purine rich element binding protein A	0006268 // DNA unwinding involved in DNA replication // not recorded//0006270 // DNA replication initiation // traceable author
1445781_at	0.003888	-3.51	-1.60	NM_001285805//NM_019778	Zbtb20	zinc finger and BTB domain containing 20	0000122 // negative regulation of transcription from RNA polymerase II promoter // inferred from direct assay//0000122 // negative
1445837_at	0.002933	-3.52	-3.41	NM_001081087	Klhl41	klf-like 41	0016567 // protein ubiquitination // not recorded//0030239 // myofibril assembly // inferred from mutant phenotype//0031275 //
1445892_at	0.006710	-3.52	-1.25	NM_146162//XM_006530287	Tmem119	transmembrane protein 119	0001503 // ossification // inferred from electronic annotation//0001649 // osteoblast differentiation // inferred from direct
1445900_at	0.001471	-3.52	-2.98	NM_026183//XM_006533992	Slc47a1	solute carrier family 47, member 1	0006810 // transport // inferred from electronic annotation//0006855 // drug transmembrane transport // not recorded//0015695 //
1445938_at 402	0.006602	-3.53	-3.67	NM_007906	Eef1a2	eukaryotic translation elongation factor 1 alpha 2	0006184 // GTP catabolic process // inferred from electronic annotation//0006412 // translation // inferred from electronic
1445966_at	0.003116	-3.53	-1.11	NM_172463//XM_006529317	Sned1	snid, nodagin and EGF-like domains 1	0007160 // cell-matrix adhesion // inferred from electronic annotation
1445984_at	0.002138	-3.53	-1.30	NM_001170669//NM_172263	Pde8b	phosphodiesterase 8B	0000160 // phosphorelay signal transduction system // inferred from electronic annotation//0001662 // behavioral fear response //
1446048_at	0.002896	-3.53	-3.64	NM_010473	Hrc	histidine rich calcium binding protein	0008016 // regulation of heart contraction // inferred from direct assay//0010881 // regulation of cardiac muscle contraction by
1446088_at 320	0.005016	-3.55	-1.18	NM_015776//XM_006506364	Mfap5	microfibrillar associated protein 5	0043206 // extracellular fibril organization // inferred from direct assay
1446124_at	0.007806	-3.56	-1.60	NM_001286653//NM_001286	Rcan2	regulator of calcineurin 2	0006950 // response to stress // inferred from genetic interaction//0006950 // response to stress // inferred from mutant
1446182_at	0.001582	-3.57	-2.68	NM_010859	Myl3	myosin, light polypeptide 3	0002026 // regulation of the force of heart contraction // not recorded//0006942 // regulation of striated muscle contraction // not
1446212_at	0.002971	-3.60	-2.52	NM_001081437//NM_007992	Fbln2	fibulin 2	0010811 // positive regulation of cell-substrate adhesion // inferred from direct assay
1446280_at	0.000504	-3.60	1.46	NM_012033//XM_006511201	Tinag	tubulointerstitial nephritis antigen	0006508 // proteolysis // inferred from electronic annotation//0006898 // receptor-mediated endocytosis // inferred from electronic
1446345_at	0.000814	-3.61	-1.53	NM_001080707//NM_001190	Gpr155	G protein-coupled receptor 155	0035556 // intracellular signal transduction // inferred from electronic annotation//0050890 // cognition // not recorded//0055085 //
1446424_at 110	0.004335	-3.60	1.52	NM_001146031//NM_176930	Nrcam	neuron-glia-CAM-related cell adhesion molecule	0001525 // angiogenesis // inferred from electronic annotation//0007155 // cell adhesion // inferred from electronic
1446440_at	0.001113	-3.62	-1.35	NM_178405	Atp1a2	ATPase, Na+/K+ transporting, alpha 2 polypeptide	0001504 // neurotransmitter uptake // inferred from mutant phenotype//0002026 // regulation of the force of heart contraction //
1446481_at	0.000655	-3.62	-1.44	NM_001110227	Cknj13	potassium inwardly-rectifying channel, subfamily J, member 13	0006810 // transport // inferred from electronic annotation//0006811 // ion transport // inferred from electronic annotation//0006813
1446547_at 145f	0.006015	-3.63	-3.60	NM_001205085//NM_020496	Tbx20	T-box 20	0000122 // negative regulation of transcription from RNA polymerase II promoter // inferred from genetic interaction//0000122 //
1446570_at	0.005114	-3.64	-1.23	NM_001199136//NM_001199	Macf1	microtubule-actin crosslinking factor 1	0001707 // mesoderm formation // inferred from mutant phenotype//0006200 // ATP catabolic process // inferred from direct
1446591_at 380	0.003823	-3.65	-1.33	NM_001160268//NM_182390	Plekha6	pleckstrin homology domain containing, family A member 6	
1446598_at	0.000658	-3.65	-2.74	NM_001005422	Stmnd1	stathmin domain containing 1	0031110 // regulation of microtubule polymerization or depolymerization // inferred from electronic annotation
1446636_at 145f	0.006826	-3.66	-1.47	NM_001145826//NM_153406	Spect11	sperm antigen with calponin homology and coiled-coil domains 1-like	0007026 // negative regulation of microtubule depolymerization // inferred from direct assay//0007049 // cell cycle // inferred from
1446656_at	0.004629	-3.67	-1.86	NM_029297	Dynlrb2	dynein light chain roodblock-type 2	0006810 // transport // inferred from electronic annotation//0008152 // metabolic process // inferred from electronic annotation
1446929_at 100	0.004217	-3.68	-3.41	NM_001271402//NM_001271	Ephx2	epoxide hydrolase 2, cytoplasmic	0002539 // prostaglandin production involved in inflammatory response // not recorded//0006629 // lipid metabolic process // inferred
1446967_at	0.004811	-3.70	-1.55	NM_001267622//NM_024477	Ttc28	tetratricopeptide repeat domain 28	0007049 // cell cycle // inferred from electronic annotation//0007067 // mitotic nuclear division // inferred from electronic
1446982_at	0.009324	-3.71	1.11	NM_001113481//NM_011350	Sema4f	sema domain, immunoglobulin domain (Ig), TM domain, and short	0007275 // multicellular organismal development // inferred from electronic annotation//0007399 // nervous system development //
1447040_at	0.008786	-3.74	-2.66	NM_001277875//NM_001277	Tpm2	tropomyosin 2, beta	0006936 // muscle contraction // traceable author statement//0043462 // regulation of ATPase activity // inferred from electronic
1447064_at	0.002727	-3.76	-1.00	NM_029947//XM_006535284	Prdm8	PR domain containing 8	0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 // regulation of transcription, DNA-templated
1447094_at	0.002351	-3.80	-1.11	NM_008120	Gja4	gap junction protein, alpha 4	0001568 // blood vessel development // inferred from mutant phenotype//0003158 // endothelium development // inferred from
1447124_at	0.005174	-3.81	-1.44	NM_001166067//XM_006505	Slc4a5	solute carrier family 4, sodium bicarbonate cotransporter, member 5	0002064 // epithelial cell development // inferred from mutant phenotype//0003014 // renal system process // inferred from mutant
1447164_at	0.008007	-3.81	-2.82	NM_001048005//NM_001253	1110017D15Rik	RIKEN cDNA 1110017D15 gene	0007283 // spermatogenesis // inferred from electronic annotation//0003014 // cell differentiation // inferred from electronic
1447174_at	0.002131	-3.82	-1.11	NM_001177503//XM_006515	Plekhd1	plekhdin domain containing, family D (with coiled-coil domains)	
1447209_at	0.000738	-3.82	-1.96	NM_001102468//NM_138304	Calm1a	calmodulin-like 4	
1447270_at	0.008951	-3.84	-3.69	NM_001289654//NM_001289	Fhod3	formin homology 2 domain containing 3	0007015 // actin filament organization // inferred from electronic annotation//000837 // negative regulation of actin filament
1447302_at	0.009950	-3.84	-1.48	NM_017391	Slc5a3	solute carrier family 5 (inositol transporters), member 3	0006020 // inositol metabolic process // inferred from mutant phenotype//0006412 // translation // inferred from electronic
1447421_at	0.001678	-3.84	-3.99	NM_009814//XM_006500947	Casq2	casein kinase 2	0002027 // regulation of heart rate // not recorded//0006937 // regulation of muscle contraction // traceable author
1447854_s_at 14	0.002274	-3.86	1.16	NM_013691//XM_006501295	Tbhs3	thrombospondin 3	0003417 // growth plate cartilage development // inferred from genetic interaction//0003417 // growth plate cartilage development //
1447896_s_at 11f	0.003974	-3.86	-2.00	NM_001044720//NM_011511	Abcc9	ATP-binding cassette, sub-family C (CFTR/MRP), member 9	0006200 // ATP catabolic process // inferred from electronic annotation//0006810 // transport // inferred from electronic
1447933_at 668	0.009986	-3.87	-1.98	NM_172864	Wdr63	WD repeat domain 63	
1447988_at	0.003999	-3.89	-1.10	NM_145463	Shisa2	shisa homolog 2 (Xenopus laevis)	0007275 // multicellular organismal development // inferred from electronic annotation
1452968_at 685	0.007491	-3.98	-3.28	NM_027150//XM_006511410	Mlip	muscular LMNA-interacting protein	
1452989_at	0.006697	-3.98	-3.02	NM_027126//XM_006502036	Hfe2	hemochromatosis type 2 (juvenile) (human homolog)	0030509 // BMP signaling pathway // inferred from genetic interaction//0030509 // BMP signaling pathway // inferred from mutant
1453326_at 75e	0.001641	-4.04	-4.58	NM_001039543//NM_010801	Mif1	myeloid leukemia factor 1	0002318 // myeloid progenitor cell differentiation // inferred from direct assay//0006351 // transcription, DNA-templated // inferred
1453492_at 329	0.000931	-4.07	-1.15	NM_001025600//NM_018770	Cadm1	cell adhesion molecule 1	0001889 // liver development // not recorded//0002376 // immune system process // inferred from electronic annotation//0006915 //
1453523_at 779	0.000623	-4.07	-2.13	NM_001164669//XM_006506	Dnah6	dynein, axonemal, heavy chain 6	0001539 // cilium or flagellum-dependent cell motility // inferred from electronic annotation//0006200 // ATP catabolic process //
1453585_at 697	0.008257	-4.09	-1.18	NM_001004363	Nuak1	NUAK family, SNF1-like kinase, 1	0006468 // protein phosphorylation // not recorded//0006974 // cellular response to DNA damage stimulus // inferred from electronic

Table S6

Gene_ID	p (Corr)	FC-RSV 1 d	FC-RSV 5 d	RefSeq Transcript ID	Gene Symbol	Gene Title	Gene Ontology Biological Process
1453619_at,1454	0.003021	-4.11	-3.58	NM_001195006//NM_145602	<i>Ndrg4</i>	N-myc downstream regulated gene 4	0010976 // positive regulation of neuron projection development // not recorded
1453640_at,1769	0.006178	-4.11	-2.62	NM_030187//NM_006516390	<i>Akr7</i>	adenylate kinase 7	0002437 // inflammatory response to antigenic stimulus // inferred from mutant phenotype//0003351 // epithelial cilium movement //
1454494_at	0.004815	-4.16	1.07	NM_173749	<i>Pamr1</i>	peptidase domain containing associated with muscle regeneration 1	0006508 // proteolysis // inferred from electronic annotation//0008152 // metabolic process // inferred from electronic annotation
1454765_at,1984	0.004709	-4.20	-1.17	NM_011584	<i>Nr1a2</i>	nuclear receptor subfamily 1, group D, member 2	0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 // regulation of transcription, DNA-templated
1454776_at,1776	0.001127	-4.20	-1.47	NM_197999//NM_006531391	<i>Ces2g</i>	carboxylesterase 2G	0006508 // proteolysis // inferred from electronic annotation//0008152 // metabolic process // --//0008152 // metabolic process //
1454874_at	0.005058	-4.21	1.18	NM_026778//NM_006521318	<i>Chrc1</i>	collagen triple helix repeat containing 1	0016477 // cell migration // not recorded//0032092 // positive regulation of protein binding // inferred from direct assay//0033690 //
1454877_at,1214	0.000939	-4.22	-1.72	NM_133660//NM_006530651	<i>Ces1e</i>	carboxylesterase 1E	0008152 // metabolic process // not recorded
1454933_at,1230	0.007882	-4.23	-1.98	NM_001160386//NM_006495	<i>Dnah7b//Dnah7c</i>	dynein, axonemal, heavy chain 7B//dynein, axonemal, heavy chain 7C	0001539 // cilium or flagellum-dependent cell motility // inferred from electronic annotation//0003341 // cilium movement // inferred
1454980_at	0.000333	-4.25	1.09	NM_011254	<i>Rbp1</i>	retinol binding protein 1, cellular	0002138 // retinoic acid biosynthetic process // inferred from electronic annotation//0006810 // transport // inferred from electronic
1455014_at,100	0.001324	-4.26	-1.25	NM_026162//NM_006497531	<i>Plxdc2</i>	plexin domain containing 2	0007275 // multicellular organismal development // inferred from electronic annotation
1455051_at,268	0.001995	-4.27	-7.56	NM_008030	<i>Fmo3</i>	flavin containing monooxygenase 3	0017144 // drug metabolic process // not recorded//0055114 // oxidation-reduction process // not recorded
1455489_at,107	0.004354	-4.39	-1.27	NM_009238	<i>Sox4</i>	SRY (sex determining region Y)-box 4	0001501 // skeletal system development // inferred from mutant phenotype//0001666 // response to hypoxia // not
1455500_at,146	0.001024	-4.40	-1.44	NM_023617//NM_006496284	<i>Aox3</i>	aldehyde oxidase 3	0055114 // oxidation-reduction process // inferred from direct assay
1455521_at	0.004595	-4.43	1.02	NM_007409	<i>Adh1</i>	alcohol dehydrogenase 1 (class I)	0001523 // retinoid metabolic process // inferred from mutant phenotype//0006068 // ethanol catabolic process // inferred from direct
1455538_at,109	0.003367	-4.46	-4.73	NM_001136062//NM_001276	<i>Eno3</i>	enolase 3, beta muscle	0006096 // glycolytic process // inferred from electronic annotation//0007568 // aging // inferred from electronic annotation//0042493
1455610_at,145	0.000555	-4.48	-1.75	NM_001113325//NM_001252	<i>Gria1</i>	glutamate receptor, ionotropic, AMPA1 (alpha 1)	0001919 // regulation of receptor recycling // not recorded//0006810 // transport // inferred from electronic annotation//0006811 //
1455665_at,244	0.004335	-4.48	-6.75	NM_001112725//NM_007436	<i>Aldh3a1</i>	aldehyde dehydrogenase family 3, subfamily A1	0001666 // response to hypoxia // not recorded//0006081 // cellular aldehyde metabolic process // not recorded//0007568 // aging //
1455735_at,252	0.008757	-4.48	-1.69	NM_183312//NM_201639//	<i>Synn</i>	synemin, intermediate filament protein	0006939 // smooth muscle contraction // inferred from direct assay//0006939 // smooth muscle contraction // inferred from mutant
1455885_at,1231	0.002558	-4.50	-3.22	NM_001161775//NM_013607	<i>Mylh11</i>	myosin, heavy polypeptide 11, smooth muscle	
1455925_at,1776	0.003859	-4.50	-3.82	NM_013712	<i>Itgbl1bp2</i>	integrin beta 1 binding protein 2	
1455951_at,1216	0.006230	-4.56	1.02	NM_017399	<i>Fabp1</i>	fatty acid binding protein 1, liver	0006810 // transport // inferred from electronic annotation//0008284 // positive regulation of cell proliferation // inferred from
1456303_at	0.002260	-4.64	-1.29	NM_001014399//NM_001014	<i>Abi3bp</i>	ABI gene family, member 3 (NESH) binding protein	0010811 // positive regulation of cell-substrate adhesion // inferred from direct assay//0030198 // extracellular matrix organization //
1456335_at,145	0.000750	-4.64	-1.92	NM_172563//NM_006533004	<i>Hlf</i>	hepatic leukemia factor	0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 // regulation of transcription, DNA-templated
1456392_at,1320	0.004038	-4.66	-1.74	NM_026481//NM_006531324	<i>Tppp3</i>	tubulin polymerization-promoting protein family member 3	0001578 // microtubule bundle formation // not recorded
1456418_at,100	0.005143	-4.67	-1.24	NM_175260//NM_006534489	<i>Mylh10</i>	myosin, heavy polypeptide 10, non-muscle	0000281 // mitotic cytokinesis // inferred from mutant phenotype//0000281 // mitotic cytokinesis // not recorded//0001701 // in utero
1456482_at,187	0.004897	-4.68	-3.38	NM_009675//NM_006532040	<i>Aoc3</i>	amine oxidase, copper containing 3	0002523 // leukocyte migration involved in inflammatory response // not recorded//0002675 // positive regulation of acute
1456640_at,269	0.008570	-4.71	-1.93	NM_010656//NM_006506916	<i>Sspn</i>	sarcospan	0000165 // MAPK cascade // inferred from electronic annotation//0006468 // protein phosphorylation // not recorded//0007254 //
1456661_at	0.002971	-4.73	-5.53	NM_001081567//NM_009158	<i>Mapk10</i>	mitogen-activated protein kinase 10	0006468 // protein phosphorylation // inferred from electronic annotation//0009103 // lipopolysaccharide biosynthetic process //
1456821_at	0.000789	-4.78	-5.12	NM_001166030//NM_006516	<i>Mylik4</i>	myosin light chain kinase family, member 4	0002026 // regulation of the force of heart contraction // not recorded//0002678 // positive regulation of chronic inflammatory
1456864_at	0.002333	-4.78	-1.13	NM_153422//NM_006501481	<i>Pde5a</i>	phosphodiesterase 5A, cGMP-specific	0006200 // ATP catabolic process // inferred from electronic annotation//0006810 // transport // inferred from electronic
1456888_at,270	0.000296	-4.82	-1.48	NM_153145//NM_006533061	<i>Abca8a</i>	ATP-binding cassette, sub-family A (ABC1), member 8a	0001502 // cartilage condensation // inferred from electronic annotation//00060348 // bone development // inferred from mutant
1456960_at	0.005853	-4.84	-3.71	NM_007689	<i>Chad</i>	chondradherin	0045214 // sarcomere organization // inferred from mutant phenotype
1457031_at,244	0.005524	-4.85	-4.53	NM_001039071//NM_001039	<i>Ldb3</i>	LIM domain binding 3	0007165 // signal transduction // inferred from electronic annotation//0007186 // G-protein coupled receptor signaling pathway //
1457042_at,100	0.001490	-4.86	-1.59	NM_011784	<i>Aplnr</i>	apelin receptor	0001701 // in utero embryonic development // inferred from genetic interaction//0002376 // immune system process // inferred from
1457069_at,145	0.009361	-4.87	1.23	NM_010406//XR_374061//X	<i>Hc</i>	hemolytic complement	0003214 // cardiac left ventricle morphogenesis // not recorded//0006508 // proteolysis // inferred from mutant phenotype//0006518
1457191_at	0.004318	-4.99	-2.71	NM_013494	<i>Cpe</i>	carboxypeptidase E	0007155 // cell adhesion // inferred from direct assay//0007156 // homophilic cell adhesion // inferred from direct assay//0007157 //
1457438_at,100	0.003455	-5.03	-3.20	NM_007664//NM_006525553	<i>Cdh2</i>	cadherin 2	0006629 // lipid metabolic process // inferred from electronic annotation//0008015 // blood circulation // traceable author
1457465_at,208	0.001757	-5.06	-3.45	NM_011134//NM_006505011	<i>Pon1</i>	paraoxonase 1	0006810 // transport // inferred from electronic annotation//0006811 // ion transport // inferred from electronic annotation//0006814
1457466_at,1987	0.002971	-5.07	-1.49	NM_009135	<i>Scn7a</i>	sodium channel, voltage-gated, type VII, alpha	
1457532_at	0.009221	-5.10	-1.32	XR_105003//XR_107805	<i>Al256396</i>	EST AI256396	
1457551_at	0.007870	-5.12	-7.54	NM_008522	<i>Ltf</i>	lactotransferrin	0001503 // ossification // inferred from electronic annotation//0001817 // regulation of cytokine production // not recorded//0002227
1457553_at	0.005964	-5.19	-1.64	NM_001289877//NM_001289	<i>Per3</i>	period circadian clock 3	0000122 // negative regulation of transcription from RNA polymerase II promoter // inferred from direct assay//0006351 //
1457589_at,270	0.001779	-5.27	-1.03	NM_001109988//NM_001109	<i>Nep</i>	neuronal regeneration related protein	0017015 // regulation of transforming growth factor beta receptor signaling pathway // inferred from direct assay//0031103 // axon
1457707_at,244	0.005986	-5.37	-1.17	NM_001014288//NM_011211	<i>Ptprd</i>	protein tyrosine phosphatase, receptor type, D	0006470 // protein dephosphorylation // inferred from electronic annotation//0007157 // heterophilic cell-cell adhesion // inferred
1457801_at,399	0.005978	-5.48	-1.25	NM_001161665//NM_177724	<i>Kif26b</i>	kinase family member 26B	0007018 // microtubule-based movement // inferred from electronic annotation//0007275 // multicellular organismal development //
1457813_at	0.008196	-5.52	-1.46	NM_183221//NM_006535484	<i>Fat4</i>	FAT tumor suppressor homolog 4 (Drosophila)	0001658 // branching involved in ureteric bud morphogenesis // inferred from mutant phenotype//0001736 // establishment of planar
1457898_at	0.001511	-5.58	-2.11	NM_008182//NM_006510814	<i>Gsta2//Gm3776//Gsta1</i>	glutathione S-transferase, alpha 2 (Yc2)//predicted gene 3776//glutathione	0006749 // glutathione metabolic process // inferred from sequence or structural similarity//0008152 // metabolic process // inferred
1457908_at	0.008837	-5.64	-6.91	NM_001081198//NM_006496	<i>Tmem182</i>	transmembrane protein 182	
1457966_at	0.003646	-5.65	-1.10	NM_011415	<i>Sno12</i>	snail family zinc finger 2	0000122 // negative regulation of transcription from RNA polymerase II promoter // inferred from direct assay//0000122 // negative
1458040_at,280	0.005543	-5.68	-7.06	NM_053098	<i>Lmod2</i>	leiomodin 2 (cardiac)	
1458089_at	0.005720	-5.83	-1.30	NM_181277//NM_006520384	<i>Col14a1</i>	collagen, type XIV, alpha 1	0003229 // ventricular cardiac muscle tissue development // inferred from mutant phenotype//0007155 // cell adhesion // inferred
1458099_at	0.003588	-5.83	-1.30	NM_010570//NM_006496441	<i>Irs1</i>	insulin receptor substrate 1	0002053 // positive regulation of mesenchymal cell proliferation // inferred from genetic interaction//0007165 // signal transduction //
1458115_at,751	0.000457	-5.84	1.01	NM_001243008//NM_001243	<i>Col6a3</i>	collagen, type VI, alpha 3	0010951 // negative regulation of endopeptidase activity // inferred from electronic annotation
1458126_at,320	0.007792	-5.84	-2.02	NM_011224	<i>Pygm</i>	muscle glycogen phosphorylase	0001666 // response to hypoxia // not recorded//0005975 // carbohydrate metabolic process // inferred from electronic
1458134_at	0.009550	-5.95	-1.32	NM_001080814//NM_006510	<i>Fat3</i>	FAT tumor suppressor homolog 3 (Drosophila)	0000904 // cell morphogenesis involved in differentiation // inferred from mutant phenotype//0001764 // neuron migration // inferred
1458135_at	0.003694	-5.95	-4.46	NM_007751	<i>Cox8b</i>	cytochrome c oxidase subunit VIIIb	0042493 // response to drug // inferred from electronic annotation//1902600 // hydrogen ion transmembrane transport // inferred
1458178_at	0.009832	-6.07	-4.97	NM_175441//NM_006530824	<i>Mylik3</i>	myosin light chain kinase 3	0002528 // regulation of vascular permeability involved in acute inflammatory response // not recorded//0006468 // protein
1458240_at	0.006775	-6.10	-5.06	NM_001033288	<i>Sbspon</i>	somatomedin B and thrombospondin, type 1 domain containing	0006898 // receptor-mediated endocytosis // inferred from electronic annotation//0006955 // immune response // inferred from
1458286_at	0.006107	-6.10	-1.38	NM_001099774	<i>Krtap17-1</i>	keratin associated protein 17-1	
1458505_at,552	0.000791	-6.39	-6.39	NM_018870	<i>Pgam2</i>	phosphoglycerate mutase 2	0006094 // gluconeogenesis // not recorded//0006096 // glycolytic process // inferred from direct assay//0006096 // glycolytic process
1458573_at	0.004237	-6.46	-4.74	NM_001003914//NM_001171	<i>Obscn</i>	obscurin, cytoskeletal calmodulin and titin-interacting RhoGEF	0006468 // protein phosphorylation // inferred from electronic annotation//0007275 // multicellular organismal development //
1458578_at,102	0.001003	-6.48	-5.87	NM_009922//NM_006509969	<i>Cnn1</i>	calponin 1	0031032 // actomyosin structure organization // inferred from electronic annotation
1458589_at	0.002713	-6.57	-1.12	NM_172479//NM_006527580	<i>Sic38a5</i>	solute carrier family 38, member 5	0003333 // amino acid transmembrane transport // not recorded//0015804 // neutral amino acid transport // not recorded//0015816
1458601_at,399	0.003563	-6.59	-4.28	NM_015825	<i>Sh3brg</i>	SH3-binding domain glutamic acid-rich protein	0045454 // cell redox homeostasis // inferred from electronic annotation
1458605_at	0.006857	-6.59	-1.70	NM_031176//NM_006525185	<i>Tnxb</i>	tenascin XB	0006629 // lipid metabolic process // inferred from mutant phenotype//0006631 // fatty acid metabolic process // inferred from mutant
1458637_x_at	0.006780	-6.67	-1.68	NM_145434	<i>Nr1d1</i>	nuclear receptor subfamily 1, group D, member 1	0000122 // negative regulation of transcription from RNA polymerase II promoter // not recorded//0005978 // glycogen biosynthetic
1458663_at	0.007672	-6.83	-7.01	NM_023868//NM_006516610	<i>Ryr2</i>	ryanodine receptor 2, cardiac	0001666 // response to hypoxia // inferred from direct assay//0002027 // regulation of heart rate // inferred from mutant
1458738_at	0.005367	-7.10	-6.22	NM_023821//NM_028225//X	<i>Cmya5</i>	cardiomyopathy associated 5	0014733 // regulation of skeletal muscle adaptation // inferred from genetic interaction//0032513 // negative regulation of protein
1458768_at,1968	0.001785	-7.50	-1.26	NM_001083917//NM_001286	<i>Scn3b</i>	sodium channel, voltage-gated, type III, beta	0006810 // transport // inferred from electronic annotation//0006811 // ion transport // inferred from electronic annotation//0006814
1458814_at,107	0.004017	-7.53	-7.30	NM_026831	<i>Mybphl</i>	myosin binding protein H-like	
1458819_at	0.005839	-7.56	-14.30	NM_054037//NM_170727	<i>Scgb3a1</i>	secretoglobin, family 3A, member 1	
1458832_at	0.003993	-7.78	-7.37	NM_007710	<i>Ckm</i>	creatine kinase, muscle	0006603 // phosphocreatine metabolic process // traceable author statement//0016310 // phosphorylation // not recorded//0046314
1459009_at	0.009824	-7.80	-3.47	NM_144930//XR_387740	<i>Ces1f</i>	carboxylesterase 1F	0008152 // metabolic process // inferred from electronic annotation//0019626 // short-chain fatty acid catabolic process // inferred
1459078_at	0.009307	-7.88	-9.38	NM_001141927//NM_023129	<i>Pln</i>	phospholamban	0002026 // regulation of the force of heart contraction // inferred from genetic interaction//0002026 // regulation of the force of heart
1459098_at	0.006560	-8.17	-7.29	NM_001013013	<i>Dhrs7c</i>	dehydrogenase/reductase (SDR family) member 7C	0008152 // metabolic process // inferred from electronic annotation//0010880 // regulation of release of sequestered calcium ion into
1459242_at	0.002885	-8.29	-5.63	NM_010174	<i>Fabp3</i>	fatty acid binding protein 3, muscle and heart	0006658 // phosphatidylcholine biosynthetic process // inferred from genetic interaction//0006810 // transport // inferred from
1459279_at	0.002198	-8.31	-6.98	NM_026671//NM_006521312	<i>Lypd2</i>	Ly6b/Plaur domain containing 2	0001775 // cell activation // not recorded
1459322_at	0.000573	-8.53	-17.86	NM_016771	<i>Sult1d1</i>	sulfotransferase family 1D, member 1	0000103 // sulfate assimilation // inferred from direct assay//0006584 // catecholamine metabolic process // inferred from electronic

Table S6

Gene_ID	p (Corr)	FC-RSV 1 d	FC-RSV 5 d	RefSeq Transcript ID	Gene Symbol	Gene Title	Gene Ontology Biological Process
1459354_at	0.000333	-8.60	-1.73	NM_001289643///NM_001289	<i>Scgb3a2</i>	secretoglobin, family 3A, member 2	0019800 // peptide cross-linking via chondroitin 4-sulfate glycosaminoglycan // inferred from direct assay
1459442_at	0.007637	-8.79	-1.10	NM_174857///XM_006527345	<i>Mamdc2</i>	MAM domain containing 2	0002025 // regulation of the force of heart contraction // not recorded///0002027 // regulation of heart rate // not recorded///0006200
1459443_at	0.003776	-8.89	-2.30	NM_080728///NM_001164171	<i>Myh7///Myh6</i>	myosin, heavy polypeptide 7, cardiac muscle, beta///myosin, heavy	0006653 // 1,2-diacyl-sn-glycero-3-phosphocholine metabolic process // traceable author statement///0006776 // vitamin A metabolic
1459453_at	0.004024	-9.00	1.25	NM_023624	<i>Lrat</i>	lecithin-retinol acyltransferase (phosphatidylcholine-retinol-O-	0006879 // growth // inferred from electronic annotation///0045444 // fat cell differentiation // inferred from mutant
1459473_at	0.005936	-9.03	-2.27	NM_145741	<i>Gdf10</i>	growth differentiation factor 10	0004007 // cellular iron ion homeostasis // inferred from direct assay///0042742 // defense response to bacterium // inferred from
1459526_at	0.004980	-9.69	-14.95	NM_032541	<i>Hamp</i>	hepcidin antimicrobial peptide	0001756 // somitogenesis // inferred from expression pattern///0003009 // skeletal muscle contraction // inferred from electronic
1459595_at	0.001055	-10.19	-5.74	NM_011540	<i>Tcap</i>	titin-cap	0010952 // positive regulation of peptidase activity // not recorded
1459632_at	0.001604	-10.52	-1.09	NM_029620	<i>Pcolce2</i>	procollagen C-endopeptidase enhancer 2	0002376 // immune system process // inferred from electronic annotation///0006508 // proteolysis // not recorded///0006957 //
1459638_at	0.005873	-10.94	-45.91	NM_001291915///NM_013459	<i>Cfd</i>	complement factor D (adipsin)	
1459691_at	0.006381	-11.15	1.01	NM_020052	<i>Scube2</i>	signal peptide, CUB domain, EGF-like 2	
1459707_at	0.008641	-11.84	-8.50	NM_021282	<i>Cyp2e1</i>	cytochrome P450, family 2, subfamily e, polypeptide 1	
1459947_at	0.002102	-13.30	-8.33	NM_009608	<i>Actc1</i>	actin, alpha, cardiac muscle 1	
1459948_at	0.000296	-13.88	-17.85	NM_001164047///NM_001164	<i>Mb</i>	myoglobin	
1460003_at 991	0.004014	-14.22	-11.45	NM_011652///NM_028004///X	<i>Ttn///LOC102641264</i>	titin//titin-like	
1460014_at 224	0.005483	-15.68	-1.57	NM_018732///XM_006499030	<i>Scn3a</i>	sodium channel, voltage-gated, type III, alpha	
1460121_at 399	0.000660	-16.56	-1.45	NM_016974///XM_006540596	<i>Dbp</i>	D site albumin promoter binding protein	
1460474_at 763	0.003706	-18.82	-6.98	NM_001198841///NM_013808	<i>Csrp3</i>	cysteine and glycine-rich protein 3	
1460522_at 778	0.008807	-20.63	-24.58	NM_009605	<i>Adipoq</i>	adiponectin, C1Q and collagen domain containing	
1460531_at	0.004090	-21.04	-42.33	NM_007812///NM_009997///X	<i>Cyp2a4///Cyp2a5</i>	cytochrome P450, family 2, subfamily a, polypeptide 4///cytochrome P450,	
1460601_at 245	0.003192	-24.19	-29.32	NM_007606	<i>Car3</i>	carbonic anhydrase 3	
1460603_at 209	0.001692	-26.48	-65.61	NM_008725	<i>Nppa</i>	natriuretic peptide type A	

Table S7. Lung genes significantly altered by respiratory syncytial virus (RSV) in C57BL/6J (B6) mice (One-Way ANOVA at p<0.01).

Blue(-): fold decrease by RSV vs vehicle. Red: fold increase by RSV vs vehicle.

Gene_ID	p (Corr)	FC-RSV 1 d	FC-RSV 5 d	RefSeq Transcript ID	Gene Symbol	Gene Title	Gene Ontology Biological Process
1416086_a	0.005197	200.44	5.63	NM_019494//NR_038116	Cxcl11	chemokine (C-X-C motif) ligand 11	0002690 // positive regulation of leukocyte chemotaxis // inferred from electronic annotation//0006935 // chemotaxis // inferred from electronic annotation//0006954 // inflammatory
1415676_a	0.001737	164.37	202.89	NM_001039594	Lce3a	late cornified envelope 3A	0008544 // epidermis development // inferred from electronic annotation
1416273_a	0.003595	157.24	3.35	NM_008392//XNM_0065185	Irg1	immunoresponsive gene 1	0002376 // immune system process // inferred from electronic annotation//0002760 // positive regulation of antimicrobial humoral response // inferred from direct assay//0002760 //
1416051_a	0.000607	155.65	7.51	NM_021274	Cxcl10	chemokine (C-X-C motif) ligand 10	0002690 // positive regulation of leukocyte chemotaxis // not recorded//0006935 // chemotaxis // not recorded//0006954 // inflammatory response // inferred from electronic
1415670_a	0.002466	151.99	233.51	NM_008475	Krt4	keratin 4	0007010 // cytoskeleton organization // not recorded//0009790 // embryo development // traceable author statement//0030855 // epithelial cell differentiation // inferred from mutant
1419112_a	0.006025	140.36	1.30	NM_009140	Cxcl2	chemokine (C-X-C motif) ligand 2	0001975 // response to amphetamine // inferred from electronic annotation//0002237 // response to molecule of bacterial origin // inferred from direct assay//0006935 // chemotaxis //
1419150_a	0.002000	125.06	1.30	NM_009111//XNM_0065407	Saa1	serum amyloid A 1	0006953 // acute-phase response // inferred from electronic annotation//0008203 // cholesterol metabolic process // inferred from direct assay//0003634 // response to stilbenoid //
1415923_a	0.006027	115.15	15.07	NM_008599	Cxcl9	chemokine (C-X-C motif) ligand 9	0006935 // chemotaxis // inferred from electronic annotation//0006935 // chemotaxis // inferred from sequence or structural similarity//0006954 // inflammatory response // inferred from
1415686_a	0.001094	111.21	113.98	NM_001018079	Lce3f	late cornified envelope 3F	0008544 // epidermis development // inferred from electronic annotation
1415680_a	0.006207	109.25	152.72	NM_001033131	Krt10p	keratinocyte differentiation associated protein	0008544 // epidermis development // not recorded//0030154 // cell differentiation // inferred from electronic annotation
1416226_a	0.002537	106.83	3.83	NM_203320	Cxcl3	chemokine (C-X-C motif) ligand 3	0006935 // chemotaxis // inferred from electronic annotation//0006954 // inflammatory response // not recorded//0006955 // immune response // inferred from electronic
1415770_a	0.000157	99.71	25.91	NM_011315	Saa3	serum amyloid A 3	0006953 // acute-phase response // inferred from electronic annotation//0035634 // response to stilbenoid // inferred from expression pattern
1416907_a	0.002452	90.52	1.95	NM_011337	Ccl3	chemokine (C-X motif) ligand 3	0001165 // MAPK cascade // inferred from sequence or structural similarity//0001649 // osteoblast differentiation // inferred from sequence or structural similarity//0001775 // cell
1416144_a	0.004656	88.19	4.73	NM_031367	Ifi44l	interferon-induced protein 44 like	0006955 // immune response // inferred from direct assay
1415710_a	0.004909	81.86	57.64	NM_198680//NM_201363	Serpinc3b//Serpinc3c	serine (or cysteine) peptidase inhibitor, clade B (ovalbumin), member	0010951 // negative regulation of endopeptidase activity // inferred from direct assay//0030162 // regulation of proteolysis // not recorded
1415701_x	0.007303	70.58	70.30	NM_001199213//NM_0279	Serpinc12	serine (or cysteine) peptidase inhibitor, clade B (ovalbumin), member 12	0002244 // hematopoietic progenitor cell differentiation // inferred from mutant phenotype//0010466 // negative regulation of peptidase activity // inferred from electronic
1415690_a	0.006867	68.27	107.25	NM_008508	Lor	loricrin	0031424 // keratinization // inferred from electronic annotation
1415682_a	0.007712	61.29	122.68	NM_028798	Crtct1	cysteine-rich C-terminal 1	0008544 // epidermis development // inferred from electronic annotation
1415694_a	0.003940	61.29	106.99	NM_028622	Lce1c	late cornified envelope 1C	0007010 // cytoskeleton organization // not recorded//0009314 // response to radiation // inferred from electronic annotation//0043587 // tongue morphogenesis // inferred from electronic
1415695_a	0.001377	60.93	106.62	NM_010662	Krt13	keratin 13	0008285 // negative regulation of cell proliferation // inferred from direct assay
1416624_a	0.002449	57.12	2.35	NM_011410//XNM_0065326	Sfn4//Sfn3	schlafen 4//schlafen 3	0001666 // response to hypoxia // not recorded//0001701 // in utero embryonic development // inferred from mutant phenotype//0001821 // histamine secretion // not
1415736_a	0.008993	56.90	33.80	NM_001272051//NM_0073	Ado	adenosine deaminase	0001665 // MAPK cascade // inferred from electronic annotation//0001525 // angiogenesis // traceable author statement//0001666 // response to hypoxia // inferred from electronic
1416522_a	0.000394	56.68	2.47	NM_011333	Ccl2	chemokine (C-X motif) ligand 2	0001665 // response to hypoxia // not recorded//0001525 // angiogenesis // inferred from direct assay//0001648 // protein processing // not recorded//0001781 // skin
1415701_x	0.007303	49.11	74.81	NM_009100	Rtn	regitin	0001665 // response to hypoxia // not recorded//0001525 // angiogenesis // inferred from direct assay//0001648 // protein processing // not recorded//0001781 // skin
1416125_a	0.000087	48.97	5.00	NM_011331	Ccl12	chemokine (C-X motif) ligand 12	0001665 // response to hypoxia // not recorded//0001525 // angiogenesis // inferred from direct assay//0002548 // monocyte chemotaxis // inferred from direct assay//0002548 // monocyte
1416244_a	0.001954	47.05	3.52	NM_001287348//NM_0087	Nppb	natriuretic peptide type B	0001666 // response to hypoxia // inferred from electronic annotation//0003085 // negative regulation of systemic arterial blood pressure // not recorded//0006182 // cGMP biosynthetic
1415683_a	0.001650	45.99	119.67	NM_027137	Lce1d	late cornified envelope 1D	0008544 // epidermis development // inferred from electronic annotation//0001277 // cellular response to calcium ion // not recorded
1415713_a	0.002131	41.83	46.16	NM_026414	Asprv1	aspartic peptidase, retroviral-like 1	0006508 // proteolysis // inferred from direct assay//0016485 // protein processing // inferred from direct assay//0016485 // protein processing // not recorded//0001781 // skin
1418517_a	0.001701	41.35	1.38	NM_145209//XNM_0065302	Oas1	2'-5' oligoadenylate synthetase-like 1	0002376 // immune system process // inferred from electronic annotation//0006955 // immune response // inferred from electronic annotation//0008152 // metabolic process // inferred
1415699_a	0.005451	41.23	95.28	NM_008631	Mt4	metallothionein 4	0006875 // cellular metal ion homeostasis // inferred from direct assay//0046686 // response to cadmium ion // not recorded
1420911_a	0.000610	41.13	1.18	NM_031168	Il6	interleukin 6	0001781 // neutrophil apoptotic process // inferred from direct assay//0001781 // neutrophil apoptotic process // inferred from mutant phenotype//0001781 // neutrophil apoptotic process
1417425_a	0.001706	38.59	1.65	NM_010846//NR_003520	Mx1	myxovirus (influenza virus) resistance 1	0002376 // immune system process // inferred from electronic annotation//0006184 // GTP catalytic process // traceable author statement//0009615 // response to virus // inferred from
1416632_a	0.005121	35.83	2.32	NM_008176	Cxcl1	chemokine (C-X-C motif) ligand 1	0002237 // response to molecule of bacterial origin // not recorded//0002526 // acute inflammatory response // not recorded//0006954 // inflammatory response // inferred from electronic
1420088_a	0.004609	34.90	1.22	NM_008768	Orm1	orosomucoid 1	0002682 // regulation of immune system process // inferred from electronic annotation//0006810 // transport // inferred from electronic annotation//0006953 // acute-phase response //
1416317_a	0.002359	34.74	3.25	NM_023137	Ubd	ubiquitin D	0006511 // ubiquitin-dependent protein catabolic process // inferred from mutant phenotype//0006511 // ubiquitin-dependent protein catabolic process // not recorded//0010243 //
1417988_a	0.003604	34.65	1.48	NM_019948	Clec4e	C-type lectin domain family 4, member e	0002376 // immune system process // inferred from electronic annotation//0006955 // immune response // inferred from mutant phenotype//00050715 // positive regulation of cytokine
1417314_a	0.000879	33.66	1.72	NM_015783//XNR_168557//	Gm9706//Isg15	predicted gene 9706//ISG15 ubiquitin-like modifier	0019941 // modification-dependent protein catabolic process // inferred from direct assay//0003197 // negative regulation of protein ubiquitination // not recorded//0032020 // ISG15-
1416165_a	0.005311	33.10	4.53	NM_026835	M540d6	membrane-spanning 4-domains, subfamily A, member 6D	0001665 // response to hypoxia // not recorded//0001525 // angiogenesis // inferred from direct assay//0001648 // protein processing // not recorded//0001781 // skin
1416312_a	0.006470	33.04	3.26	NM_020498//XNM_0065212	Ly6i	lymphocyte antigen 6 complex, locus I	0002376 // immune system process // inferred from electronic annotation//0006164 // purine nucleotide biosynthetic process // inferred from direct assay//0006955 // immune response //
1416527_a	0.000159	32.72	2.46	NM_133871//XNM_0065024	Ifi44	interferon-induced protein 44	0002376 // immune system process // inferred from electronic annotation//0002819 // regulation of adaptive immune response // not recorded//0006351 // transcription, DNA-templated //
1417133_a	0.007896	31.88	1.61	NM_145226	Oas3	2'-5' oligoadenylate synthetase 3	0001775 // cell activation // not recorded//0007568 // aging // inferred from electronic annotation//0008284 // positive regulation of cell proliferation // not recorded//0010033 // response
1416889_a	0.005874	31.64	1.97	NM_001252600//NM_0012	Irf7	interferon regulatory factor 7	0002376 // immune system process // inferred from electronic annotation//0006508 // proteolysis // inferred from electronic annotation//0006956 // complement activation // not
1416686_a	0.006182	31.40	2.23	NM_001004384//NM_0012	Timp1	tissue inhibitor of metalloproteinase 1	0010466 // negative regulation of peptidase activity // not recorded//0010951 // negative regulation of endopeptidase activity // not recorded//0030162 // regulation of proteolysis //
1416251_a	0.003568	29.07	3.44	NM_001142706//NM_0081	Cfb	complement factor B	0006935 // chemotaxis // inferred from electronic annotation//0006954 // inflammatory response // not recorded//0006955 // immune response // inferred from electronic
1415726_a	0.002560	28.54	34.85	NM_009126	Serpinc3a	serine (or cysteine) peptidase inhibitor, clade B (ovalbumin), member 3A	0002376 // immune system process // inferred from electronic annotation//0006184 // GTP catalytic process // traceable author statement//0009615 // response to virus // inferred from
1417399_a	0.004640	27.23	1.66	NM_013654	Ccl7	chemokine (C-X motif) ligand 7	0006935 // chemotaxis // inferred from electronic annotation//0006954 // inflammatory response // inferred from electronic annotation//0006955 // immune response // inferred from
1417562_a	0.002639	26.84	1.61	NM_015783//XNR_168557//	Gm9706//Isg15	predicted gene 9706//ISG15 ubiquitin-like modifier	0019941 // modification-dependent protein catabolic process // inferred from direct assay//0003197 // negative regulation of protein ubiquitination // not recorded//0032020 // ISG15-
1415791_a	0.001423	25.83	23.40	NM_001164787//NM_0114	Spr2a1//Spr2a2//Spr2a3	small proline-rich protein 2A1//small proline-rich protein 2A2//small	0008360 // regulation of cell shape // traceable author statement//0008544 // epidermis development // non-traceable author statement//0030216 // keratinocyte differentiation // non-
1417865_a	0.001289	25.65	1.52	NM_001039701//NM_0011	Il1rn	interleukin 1 receptor antagonist	0001660 // fever generation // not recorded//0001960 // negative regulation of cytokine-mediated signaling pathway // not recorded//0002439 // chronic inflammatory response to antigenic
1415702_a	0.006255	25.40	60.70	NM_026394	Lce1f	late cornified envelope 1F	0008544 // epidermis development // inferred from electronic annotation
1418453_a	0.006656	25.24	1.39	NM_013652	Ccl4	chemokine (C-X motif) ligand 4	0006935 // chemotaxis // inferred from electronic annotation//0006954 // inflammatory response // not recorded//0006955 // immune response // inferred from electronic
1416371_a	0.000726	24.98	3.00	NM_018866	Cxcl13	chemokine (C-X-C motif) ligand 13	0002518 // lymphocyte chemotaxis across high endothelial venule // inferred from mutant phenotype//0006935 // chemotaxis // inferred from electronic annotation//0006954 //
1415754_a	0.008547	24.71	29.43	NM_020036	Calmd4	calmodulin 4	0007165 // signal transduction // inferred from electronic annotation
1420889_a	0.003668	24.63	1.18	NM_013606//NR_003508	Mx2	myxovirus (influenza virus) resistance 2	0002376 // immune system process // inferred from electronic annotation//0006184 // GTP catalytic process // traceable author statement//0009615 // response to virus // inferred from
1418991_a	0.003411	24.52	1.31	NM_008361//XNM_0064987	Il1b	interleukin 1 beta	0000122 // negative regulation of transcription from RNA polymerase II promoter // not recorded//0001665 // MAPK cascade // not recorded//0000187 // activation of MAPK activity // not
1415730_a	0.001588	23.47	34.01	NM_019728	Defb4	defensin beta 4	0006952 // defense response // inferred from electronic annotation//0042742 // defense response to bacterium // inferred from electronic annotation
1416576_a	0.007974	23.05	2.44	NM_010555//XNM_0064957	Il1r2	interleukin 1 receptor, type II	0019221 // cytokine-mediated signaling pathway // inferred from electronic annotation
1416511_a	0.000369	23.04	2.48	NM_001139519//NM_0213	Zbp1	Z-DNA binding protein 1	0002376 // immune system process // inferred from electronic annotation//0008152 // metabolic process // inferred from electronic annotation//0016032 // viral process // inferred from
1415822_a	0.000171	22.64	20.50	NM_009638//XNM_0065235	Crisp1	cysteine-rich secretory protein 1	0002376 // immune system process // inferred from electronic annotation//0009615 // response to virus // inferred from mutant phenotype//0035457 // cellular response to interferon-
1418061_a	0.000332	22.47	1.46	NM_008331	Ifi1	interferon-induced protein with tetratricopeptide repeats 1	0008544 // epidermis development // inferred from electronic annotation
1415750_a	0.004741	22.45	31.23	NM_026822	Lce1b	late cornified envelope 1B	0002639 // positive regulation of immunoglobulin production // inferred from mutant phenotype//0002925 // positive regulation of humoral immune response mediated by circulating
1418983_a	0.000587	22.31	1.31	NM_017371	Hpx	hemopexin	0002682 // regulation of immune system process // inferred from electronic annotation//0006810 // transport // inferred from electronic annotation//0006953 // acute-phase response //
1422002_a	0.000131	22.18	1.14	NM_011016	Orm2	orosomucoid 2	0008360 // regulation of cell shape // traceable author statement//0008544 // epidermis development // non-traceable author statement//0030216 // keratinocyte differentiation // non-
1415806_a	0.004608	22.13	20.79	NM_001164787//NM_0114	Spr2a1//Spr2a2//Spr2a3	small proline-rich protein 2A1//small proline-rich protein 2A2//small	0006629 // lipid metabolic process // inferred from electronic annotation//0006633 // fatty acid biosynthetic process // inferred from electronic annotation//0006694 // steroid biosynthetic
1416217_a	0.000762	21.64	3.92	NM_009890	Ch25h	cholesterol 25-hydroxylase	0006810 // transport // inferred from electronic annotation//0006811 // ion transport // inferred from electronic annotation
1416188_a	0.009275	21.39	4.12	NM_175449	Fam20f	family with sequence similarity 26, member F	0006955 // immune response // inferred from electronic annotation//0008284 // positive regulation of cell proliferation // not recorded//0014068 // positive regulation of
1424080_a	0.006181	20.73	1.05	NM_009971//XNM_0065321	Cs3	colony stimulating factor 3 (granulocyte)	0006351 // transcription, DNA-templated // inferred from sequence or structural similarity//0006810 // transport // inferred from electronic annotation//0007166 // cell surface receptor
1417724_a	0.003826	20.44	1.55	NM_001171024//NM_0102	Il4i1//Nup62-ii4i1	interleukin 4 induced 1//Nup62-II4i1 protein	0032496 // response to lipopolysaccharide // inferred from electronic annotation//0042088 // T-helper 1 type immune response // not recorded//0007031 // cellular response to hydrogen
1416958_a	0.003426	20.36	1.90	NM_010531//XNM_0065073	Il18bp	interleukin 18 binding protein	0002376 // immune system process // inferred from electronic annotation//0006164 // purine nucleotide biosynthetic process // inferred from direct assay//0006955 // immune response //
1416708_a	0.008399	20.28	2.16	NM_145211//XNM_0065303	Oas1a	2'-5' oligoadenylate synthetase 1A	0002376 // immune system process // inferred from electronic annotation//0006915 // apoptotic process // inferred from electronic annotation//0010466 // negative regulation of peptidase
1416104_a	0.008154	19.37	3.34	NM_009251//XNM_0065430	Serpina3g	serine (or cysteine) peptidase inhibitor, clade A, member 3G	0006629 // lipid metabolic process // inferred from electronic annotation//0016042 // lipid catabolic process // inferred from electronic annotation
1416629_a	0.004949	19.31	2.33	NM_134102//XNM_0065227	Plg1a	phospholipase A1 member A	0018149 // peptide cross-linking // inferred from electronic annotation//0031424 // keratinization // inferred from electronic annotation
1415780_a	0.005391	19.25	24.54	NM_00120442//NM_0114	Spr3	small proline-rich protein 3	0001660 // fever generation // inferred from electronic annotation//0006954 // inflammatory response // inferred from electronic annotation//0006955 // immune response // inferred from
1417608_a	0.001313	19.00	1.59	NM_010554//XNM_0064987	Il1a	interleukin 1 alpha	0006508 // proteolysis // inferred from mutant phenotype//0006511 // ubiquitin-dependent protein catabolic process // inferred from electronic annotation//0032020 // ISG15-protein
1421064_a	0.002416	18.55	1.17	NM_011909	Usp18	ubiquitin specific peptidase 18	0001781 // neutrophil apoptotic process // not recorded//0006915 // apoptotic process // inferred from electronic annotation//0007165 // signal transduction // inferred from electronic
1416471_a	0.006652	18.35	2.57	NM_030701	Hcar2	hydroxycarboxylic acid receptor 2	0001788 // antibody-dependent cellular cytotoxicity // inferred from mutant phenotype//0001798 // positive regulation of type Ila hypersensitivity // inferred from mutant
1416713_a	0.001179	18.10	2.15	NM_026862//XNM_0065403	Cd177	antigen	0002376 // immune system process // inferred from electronic annotation//0006915 // apoptotic process // inferred from electronic annotation//0006915 // response to virus // inferred
1416351_a	0.001333	17.95	3.02	NM_010186	Fcgr1	Fc receptor, IgG, high affinity 1	0006508 // proteolysis // not recorded//0030574 // collagen catabolic process // inferred from electronic annotation
1422844_a	0.001042	17.63	1.10	NM_008332//XNM_0065267	Ifi12	interferon-induced protein with tetratricopeptide repeats 2	0001503 // ossification // not recorded//0002376 // immune system process // inferred from electronic annotation//0008152 // metabolic process // inferred from electronic
1419364_a	0.009000	17.56	1.27	NM_008611	Mmp8	matrix metalloproteinase 8	0008544 // epidermis development // inferred from electronic annotation
1425190_a	0.000775	17.33	1.01	NM_021384//XNM_0065151	Rsd2	radical S-adenosyl methionine domain containing 2	0006351 // transcription, DNA-templated // inferred from sequence or structural similarity//0006810 // transport // inferred from electronic annotation//0007166 // cell surface receptor
1415727_a	0.000720	16.99	34.77	NM_025984	Lce1a1	late cornified envelope 1A1	0008544 // epidermis development // inferred from electronic annotation
1417738_a	0.005761	16.05	1.55	NM_001171024//NM_0102	Il4i1//Nup62-ii4i1	interleukin 4 induced 1//Nup62-II4i1 protein	0006351 // transcription, DNA-templated // inferred from sequence or structural similarity//0006810 // transport // inferred from electronic annotation//0007166 // cell surface receptor
1415716_a	0.000762	15.45	38.13	NM_028625	Lce1a2	late cornified envelope 1A2	0008544 // epidermis development // inferred from electronic annotation
1418992_a	0.000258	15.45	1.31	NM_001159738//NM_0169	Ccl20	chemokine (C-X motif) ligand 20	0006935 // chemotaxis // not recorded//0006954 // inflammatory response // inferred from electronic annotation//0006955 // immune response // inferred from electronic
1418641_a	0.002052	15.38	1.36	NM_011407	Sfn1	schlafen 1	0000122 // negative regulation of transcription from RNA polymerase II promoter // inferred from direct assay//0001933 // negative regulation of protein phosphorylation // inferred from

Table S7

Gene ID	p (Corr)	FC-RSV 1 d	FC-RSV 5 d	RefSeq Transcript ID	Gene Symbol	Gene Title	Gene Ontology Biological Process
1434554_a	0.001326	15.36	-1.13	NM_011409//NM_0065326	<i>Slf3n3//Slfn4</i>	schlafen 3//schlafen 4	0008285 // negative regulation of cell proliferation // inferred from direct assay
1415831_a	0.000623	15.11	18.88	NM_183278	<i>Fam25c</i>	family with sequence similarity 25, member C	
1416506_a	0.000826	14.68	2.50	NM_001163161//NM_0108	<i>Clec4d</i>	C-type lectin domain family 4, member d	0002376 // immune system process // inferred from electronic annotation//00045087 // innate immune response // inferred from electronic annotation
1416330_a	0.001818	14.66	3.12	NM_0021893//NM_0065272	<i>Cd274</i>	CD274 antigen	0006955 // immune response // not recorded//0007165 // signal transduction // not recorded//0007166 // cell surface receptor signaling pathway // not recorded//0031295 // T cell
1417903_a	0.000952	14.47	1.50	NM_001162883//NM_0011	<i>Apol9a//Apol9b</i>	apolipoprotein L 9a//apolipoprotein L 9b	0006869 // lipid transport // inferred from electronic annotation//00042157 // lipoprotein metabolic process // inferred from electronic annotation
1417556_a	0.000020	14.30	1.61	NM_001172588//NM_1531	<i>Mrgpra2a//Mrgpra2b</i>	MAS-related GPR, member A2a//MAS-related GPR, member A2b	0007165 // signal transduction // inferred from electronic annotation//0007186 // G-protein coupled receptor signaling pathway // inferred from electronic annotation
1420699_a	0.000680	13.75	1.19	NM_008630	<i>Mt2</i>	metallothionein 2	0006882 // cellular zinc ion homeostasis // inferred from mutant phenotype//0007263 // nitric oxide mediated signal transduction // inferred from mutant phenotype//0010273 //
1424274_a	0.007566	13.60	1.04	NM_029499//NM_0065272	<i>M54dc4</i>	membrane-spanning 4-domains, subfamily A, member 4C	0002376 // immune system process // inferred from electronic annotation//0006164 // purine nucleotide biosynthetic process // not recorded//0006401 // RNA catabolic process // inferred
1417321_a	0.001060	13.50	1.68	NM_145322//NM_0065303	<i>Oas2</i>	2'-5' oligoadenylate synthetase 2	0007165 // signal transduction // inferred from electronic annotation//0007186 // G-protein coupled receptor signaling pathway // inferred from electronic annotation
1417446_a	0.000852	13.49	1.64	NM_030720//NM_0065215	<i>Gpr84</i>	G protein-coupled receptor 84	0010466 // negative regulation of peptidase activity // inferred from electronic annotation//0010951 // negative regulation of endopeptidase activity // not recorded
1415740_a	0.003031	13.43	32.65	NM_001032339	<i>Ctata1</i>	cystatin A1	0000302 // response to reactive oxygen species // inferred from mutant phenotype//0000302 // response to reactive oxygen species // not recorded//0006006 // glucose metabolic process
1418021_a	0.001525	13.02	1.47	NM_007470//NM_0065217	<i>Apod</i>	apolipoprotein D	0002244 // hematopoietic progenitor cell differentiation // inferred from mutant phenotype//0007275 // multicellular organismal development // inferred from electronic
1415800_a	0.007518	12.97	22.07	NM_133698//NM_0065019	<i>Hmr</i>	hormerin	0002376 // immune system process // inferred from electronic annotation//0008285 // negative regulation of cell proliferation // inferred from sequence or structural similarity//0009615 //
1423164_a	0.000267	12.77	1.09	NM_010501	<i>Ifit3</i>	interferon-induced protein with tetratricopeptide repeats 3	0006953 // acute-phase response // inferred from electronic annotation//0035634 // response to stilbenoid // inferred from expression pattern
1424778_a	0.002713	12.77	1.03	NM_011314//NM_0065407	<i>Saa2</i>	serum amyloid A 2	001819 // positive regulation of cytokine production // inferred from direct assay//0006954 // inflammatory response // inferred from electronic annotation//0032755 // positive regulation
1417663_a	0.004132	12.74	1.57	NM_153511	<i>Il1f9</i>	interleukin 1 family, member 9	0002376 // immune system process // inferred from electronic annotation//0006164 // purine nucleotide biosynthetic process // inferred from direct assay//0006955 // immune response //
1426595_a	0.003827	12.62	-1.03	NM_011854//NM_0065303	<i>Oas2</i>	2'-5' oligoadenylate synthetase-like 2	
1415947_a	0.001352	12.45	14.16	NM_028629	<i>Kprp</i>	keratinocyte expressed, proline-rich	
1415829_a	0.001604	12.33	19.41	NM_001081375//NM_0282	<i>Cnfn</i>	cornifelin	0031424 // keratinization // inferred from electronic annotation
1416884_a	0.000673	12.17	2.00	NM_007482	<i>Arg1</i>	arginase, liver	0000050 // urea cycle // not recorded//0001889 // liver development // inferred from electronic annotation//0001938 // positive regulation of endothelial cell proliferation // not
1416617_a	0.003115	12.07	2.40	NM_024495	<i>Cor13</i>	carbonic anhydrase 13	0006730 // one-carbon metabolic process // inferred from electronic annotation
1415995_a	0.006778	12.06	11.31	NM_025867	<i>Serpinb11</i>	serine (or cysteine) peptidase inhibitor, clade B (ovalbumin), member 11	0010466 // negative regulation of peptidase activity // inferred from electronic annotation//0010951 // negative regulation of endopeptidase activity // not recorded//0030162 // regulation
1416628_a	0.000252	11.89	2.33	NM_023044	<i>Slc15a3</i>	solute carrier family 15, member 3	0006810 // transport // inferred from electronic annotation//0006857 // oligopeptide transport // inferred from electronic annotation//0015031 // protein transport // inferred from
1417668_a	0.009682	11.74	1.57	NM_001013832	<i>Gpr31b</i>	G protein-coupled receptor 31, D17Leh66b region	0007165 // signal transduction // inferred from electronic annotation//0007186 // G-protein coupled receptor signaling pathway // inferred from electronic annotation
1416441_a	0.001013	11.65	2.85	NM_027988//NM_0065249	<i>Naxo1</i>	NADPH oxidase organizer 1	0006801 // superoxide metabolic process // inferred from direct assay//0007154 // cell communication // inferred from electronic annotation//0022617 // extracellular matrix disassembly //
1416723_a	0.002166	11.61	2.14	NM_172295	<i>Mab21l3</i>	mab-21-like 3 (C. elegans)	
1417691_a	0.004594	11.60	1.57	NM_001167743//NM_1815	<i>Sfn8</i>	schlafen 8	
1416239_a	0.000786	11.46	3.67	NM_001033767//NM_0065	<i>Gm4951</i>	predicted gene 4951	0008152 // metabolic process // inferred from electronic annotation//0035458 // cellular response to interferon-beta // inferred from direct assay
1416500_a	0.007475	11.25	2.51	NM_001113326//NM_0311	<i>Msr1</i>	macrophage scavenger receptor 1	0006897 // endocytosis // inferred from electronic annotation//0006898 // receptor-mediated endocytosis // inferred from electronic annotation//0010744 // positive regulation of
1415722_a	0.003810	11.23	34.97	NR_001592//NR_030416	<i>H19//Mir675</i>	H19, imprinted maternally expressed transcript//microRNA 675	0008285 // negative regulation of cell proliferation // inferred from genetic interaction//0010468 // regulation of gene expression // inferred from direct assay
1416567_a	0.003880	11.11	2.44	NM_001289493//NM_0012	<i>Gbp3</i>	guanylate binding protein 3	0006184 // GTP catabolic process // inferred from sequence or structural similarity//0035458 // cellular response to interferon-beta // inferred from direct assay//0042832 // defense
1416141_a	0.002863	11.09	4.80	NM_011867//NM_0065150	<i>Sk26a4</i>	solute carrier family 26, member 4	0006810 // transport // inferred from electronic annotation//0006820 // anion transport // inferred from sequence or structural similarity//0006821 // chloride transport // not
1418970_a	0.004401	11.07	1.31	NM_013737//NM_0065243	<i>Pla2g7</i>	phospholipase A2, group VII (platelet-activating factor acetylhydrolase,	0006508 // proteolysis // inferred from electronic annotation//0006629 // lipid metabolic process // inferred from electronic annotation//0006954 // inflammatory response // traceable
1416282_a	0.003371	10.84	3.33	NM_001081957	<i>Wfdc17</i>	WAP four-disulfide core domain 17	0010466 // negative regulation of peptidase activity // inferred from electronic annotation
1418347_a	0.004017	10.72	1.40	NM_013468	<i>Ankrd1</i>	ankyrin repeat domain 1 (cardiac muscle)	0001122 // negative regulation of transcription from RNA polymerase II promoter // not recorded//0006357 // regulation of transcription from RNA polymerase II promoter // inferred from
1415950_a	0.000762	10.65	13.58	NM_025416	<i>Them5</i>	thioesterase superfamily member 5	0006629 // lipid metabolic process // inferred from electronic annotation//0006631 // fatty acid metabolic process // inferred from electronic annotation//0035336 // long-chain fatty-acyl-
1452070_a	0.006149	10.65	-1.29	NM_009252	<i>Serpin3n</i>	serine (or cysteine) peptidase inhibitor, clade A, member 3N	0006953 // acute-phase response // inferred from electronic annotation//0006954 // inflammatory response // inferred from electronic annotation//0010466 // negative regulation of
1417045_a	0.000237	10.60	1.85	NM_011087//NM_011088//	<i>Pira1//Pira11//Pira2//Pira5</i>	paired-Ig-like receptor A1//paired-Ig-like receptor A11//paired-Ig-like	0001782 // B cell homeostasis // inferred from mutant phenotype//0002376 // immune system process // inferred from electronic annotation//0019221 // cytokine-mediated signaling
1416509_a	0.004030	10.41	2.49	NM_001040201//NM_1453	<i>BC023105</i>	cDNA sequence BC023105	0008152 // metabolic process // inferred from electronic annotation
1416239_a	0.000805	10.36	3.58	NM_144559	<i>Fcgr4</i>	Fc receptor, IgG, low affinity IV	0001866 // NK T cell proliferation // not recorded//0051930 // regulation of sensory perception of pain // not recorded//0071222 // cellular response to lipopolysaccharide // not recorded
1419662_a	0.000734	10.32	1.24	NM_030150	<i>Dhx58</i>	DEXH (Asp-Glu-X-His) box polypeptide 58	0002376 // immune system process // inferred from electronic annotation//0008152 // metabolic process // inferred from electronic annotation//0009615 // response to virus // inferred
1421384_a	0.000690	10.30	1.16	NM_025993//NM_028861	<i>Herc6</i>	hect domain and RLD 6	0002244 // hematopoietic progenitor cell differentiation // inferred from genetic interaction//0002376 // immune system process // inferred from electronic annotation//0016567 // protein
1417172_a	0.005672	10.27	1.26	NM_009709	<i>Arg2</i>	arginase type II	0000050 // urea cycle // inferred from electronic annotation//0001657 // ureteric bud development // inferred from expression pattern//0006525 // arginine metabolic process // not
1416679_a	0.001083	10.27	2.25	NM_001122954//NM_0111	<i>Pla2g5</i>	phospholipase A2, group V	0006629 // lipid metabolic process // inferred from electronic annotation//000664 // phospholipid metabolic process // inferred from direct assay//0006663 // platelet activating factor
1419510_a	0.004010	10.14	1.26	NM_029005//NM_0065314	<i>Mkl1</i>	mixed lineage kinase domain-like	0006468 // protein phosphorylation // inferred from electronic annotation//0012501 // programmed cell death // inferred from electronic annotation//0070207 // protein homotrimerization
1416728_a	0.008156	10.00	2.13	NM_054098	<i>Steap4</i>	STEAP family member 4	0006810 // transport // inferred from electronic annotation//0006811 // ion transport // inferred from electronic annotation//0015677 // copper ion import // inferred from direct
1415979_a	0.001483	9.76	12.11	NM_146189//NM_0065408	<i>Mybpc2</i>	myosin binding protein C, fast-type	0006936 // muscle contraction // inferred from direct assay//0007155 // cell adhesion // inferred from electronic annotation
1417294_a	0.002031	9.45	1.73	NM_011087//NM_011088//	<i>Pira1//Pira11//Pira2//Pira5</i>	paired-Ig-like receptor A1//paired-Ig-like receptor A11//paired-Ig-like	0001782 // B cell homeostasis // inferred from mutant phenotype//0002376 // immune system process // inferred from electronic annotation//0019221 // cytokine-mediated signaling
1425008_a	0.000852	9.39	1.02	NM_198095	<i>Bst2</i>	bone marrow stromal cell antigen 2	0002376 // immune system process // inferred from electronic annotation//0002737 // negative regulation of plasmacytoid dendritic cell cytokine production // inferred from electronic
1415827_a	0.005628	9.35	19.49	NM_001291804//NM_0135	<i>Dsc1</i>	desmocollin 1	0007155 // cell adhesion // inferred from electronic annotation//0007156 // homophilic cell adhesion // inferred from electronic annotation
1416453_a	0.009491	9.34	2.69	NM_008491	<i>Lcn2</i>	lipocalin 2	0002376 // immune system process // inferred from electronic annotation//0006810 // transport // inferred from electronic annotation//0006811 // ion transport // inferred from electronic
1425242_a	0.007983	9.04	1.01	NM_001081215//NM_0012	<i>Ddx60</i>	DEAD (Asp-Glu-Ala-Asp) box polypeptide 60	0008152 // metabolic process // inferred from electronic annotation//0009615 // response to virus // not recorded//0051607 // defense response to virus // inferred from direct
1416695_a	0.000025	8.86	2.22	NM_001293690//NM_0083	<i>Ido1</i>	indoleamine 2,3-dioxygenase 1	0002534 // cytokine production involved in inflammatory response // inferred from mutant phenotype//0002666 // positive regulation of T cell tolerance induction // inferred from mutant
1417968_a	0.001190	8.80	1.49	NM_001164323//NM_1990	<i>Phf11d</i>	PHD finger protein 11D	0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 // regulation of transcription, DNA-templated // inferred from electronic annotation
1419658_a	0.000469	8.63	1.24	NM_011150//NM_0065325	<i>Lgals3bp</i>	lectin, galactoside-binding, soluble, 3 binding protein	0006898 // receptor-mediated endocytosis // inferred from sequence or structural similarity//0007155 // cell adhesion // inferred from electronic annotation
1418345_a	0.000896	8.61	1.40	NM_001012236//NM_0116	<i>Atrip//Trex1</i>	ATR interacting protein//three prime repair exonuclease 1	0000738 // DNA catabolic process, exonucleolytic // inferred from direct assay//0006259 // DNA metabolic process // inferred from direct assay//0006281 // DNA repair // inferred from
1416276_a	0.001356	8.58	3.34	NM_019467//NM_0065235	<i>Aif1</i>	allograft inflammatory factor 1	0001774 // microglial cell activation // non-traceable author statement//0001934 // positive regulation of protein phosphorylation // not recorded//0006911 // phagocytosis, engulfment //
1417365_a	0.002506	8.39	1.67	NM_001161790//NM_0011	<i>Mefv</i>	Mediterranean fever	0002376 // immune system process // inferred from electronic annotation//0006954 // inflammatory response // not recorded//0032691 // negative regulation of interleukin-1 beta
1419536_a	0.005899	8.37	1.25	NM_001081249//NM_0011	<i>Vcan</i>	versican	0001649 // osteoblast differentiation // not recorded//0001657 // ureteric bud development // inferred from expression pattern//0007155 // cell adhesion // inferred from electronic
1417836_a	0.005623	8.33	1.52	NM_011347	<i>Slp1</i>	selectin, platelet	0002587 // positive regulation of leukocyte migration // inferred from genetic interaction//0002587 // positive regulation of leukocyte migration // inferred from mutant phenotype//0002691
1418145_a	0.002598	8.33	1.44	NM_009627	<i>Adm</i>	adrenomedullin	0001570 // vasculogenesis // not recorded//0001666 // response to hypoxia // inferred from electronic annotation//0001843 // neural tube closure // inferred from mutant
1417932_a	0.009317	8.21	1.50	NM_010807	<i>Marcks1</i>	MARCKS-like 1	0008284 // positive regulation of cell proliferation // inferred from direct assay
1416652_a	0.001748	8.17	2.28	NM_001291892//NM_0012	<i>Gp49a//Lilrb4</i>	glycoprotein 49 A//leukocyte immunoglobulin-like receptor, subfamily B,	0002376 // immune system process // inferred from electronic annotation
1416683_a	0.004921	8.15	2.23	NM_009763//NM_0065037	<i>Bst1</i>	bone marrow stromal cell antigen 1	0008152 // metabolic process // inferred from electronic annotation
1416778_a	0.006743	8.10	2.09	NM_009912	<i>Ccr1</i>	chemokine (C-C motif) receptor 1	0006816 // calcium ion transport // not recorded//0006874 // cellular calcium ion homeostasis // not recorded//0006887 // exocytosis // not recorded//0006935 // chemotaxis // inferred
1426678_a	0.001662	8.06	-1.03	NM_008871	<i>Serpin1e</i>	serine (or cysteine) peptidase inhibitor, clade E, member 1	0001300 // chronological cell aging // inferred from electronic annotation//0001525 // angiogenesis // inferred from electronic annotation//0008585 // female gonad development // not
1416804_a	0.004366	8.05	2.08	NM_008039	<i>Fpr2</i>	formyl peptide receptor 2	0006935 // chemotaxis // inferred from electronic annotation//0007165 // signal transduction // inferred from electronic annotation//0007186 // G-protein coupled receptor signaling
1416005_a	0.004021	7.93	9.82	NM_001113387//NM_0212	<i>My1l</i>	myosin, light polypeptide 1	0006936 // muscle contraction // not recorded//0006048 // cardiac muscle contraction // not recorded
1416366_a	0.001178	7.91	3.00	NM_001145164//NM_0115	<i>Tgtp1//Tgtp2</i>	T cell specific GTPase 1//T cell specific GTPase 2	0006184 // GTP catabolic process // inferred from direct assay//0006955 // immune response // non-traceable author statement//0008152 // metabolic process // inferred from electronic
1416021_a	0.001377	7.91	8.61	NM_011414	<i>Sipi</i>	secretory leukocyte peptidase inhibitor	0006508 // proteolysis // inferred from electronic annotation//0010466 // negative regulation of peptidase activity // inferred from electronic annotation//0010951 // negative regulation of
1417963_a	0.000539	7.84	1.49	NM_009899//NM_0065009	<i>Cka1//Cka2</i>	chloride channel calcium activated 1//chloride channel calcium activated 2	0006821 // chloride transport // inferred from direct assay//1902476 // chloride transmembrane transport // inferred from direct assay//0006821 // chloride transport // not
1416055_a	0.001702	7.81	6.98	NM_133743	<i>Lypd3</i>	Ly6/Plaur domain containing 3	0006928 // cellular component movement // not recorded//0007160 // cell-matrix adhesion // not recorded
1415970_a	0.001705	7.77	13.06	NM_212487//NM_0065211	<i>Krt78</i>	keratin 78	
1415764_a	0.003691	7.70	25.98	NM_001033621//NM_0065	<i>Myot</i>	myotilin	0006184 // GTP catabolic process // inferred from electronic annotation//0008544 // epidermis development // traceable author statement//0018149 // peptide cross-linking // not
1415998_a	0.004776	7.66	10.14	NM_005974//NM_0064991	<i>Tgrip3</i>	transglutininase 3, E polypeptide	0000060 // protein import into nucleus, translocation // not recorded//0001022 // negative regulation of transcription from RNA polymerase II promoter // inferred from direct
1417122_a	0.000377	7.54	1.82	NM_001278601//NM_0136	<i>Tnfr</i>	tumor necrosis factor	0007738 // DNA catabolic process, exonucleolytic // inferred from direct assay//0006259 // DNA metabolic process // inferred from direct assay//0006281 // DNA repair // inferred from
1418907_a	0.005290	7.51	1.32	NM_001012236//NM_0116	<i>Atrip//Trex1</i>	ATR interacting protein//three prime repair exonuclease 1	0006915 // apoptotic process // inferred from electronic annotation//0013333 // negative regulation of protein complex assembly // not recorded//0035456 // response to interferon-beta //
1426787_a	0.003735	7.45	-1.03	NM_001033771//NM_0012	<i>Xaf1</i>	XIAP associated factor 1	0006508 // proteolysis // not recorded//0006508 // proteolysis // inferred from reviewed computational analysis//0006915 // apoptotic process // inferred from electronic
1417225_a	0.006637	7.41	1.76	NM_007609//NM_0065098	<i>Casp4</i>	caspase 4, apoptosis-related cysteine peptidase	0001892 // embryonic/placenta development // inferred from mutant phenotype//0006955 // immune response // inferred from electronic annotation//0008284 // positive regulation of cell
1417317_a	0.006068	7.40	1.70	NM_009969//NM_0065321	<i>Csf2</i>	colony stimulating factor 2 (granulocyte-macrophage)	0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 // regulation of transcription, DNA-templated // inferred from electronic annotation//0030154 //
1416877_a	0.009978	7.39	2.01	NM_028967//NM_0065318	<i>Batf2</i>	basic leucine zipper transcription factor, ATF-like 2	0006810 // transport // inferred from electronic annotation//0006811 // ion transport // inferred from electronic annotation//0006826 // iron ion transport // inferred from direct
1419026_a	0.000135	7.36	1.31	NM_001135151//NM_0011	<i>Sk39a14</i>	solute carrier family 39 (zinc transporter), member 14	0001782 // B cell homeostasis // inferred from mutant phenotype//0002376 // immune system process // inferred from electronic annotation//0019221 // cytokine-mediated signaling
1417852_a	0.000214	7.36	1.52	NM_011087//NM_011088//	<i>Pira1//Pira11//Pira2//Pira5</i>	paired-Ig-like receptor A1//paired-Ig-like receptor A11//paired-Ig-like	0006508 // proteolysis // inferred from direct assay//0006508 // proteolysis // not recorded//0042742 // defense response to bacterium // inferred from genetic interaction
1418200_a	0.002476	7.26	1.43	NM_127845	<i>Adams4</i>	a disintegrin-like and metallopeptidase (reprolysin type) with	0002430 // complement receptor mediated signaling pathway // not recorded//0002462 // tolerance induction to nonself antigen // not recorded//0006935 // chemotaxis // inferred from
1416189_a	0.007928	7.24	4.11	NM_009779	<i>C3ar1</i>	complement component 3a receptor 1	0007186 // G-protein coupled receptor signaling pathway // inferred from electronic annotation
1417303_a	0.002495	7.24	1.72	NM_001081746//NM_0336	<i>Cpsrs//Gm15433//Gm2666//</i>	component of Sp100-rs//predicted pseudogene 15433	

Table S7

Gene ID	p (Corr)	FC-RSV 1 d	FC-RSV 5 d	RefSeq Transcript ID	Gene Symbol	Gene Title	Gene Ontology Biological Process
1429354_a	0.00036	7.19	-1.37	NM_011227	<i>Rob20</i>	RAB20, member RAS oncogene family	0006184 // GTP catabolic process // inferred from electronic annotation // 0006810 // transport // inferred from electronic annotation // 0007165 // signal transduction // inferred from
1423727_a	0.00243	7.11	1.06	NM_030601//XM_0065023	<i>Cla201//Ccla1</i>	chloride channel calcium activated 2 //chloride channel calcium activated 1	0006821 // chloride transport // not recorded // 00043276 // anoikis // inferred from direct assay // 0007192 // extrinsic apoptotic signaling pathway in absence of ligand // inferred from
1416981_a	0.008822	6.98	1.89	NM_012060//XM_0065010	<i>Gbp2</i>	guanylate binding protein 2	0006184 // GTP catabolic process // inferred from sequence or structural similarity // 00035458 // cellular response to interferon-beta // inferred from direct assay // 00042832 // defense
1416469_a	0.001775	6.91	2.60	NM_001169153//NM_1456	<i>Cd300f</i>	CD300 antigen like family member F	0002376 // immune system process // inferred from electronic annotation // 00030316 // osteoclast differentiation // inferred from direct assay
1417068_a	0.001136	6.88	1.83	NM_001045481//NM_0083	<i>Gm16340//lfi203//LOC10086</i>	predicted gene 16340//interferon activated gene 203//floculation	0030308 // negative regulation of cell growth // inferred from mutant phenotype // 00035458 // cellular response to interferon-beta // inferred from direct assay // 00040008 // regulation of
1450481_a	0.002008	6.87	-1.24	NM_020551//XR_381188	<i>Cmpk2</i>	cytidine monophosphate (UMP-CMP) kinase 2, mitochondrial	0006165 // nucleoside diphosphate phosphorylation // not recorded // 0006221 // pyrimidine nucleotide biosynthetic process // inferred from electronic annotation // 0006227 // dUDP
1453640_a	0.008091	6.86	-1.93	NM_001101605//NM_0011	<i>Gm14466</i>	predicted gene 14466	0009615 // response to virus // inferred from electronic annotation // 00050688 // regulation of defense response to virus // inferred from electronic annotation // 00071357 // cellular response
1451975_a	0.000324	6.86	12.93	NM_013456	<i>Actn3</i>	actinin alpha 3	0006936 // muscle contraction // inferred from direct assay
1417287_a	0.001373	6.85	1.74	NM_001161701//NM_0136	<i>Tap1</i>	transporter 1, ATP-binding cassette, sub-family B (MDR/TAP)	0002237 // positive regulation of T cell mediated cytotoxicity // — // 0002376 // immune system process // inferred from electronic annotation // 0006300 // ATP catabolic process // not
1417780_a	0.007952	6.81	1.54	NM_030218//XM_0065143	<i>Misp</i>	mitotic spindle positioning	0007049 // cell cycle // inferred from electronic annotation // 0007061 // mitotic nuclear division // inferred from electronic annotation // 00051301 // cell division // inferred from electronic
1416099_a	0.001720	6.79	5.40	NM_001174170//NM_0111	<i>Serpinh2</i>	serine (or cysteine) peptidase inhibitor, clade B, member 2	0010466 // negative regulation of peptidase activity // inferred from electronic annotation // 00010951 // negative regulation of endopeptidase activity // not recorded // 00030162 // regulation
1423868_a	0.001723	6.77	1.06	NM_010220	<i>Fkbp5</i>	FK506 binding protein	0000413 // protein peptidyl-prolyl isomerization // not recorded // 0006457 // protein folding // inferred from electronic annotation // 00018208 // peptidyl-proline modification // not
1428240_a	0.003555	6.75	-1.34	NM_017466//NM_0065121	<i>Ccr2</i>	chemokine (C-C motif) receptor-like 2	0006935 // chemotaxis // inferred from electronic annotation // 0006954 // inflammatory response // inferred from direct assay // 0007165 // signal transduction // inferred from electronic
1434888_a	0.001060	6.70	-1.13	NM_019963//XM_0065134	<i>Stat2</i>	signal transducer and activator of transcription 2	0006351 // transcription, DNA-templated // inferred from electronic annotation // 0006355 // regulation of transcription, DNA-templated // inferred from electronic annotation // 0007165 //
1416038_a	0.004687	6.62	7.81	NM_033175//XM_0065023	<i>Lce3c</i>	late cornified envelope 3C	0008544 // epidermis development // inferred from electronic annotation
1416055_a	0.001702	6.59	7.25	NM_009264	<i>Spr1a</i>	small proline-rich protein 1A	0018149 // peptide cross-linking // not recorded // 00030216 // keratinocyte differentiation // not recorded // 00031424 // keratinization // inferred from electronic annotation
1424560_a	0.000747	6.58	1.03	NM_001113527//NM_0012	<i>Isg20</i>	interferon-stimulated protein	0000738 // DNA catabolic process, exonucleolytic // not recorded // 0002376 // immune system process // inferred from electronic annotation // 0006364 // rRNA processing // inferred from
1422953_a	0.001733	6.57	1.10	NM_023141	<i>Tor3a</i>	tor1in family 3, member A	0006200 // ATP catabolic process // not recorded // 00051085 // chaperone mediated protein folding requiring cofactor // inferred from electronic annotation
1437517_x	0.000020	6.54	-1.54	NM_009253//XM_0065156	<i>Serpina3m</i>	serine (or cysteine) peptidase inhibitor, clade A, member 3M	0010466 // negative regulation of peptidase activity // inferred from electronic annotation // 00010951 // negative regulation of endopeptidase activity // not recorded // 00030162 // regulation
1416762_a	0.008200	6.53	2.09	NM_009396//XM_0065157	<i>Tnfrsf2</i>	tumor necrosis factor, alpha-induced protein 2 //NM muscululus 7 days	0001525 // angiogenesis // inferred from electronic annotation // 0006687 // exocytosis // inferred from electronic annotation // 0007275 // multicellular organismal development // inferred
1415802_a	0.006743	6.53	21.33	NM_009405//XM_0065085	<i>Tnni2</i>	troponin I, skeletal, fast 2	0003009 // skeletal muscle contraction // not recorded // 0006937 // regulation of muscle contraction // not recorded // 00045893 // positive regulation of transcription, DNA-templated //
1417247_a	0.009197	6.52	1.75	NM_011905//XM_0065014	<i>Tir2</i>	tol-like receptor 2	0001666 // response to hypoxia // inferred from electronic annotation // 0001774 // microglial cell activation // not recorded // 0002224 // toll-like receptor signaling pathway // not
1451653_a	0.000876	6.51	-1.28	NM_001033196//NM_0012	<i>Znfx1</i>	zinc finger, NFκ1-type containing 1	0006355 // regulation of transcription, DNA-templated // inferred from electronic annotation
1417290_a	0.000634	6.48	1.74	NM_001242368//NM_0079	<i>F10</i>	coagulation factor X	0006508 // proteolysis // not recorded // 0007596 // blood coagulation // not recorded // 0007599 // hemostasis // inferred from electronic annotation // 00051897 // positive regulation of
1427008_a	0.002896	6.43	-1.04	NM_008207//XM_0065237	<i>H2-T24</i>	histocompatibility 2, T region locus 24	0001916 // positive regulation of T cell mediated cytotoxicity // inferred from electronic annotation // 0002474 // antigen processing and presentation of peptide antigen via MHC class I // not
1419057_a	0.001218	6.42	1.31	NM_023386//XM_0065224	<i>Rtp4</i>	mitotic spindle positioning	0001580 // detection of chemical stimulus involved in sensory perception of bitter taste // not recorded // 0006612 // protein targeting to membrane // not recorded
1415892_a	0.003886	6.39	16.61	NM_029667	<i>Lce1i</i>	late cornified envelope 1i	0008544 // epidermis development // inferred from electronic annotation
1416032_a	0.000795	6.38	8.15	NM_148941	<i>Elovl4</i>	elongation of very long chain fatty acids (FEN1/Elo2, SUR4/Elo3, yeast)-like	0006629 // lipid metabolic process // inferred from electronic annotation // 0006631 // fatty acid metabolic process // inferred from electronic annotation // 0006633 // fatty acid biosynthetic
1417460_a	0.000290	6.36	1.63	NM_001081746//NM_0336	<i>Cpsrs//Gm2666//Gm7609//</i>	component of Sp100-rs//predicted gene 2666//predicted pseudogene	0007186 // G-protein coupled receptor signaling pathway // inferred from electronic annotation
1416109_a	0.007186	6.30	5.30	NM_001163525//NM_0011	<i>S100a14</i>	S100 calcium binding protein A14	0006915 // apoptotic process // inferred from electronic annotation // 00032496 // response to lipopolysaccharide // inferred from electronic annotation // 00034142 // toll-like receptor 4
1416498_a	0.000689	6.27	2.53	NM_001161714//NM_0011	<i>Tgm1</i>	transglutaminase 1, K polypeptide	0009887 // organ morphogenesis // inferred from mutant phenotype // 00018149 // peptide cross-linking // inferred from electronic annotation // 00019538 // protein metabolic process //
1428804_a	0.000767	6.26	-1.36	NM_001166402//NM_0093	<i>Tnfrsf3</i>	tumor necrosis factor, alpha-induced protein 3	0001922 // B-1 B cell homeostasis // inferred from mutant phenotype // 0002237 // response to molecule of bacterial origin // inferred from direct assay // 0002237 // response to molecule of
1420672_a	0.000361	6.24	1.19	NM_001199733//NM_0078	<i>Daxx</i>	Fas death domain-associated protein	0000281 // mitotic cytokinesis // inferred from mutant phenotype // 0006334 // nucleosome assembly // not recorded // 0006338 // chromatin remodeling // not recorded // 0006351 //
1415922_x	0.001128	6.22	16.08	NM_010889//XM_0064977	<i>Neblin</i>	nebulin	0003832 // regulation of actin filament length // traceable author statement // 00045214 // sarcomere organization // traceable author statement
1418551_a	0.009516	6.22	1.37	NM_001281830//NM_0298	<i>Ifi272a</i>	interferon, alpha-inducible protein 27 like 2A	0007568 // aging // inferred from direct assay // 00009615 // response to virus // inferred from direct assay
1419004_x	0.001650	6.18	1.31	NM_019777//XM_0065297	<i>ikbke</i>	inhibitor of kappaB kinase epsilon	0006468 // protein phosphorylation // not recorded // 0006974 // cellular response to DNA damage stimulus // inferred from electronic annotation // 0007252 // I-kappaB phosphorylation //
1417402_a	0.002410	6.16	1.65	NM_001033130//XM_0065	<i>D13Ert608e//LOC10263150</i>	DNA segment, Chr 13, ERATO D01 68, expressed//uncharacterized	0001782 // B cell homeostasis // inferred from mutant phenotype // 0002376 // immune system process // inferred from electronic annotation // 00019221 // cytokine-mediated signaling
1427102_a	0.002157	6.14	-1.02	NM_001166672//NM_0012	<i>Gm10693//Gm14548//leukocyte</i>	predicted pseudogene 10693//predicted gene 14548//leukocyte	0009002 // cell morphogenesis // inferred from electronic annotation // 0002376 // immune system process // inferred from electronic annotation // 0006955 // immune response // inferred
1416885_a	0.001588	6.14	1.99	NM_010734	<i>Lst1</i>	leukocyte specific transcript 1	0005975 // carbohydrate metabolic process // inferred from electronic annotation // 0006006 // glucose metabolic process // inferred from electronic annotation // 0006086 // acetyl-CoA
1416727_a	0.006916	6.04	2.13	NM_013743	<i>Pdk4</i>	pyruvate dehydrogenase kinase, isoenzyme 4	
1422013_a	0.002096	6.03	1.13	NM_022430	<i>Ms40a8</i>	membrane-spanning 4-domains, subfamily A, member 8A	
1427705_a	0.005908	6.01	-1.06	NM_011783	<i>Agp2</i>	anterior gradient 2	
1418620_a	0.002945	6.01	1.36	NM_009841	<i>Cd14</i>	CD14 antigen	
1416007_a	0.000369	5.98	8.79	NM_019645//XM_0065292	<i>Pkp1</i>	plakophilin 1	
1416185_a	0.004999	5.97	4.21	NM_001083904//NM_0010	<i>Fetub</i>	fetuin beta	
1418570_a	0.000216	5.91	1.37	NM_011408	<i>Sfn2</i>	schlafen 2	
1420642_a	0.000764	5.90	1.19	NM_001039530//XM_0065	<i>Parp14</i>	poly (ADP-ribose) polymerase family, member 14	
1417606_a	0.002013	5.89	1.59	NM_010045	<i>Ackr1</i>	atypical chemokine receptor 1 (Duffy blood group)	
1418171_a	0.002352	5.87	1.43	NM_001163540//NM_0011	<i>Parp10//Plec</i>	poly (ADP-ribose) polymerase family, member 10//plectin	
1417355_a	0.002253	5.85	1.67	NM_008690//XM_0065237	<i>Nfkbie</i>	nuclear factor of kappa light polypeptide gene enhancer in B cells inhibitor, epsilon	
1417130_x	0.001697	5.84	1.81	NM_001271676//NM_0012	<i>Ifi47</i>	interferon gamma inducible protein 47	
1417573_a	0.005771	5.81	1.60	NM_001077508//NM_0010	<i>Tnfrsf9</i>	tumor necrosis factor receptor superfamily, member 9	
1416648_a	0.001651	5.78	2.30	NM_009917	<i>Ccr5</i>	chemokine (C-C motif) receptor 5	
1416056_a	0.001105	5.76	6.75	NM_001164210//NM_0012	<i>Spfssb</i>	serine palmitoyltransferase, small subunit B	
1416050_a	0.000623	5.76	7.69	NM_019450	<i>Il1f6</i>	interleukin 1 family, member 6	
1419879_x	0.000058	5.72	1.23	NM_010751//XM_0065056	<i>Mxd1</i>	MAX dimerization protein 1	
1418103_a	0.005613	5.65	1.44	NM_030253//XM_0065227	<i>Parp9</i>	poly (ADP-ribose) polymerase family, member 9	
1420798_x	0.000789	5.59	1.19	NM_001040005//XM_0065	<i>Rnf213</i>	ring finger protein 213	
1419186_a	0.001616	5.59	1.29	NM_033075	<i>D17H6556E-5</i>	DNA segment, Chr 17, human D6556 5	
1424528_a	0.008771	5.51	1.03	NM_021407//XM_0065247	<i>Trem3</i>	triggering receptor expressed on myeloid cells 3	
1415776_a	0.003143	5.47	24.68	NM_001163664//NM_0011	<i>Tnni3</i>	troponin T3, skeletal, fast	
1416453_x	0.009491	5.44	2.80	NM_009463	<i>Ucp1</i>	uncoupling protein 1 (mitochondrial, proton carrier)	
1427906_a	0.003119	5.42	-1.06	NM_008329//XM_0064966	<i>Ifi204//lfi205//Mnda//Mnd</i>	interferon activated gene 204//interferon activated gene 205//myeloid	
1416055_a	0.001702	5.40	7.12	NM_027416	<i>Calm3</i>	calmodulin-like 3	
1418762_a	0.001800	5.40	1.34	NM_011530//XM_0065239	<i>Tap2</i>	transporter 2, ATP-binding cassette, sub-family B (MDR/TAP)	
1419846_a	0.004221	5.39	1.23	NM_001177627//NM_1726	<i>Slc20a6</i>	solute carrier family 2 (facilitated glucose transporter), member 6	
1418854_a	0.000334	5.39	1.33	NM_011338	<i>Ccl9</i>	chemokine (C-C motif) ligand 9	
1417685_a	0.001170	5.39	1.57	NM_001081746//NM_0336	<i>Cpsrs//Gm2666//Gm7609//</i>	component of Sp100-rs//predicted gene 2666//predicted pseudogene	
1415996_a	0.001042	5.37	10.31	NM_007710	<i>Ckm</i>	creatine kinase, muscle	
1416058_a	0.005494	5.36	6.69	NM_009659	<i>Alox12b</i>	arachidonate 12-lipoxygenase, 12R type	
1422821_x	0.004550	5.36	1.10	NM_001005846//NM_0266	<i>Mcoln2</i>	microclpin 2	
1448752_a	0.000826	5.34	-1.19	NM_001159301//NM_0107	<i>Lgal9</i>	lectin, galactose binding, soluble 9	
1448303_a	0.000877	5.30	-1.17	NM_001267707//NM_1308	<i>Slc10a5</i>	solute carrier organic anion transporter family, member 1a5	
1416035_a	0.003669	5.30	7.82	NM_001083903//NM_1722	<i>Sbn</i>	suprabasin	
1418571_a	0.001299	5.29	1.37	NM_205820//XM_0065280	<i>THY13</i>	thiol-like receptor 13	
1422637_a	0.006320	5.28	1.11	NM_001082963//NM_0084	<i>Itpom</i>	integrin alpha M	
1417131_a	0.007001	5.22	1.81	NM_010724//XM_0065365	<i>Pim3</i>	protein kinase (prosome, macropain) subunit, beta type B (large	
1416904_a	0.000657	5.22	1.96	NM_001281854//NM_0120	<i>Aoxh</i>	acyloxyacyl hydrolase	
1417611_a	0.002896	5.22	1.59	NM_001163621//NM_0280	<i>Apol6</i>	apolipoprotein L 6	
1418186_a	0.004065	5.20	1.43	NM_007707//XM_0065321	<i>Socs3</i>	suppressor of cytokine signaling 3	
1416016_a	0.002884	5.17	8.69	NM_175249	<i>Pspal1</i>	prospalin-like 1	
1416668_a	0.004585	5.15	2.27	NM_001134393//NM_0311	<i>Apobec1</i>	apolipoprotein B mRNA editing enzyme, catalytic polypeptide 1	
1418831_a	0.000532	5.15	1.33	NM_008987	<i>Ptx3</i>	pentraxin related gene	
1423903_a	0.006099	5.14	1.06	NM_009994//XM_0065235	<i>Cyp11b1</i>	cytochrome P450, family 1, subfamily B, polypeptide 1	
1416088_a	0.006113	5.13	5.61	NM_025501	<i>Lce3b</i>	late cornified envelope 3B	
1418109_a	0.001772	5.11	1.44	NM_008289	<i>Hsd11b2</i>	hydroxysteroid 11-beta dehydrogenase 2	
1417145_a	0.005761	5.10	1.80	NM_001205313//NM_0012	<i>Stat1</i>	signal transducer and activator of transcription 1	
1417872_a	0.000087	5.10	1.51	NM_001159401//NM_0011	<i>Upp1</i>	uridine phosphorylase 1	

Table S7

Gene ID	p (Corr)	FC-RSV 1 d	FC-RSV 5 d	RefSeq Transcript ID	Gene Symbol	Gene Title	Gene Ontology Biological Process
1419553_a	0.009682	5.07	1.25	NM_001163470//NM_1722	<i>Traf1d</i>	TRAF type zinc finger domain containing 1	0034097 // response to cytokine // inferred from electronic annotation//0045824 // negative regulation of innate immune response // inferred from mutant phenotype
1417943_a	0.000277	5.06	1.50	NM_145373//X/M_0065327	<i>Sectm1a</i>	secreted and transmembrane 1A	0007165 // signal transduction // not recorded//0043123 // positive regulation of l-kappa kinase/NF-kappaB signaling // not recorded
1416486_a	0.004120	5.06	2.54	NM_175132//X/M_0065194	<i>Synpo2l</i>	synaptopodin 2-like	
1422771_a	0.002764	5.05	1.10	NM_008102	<i>Gch1</i>	GTP cyclohydrolase 1	0006184 // GTP catabolic process // not recorded//0006461 // protein complex assembly // not recorded//0006729 // tetrahydrobiopterin biosynthetic process // inferred by
1422912_a	0.003321	5.05	1.10	NM_0252651//NM_0077	<i>Csf3r</i>	colony stimulating factor 3 receptor (granulocyte)	0007155 // cell adhesion // inferred from electronic annotation//0019221 // cytokine-mediated signaling pathway // inferred from electronic annotation//0030593 // neutrophil chemotaxis
1434867_a	0.008946	4.99	-1.47	NM_001172472//NM_0011	<i>Sphk1</i>	sphingosine kinase 1	0001568 // blood vessel development // inferred from genetic interaction//0001934 // positive regulation of protein phosphorylation // not recorded//0001956 // positive regulation of
1416137_a	0.000449	4.93	4.82	NM_008125	<i>Gjb2</i>	gap junction protein, beta 2	0007154 // cell communication // inferred from electronic annotation//0007267 // cell-cell signaling // inferred from direct assay//0007605 // sensory perception of sound // inferred from
1426364_a	0.001914	4.92	-1.02	NM_001164477//NM_0278	<i>Ifih1</i>	interferon induced with helicase C domain 1	0002376 // immune system process // inferred from electronic annotation//0008152 // metabolic process // inferred from electronic annotation//0009615 // response to virus // inferred
1416102_a	0.007853	4.92	5.39	NM_009265	<i>Spr11b</i>	small proline-rich protein 11b	0008360 // regulation of cell shape // traceable author statement//0018149 // peptide cross-linking // inferred from electronic annotation//0031424 // keratinization // inferred from
1419282_a	0.000869	4.89	1.28	NM_007494//NR_002687	<i>Assl1//Gm5424</i>	argininosuccinate synthetase 1//argininosuccinate synthase pseudogene	0000050 // urea cycle // not recorded//000053 // argininosuccinate metabolic process // not recorded//0000536 // arginine biosynthetic process // not recorded//0008652 // cellular
1422480_a	0.004498	4.88	1.12	NM_021406//X/M_0065247	<i>Trem1</i>	triggering receptor expressed on myeloid cells 1	0002374 // cytokine secretion involved in immune response // inferred from genetic interaction//0016477 // cell migration // inferred from genetic interaction//0030593 // neutrophil
1418115_s	0.000164	4.87	1.44	NM_153159	<i>Zc3h12a</i>	zinc finger CCH type containing 12A	0001525 // angiogenesis // inferred from electronic annotation//0006915 // apoptotic process // inferred from electronic annotation//0007275 // multicellular organismal development //
1422636_a	0.006113	4.86	1.11	NM_030691//X/M_0065083	<i>Igfb6</i>	immunoglobulin superfamily, member 6	
1418510_s	0.009083	4.86	1.38	NM_007825//X/M_0065353	<i>Cyp7b1</i>	cytochrome P450, family 7, subfamily b, polypeptide 1	0006629 // lipid metabolic process // inferred from electronic annotation//0000699 // bile acid biosynthetic process // inferred from direct assay//0007586 // digestion // traceable author
1416812_a	0.008410	4.84	2.07	NM_011355//X/M_0064990	<i>Spl1</i>	spleen focus forming virus (SFFV) proviral integration oncogene	0001122 // negative regulation of transcription from RNA polymerase II promoter // inferred from direct assay//0001944 // vasculature development // inferred from mutant
1416855_a	0.002830	4.83	2.03	NM_019440	<i>Irgm2</i>	immunity-related GTPase family M member 2	0006184 // GTP catabolic process // inferred from sequence or structural similarity//0008152 // metabolic process // inferred from electronic annotation//0043431 // response to interferon-
1438480_a	0.004940	4.83	-1.16	NM_001168333//NM_0234	<i>Tinag1l</i>	tubulointerstitial nephritis antigen-like 1	0006508 // proteolysis // inferred from electronic annotation//0006898 // receptor-mediated endocytosis // inferred from electronic annotation//0006955 // immune response // inferred
1420847_a	0.002311	4.81	1.18	NM_010404//NM_177981	<i>Hap1</i>	huntingtin-associated protein 1	0008104 // protein localization // not recorded//0010976 // positive regulation of neuron projection development // not recorded//0047496 // vesicle transport along microtubule // inferred
1416799_a	0.006102	4.81	2.08	NM_008657//X/M_0065133	<i>Myf6</i>	myogenic factor 6	0001756 // somitogenesis // inferred from mutant phenotype//0006355 // regulation of transcription, DNA-templated // inferred from electronic annotation//0006357 // regulation of
1418072_a	0.001274	4.78	1.46	NM_145133//X/M_0065012	<i>Tifa</i>	TRAF-interacting protein with forkhead-associated domain	0007249 // l-kappaB kinase/NF-kappaB signaling // inferred from direct assay
1416669_s	0.001211	4.75	2.27	NM_001033207//X/M_0065	<i>Nlr5</i>	NLR family, CARD domain containing 5	0002376 // immune system process // inferred from electronic annotation//0006952 // defense response // inferred from electronic annotation//0032088 // negative regulation of NF-
1424010_a	0.000960	4.75	1.05	NM_197944	<i>Hsh2d</i>	hematopoietic SH2 domain containing	0002903 // negative regulation of B cell apoptotic process // inferred from direct assay//0009967 // positive regulation of signal transduction // inferred from direct assay//0042110 // T cell
1420825_s	0.003374	4.74	1.19	NM_001172205//NM_0011	<i>Arid5a</i>	AT rich interactive domain 5A (MRF1-like)	0002062 // chondrocyte differentiation // inferred from direct assay//0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 // regulation of transcription,
1419310_s	0.006635	4.74	1.28	NM_023738	<i>Uba7</i>	ubiquitin-like modifier activating enzyme 7	0006464 // cellular protein modification process // not recorded//0016567 // protein ubiquitination // --//0019941 // modification-dependent protein catabolic process // inferred from
1418357_a	0.006985	4.71	1.40	NM_013463	<i>Gla</i>	galactosidase, alpha	0005975 // carbohydrate metabolic process // inferred from electronic annotation//0008152 // metabolic process // inferred from electronic annotation//0009311 // oligosaccharide
1440254_a	0.004671	4.66	-1.21	NM_172612	<i>Rnd1</i>	Rho family GTPase 1	0001184 // GTP catabolic process // inferred from electronic annotation//0007015 // actin filament organization // not recorded//0007162 // negative regulation of cell adhesion // not
1417317_s	0.006068	4.63	1.70	NM_008677//X/M_0065205	<i>Ncf4</i>	neutrophil cytosolic factor 4	0007154 // cell communication // inferred from electronic annotation//0043085 // positive regulation of catalytic activity // not recorded
1416457_a	0.001276	4.63	2.65	NM_001005423//X/M_0064	<i>Mreg</i>	melanoregulin	0003018 // melanocyte differentiation // inferred from mutant phenotype//0032402 // melanosome transport // inferred from direct assay//0042640 // anagen // inferred from mutant
1419469_a	0.008819	4.61	1.26	NM_007494//NR_002687	<i>Assl1//Gm5424</i>	argininosuccinate synthetase 1//argininosuccinate synthase pseudogene	0000050 // urea cycle // not recorded//000053 // argininosuccinate metabolic process // not recorded//0000526 // arginine biosynthetic process // not recorded//0008652 // cellular
1420401_a	0.007896	4.61	1.21	NM_029796	<i>Lrg1</i>	leucine-rich alpha-2-glycoprotein 1	0001938 // positive regulation of endothelial cell proliferation // inferred from mutant phenotype//0030511 // positive regulation of transforming growth factor beta receptor signaling
1418454_a	0.000440	4.61	1.39	NM_007769//X/M_0065072	<i>Dmb1</i>	deleted in malignant brain tumors 1	0001824 // blastocyst development // inferred from mutant phenotype//0001833 // inner cell mass cell proliferation // inferred from direct assay//0006810 // transport // inferred from
1416233_a	0.004999	4.56	3.76	NM_007697//X/M_0065054	<i>Ch1</i>	cell adhesion molecule with homology to L1CAM	0001764 // neuron migration // inferred from mutant phenotype//0007155 // cell adhesion // inferred from electronic annotation//0007156 // homophilic cell adhesion // inferred from
1419192_a	0.000833	4.53	1.29	NM_016748//X/M_0065032	<i>Ctps</i>	cytidine 5'-triphosphate synthase	0006221 // pyrimidine nucleotide biosynthetic process // inferred from electronic annotation//0006241 // CTP biosynthetic process // not recorded//0006541 // glutamine metabolic process
1448377_a	0.000118	4.51	-1.18	NM_019949	<i>Ube2l6</i>	ubiquitin-conjugating enzyme E2L 6	0016567 // protein ubiquitination // inferred from electronic annotation//0019941 // modification-dependent protein catabolic process // inferred from direct assay//0032020 // ISG15-
1417063_a	0.002359	4.51	1.83	NM_028808	<i>P2ry13</i>	purinergic receptor P2Y, G-protein coupled 13	0007165 // signal transduction // inferred from electronic annotation//0007186 // G-protein coupled receptor signaling pathway // inferred from electronic annotation//0007194 // negative
1420023_a	0.001105	4.48	1.22	NM_001113529//NM_0011	<i>Cs1</i>	colony stimulating factor 1 (macrophage)	0001503 // ossification // not recorded//0001954 // positive regulation of cell-matrix adhesion // inferred from genetic interaction//0002158 // osteoclast proliferation // inferred from direct
1417662_a	0.001297	4.47	1.58	NM_001168615//NM_1459	<i>Tfab</i>	TRAF-interacting protein with forkhead-associated domain, family member	
1417273_a	0.004493	4.44	1.75	NM_138684	<i>Wfdc12</i>	WAP four-disulfide core domain 12	0010466 // negative regulation of peptidase activity // inferred from electronic annotation//0010951 // negative regulation of endopeptidase activity // inferred from electronic
1417703_a	0.004570	4.40	1.56	NM_033601//X/M_0065394	<i>Bcl3</i>	B cell leukemia lymphoma 3	0000060 // protein import into nucleus, translocation // not recorded//0002268 // follicular dendritic cell differentiation // inferred from mutant phenotype//0002315 // marginal zone B cell
1415940_a	0.002478	4.40	1.77	NM_007504//X/M_0065072	<i>Atp2a1</i>	ATPase, Ca++ transporting, cardiac muscle, fast twitch 1	0006200 // ATP catabolic process // not recorded//0006810 // transport // inferred from electronic annotation//0006811 // ion transport // inferred from electronic annotation//0006812 //
1417791_a	0.004793	4.39	1.54	NM_013611//X/M_0064957	<i>Slc11a1</i>	solute carrier family 11 (proton-coupled divalent metal ion transporters),	0000060 // protein import into nucleus, translocation // inferred from mutant phenotype//0000165 // MAPK cascade // not recorded//0001818 // negative regulation of cytokine production
1420559_a	0.000635	4.36	1.20	NM_013671	<i>Sod2</i>	superoxide dismutase 2, mitochondrial	0003022 // response to reactive oxygen species // inferred from mutant phenotype//0000303 // response to superoxide // inferred from mutant phenotype//0000303 // response to
1423864_a	0.007469	4.36	1.39	NM_139198	<i>Plac8</i>	placenta-specific 8	0008284 // positive regulation of cell proliferation // inferred from direct assay//0009409 // response to cold // inferred from mutant phenotype//0040015 // negative regulation of
1417422_a	0.000827	4.35	1.65	NM_010185//X/M_0064966	<i>Fcer1g</i>	Fc receptor, IgE, high affinity I, gamma polypeptide	0001798 // positive regulation of type II hypersensitivity // inferred from mutant phenotype//0001805 // positive regulation of type III hypersensitivity // inferred from mutant
1416949_s	0.002860	4.35	1.91	NM_183249	<i>Wfdc12</i>	WAP four-disulfide core domain 21	0010466 // negative regulation of peptidase activity // inferred from electronic annotation//0032496 // response to lipopolysaccharide // inferred from direct assay//0034612 // response to
1419410_a	0.001114	4.33	1.27	NM_001083925//NR_00350	<i>Oas1b</i>	2'-5' oligoadenylate synthetase 1B	0002376 // immune system process // inferred from electronic annotation//0006955 // immune response // inferred from electronic annotation//0008152 // metabolic process // inferred
1418715_s	0.000564	4.33	1.35	NM_011990//X/M_0065007	<i>Slc7a11</i>	solute carrier family 7 (cationic amino acid transporter, y+ system), member	0003333 // amino acid transmembrane transport // inferred from electronic annotation//0006810 // transport // inferred from electronic annotation//0006865 // amino acid transport //
1432143_a	0.009810	4.32	-1.10	NM_001033122//X/M_0065	<i>Cd69</i>	CD69 antigen	0035690 // cellular response to drug // inferred from expression pattern
1421282_a	0.002495	4.30	1.16	NM_020581	<i>Angptl4</i>	angiopoietin-like 4	0001525 // angiogenesis // inferred from electronic annotation//0001666 // response to hypoxia // inferred from electronic annotation//0009267 // cellular response to starvation // non-
1438003_a	0.000374	4.29	-1.54	NM_001033632	<i>Ifitm6</i>	interferon induced transmembrane protein 6	0009607 // response to biotic stimulus // inferred from electronic annotation
1416960_a	0.008302	4.27	1.90	NM_053108//X/M_0065174	<i>Glxr</i>	glutaredoxin	0006810 // transport // inferred from electronic annotation//0045454 // cell redox homeostasis // inferred from electronic annotation//0055114 // oxidation-reduction process // traceable
1417406_a	0.009702	4.26	1.65	NM_008638//X/M_0065056	<i>Mthfd2</i>	methylentetrahydrofolate dehydrogenase (NAD+ dependent),	0006730 // one-carbon metabolic process // not recorded//0008152 // metabolic process // inferred from electronic annotation//0009396 // folic acid-containing compound biosynthetic
1417432_a	0.001094	4.25	1.64	NM_145827//X/M_0065328	<i>Nlrp3</i>	NLR family, pyrin domain containing 3	0002674 // negative regulation of acute inflammatory response // not recorded//0006915 // apoptotic process // inferred from electronic annotation//0006919 // activation of cysteine-type
1416148_a	0.007843	4.24	4.73	NM_027011	<i>Krt5</i>	keratin 5	
1434620_s	0.000587	4.22	-1.13	NM_007746//X/M_0065259	<i>Map3k8</i>	mitogen-activated protein kinase kinase kinase 8	0000165 // MAPK cascade // not recorded//0000186 // activation of MAPKK activity // not recorded//0002376 // immune system process // inferred from electronic annotation//0006468 //
1417523_a	0.000216	4.19	1.62	NM_001033308	<i>Themis2</i>	thymocyte selection associated family member 2	0002376 // immune system process // inferred from electronic annotation//0006954 // inflammatory response // inferred from electronic annotation//0005082 // cell receptor signaling
1423596_a	0.003880	4.17	1.07	NM_199223//X/M_0064995	<i>Rtn4r2</i>	reticulon 4 receptor-like 2	0031103 // axon regeneration // traceable author statement
1421040_a	0.003805	4.17	1.17	NM_001290457//NM_0090	<i>Relb</i>	avian reticuloendotheliosis viral (v-rel) oncogene related B	0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 // regulation of transcription, DNA-templated // inferred from electronic annotation//0010628 //
1419145_a	0.003103	4.16	1.30	NM_133888	<i>Spmpd3b</i>	sphingomyelin phosphodiesterase, acid-like 3B	0006685 // sphingomyelin catabolic process // inferred from electronic annotation//0008152 // metabolic process // inferred from electronic annotation
1427346_a	0.002360	4.14	-1.05	NM_172689	<i>Ddc58</i>	DEAD (Asp-Glu-Ala-Asp) box polypeptide 58	0002230 // positive regulation of defense response to virus by host // not recorded//0002376 // immune system process // inferred from electronic annotation//0008152 // metabolic
1416944_a	0.000341	4.14	1.91	NM_145158//X/M_0065242	<i>Emilin2</i>	elastin microfibril interfacer 2	0007155 // cell adhesion // inferred from electronic annotation
1416010_a	0.000297	4.13	8.77	NM_001081664	<i>4833423E24Rik</i>	RIKEN cDNA 4833423E24 gene	0006629 // lipid metabolic process // inferred from electronic annotation//0006631 // fatty acid metabolic process // inferred from electronic annotation//0006633 // fatty acid biosynthetic
1418072_a	0.002174	4.12	1.46	NM_020268	<i>Klk1b27</i>	kallikrein 1-related peptidase b27	0006508 // proteolysis // inferred from direct assay
1416119_a	0.001119	4.11	5.12	NM_001166173//NM_0011	<i>Dmkn</i>	dermokine	0030154 // cell differentiation // inferred from electronic annotation
1416083_a	0.001733	4.10	5.64	NM_026415	<i>Cysrt1</i>	cysteine rich tail 1	
1417876_a	0.000637	4.09	1.51	NM_023143//NM_0011133	<i>C1ra//C1rb</i>	complement component 1, r subcomponent A//complement component	0002376 // immune system process // inferred from electronic annotation//0006508 // proteolysis // not recorded//0006956 // complement activation // inferred from electronic
1416073_a	0.000388	4.08	6.28	NM_009257//X/M_0065292	<i>Serpinb5</i>	serine (or cysteine) peptidase inhibitor, clade B, member 5	0002009 // morphogenesis of an epithelium // inferred from mutant phenotype//0010951 // negative regulation of endopeptidase activity // not recorded//0030162 // regulation of
1418018_a	0.007228	4.07	1.47	NM_026438	<i>Ppa1</i>	pyrophosphatase (inorganic)	0006796 // phosphate-containing compound metabolic process // inferred by curator
1429239_a	0.004982	4.05	-1.09	NM_001042725//NM_0075	<i>Calcr</i>	calcitonin receptor	0007165 // signal transduction // inferred from electronic annotation//0007166 // cell surface receptor signaling pathway // inferred from electronic annotation//0007186 // G-protein
1417614_a	0.006230	4.05	1.59	NM_008152	<i>Gpr65</i>	G-protein coupled receptor 65	0006915 // apoptotic process // traceable author statement//0007165 // signal transduction // inferred from electronic annotation//0007186 // G-protein coupled receptor signaling pathway
1427484_a	0.001284	4.05	-1.06	NM_001033450//NM_0011	<i>Ifi202//Ifi205//Mndu//Mnd</i>	interferon activated gene 204//Interferon activated gene 205//myeloid	0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 // regulation of transcription, DNA-templated // inferred from electronic annotation//0006357 //
1416059_s	0.000488	4.03	6.64	NM_001164201//X/M_0065	<i>Cers3</i>	ceramide synthase 3	0006355 // regulation of transcription, DNA-templated // inferred from electronic annotation//0006629 // lipid metabolic process // inferred from electronic annotation//0030148 //
1417369_a	0.001862	4.02	1.67	NM_013484//X/M_0065235	<i>C2</i>	complement component 2 (within H-2S)	0002376 // immune system process // inferred from electronic annotation//0006508 // proteolysis // inferred from electronic annotation//0006956 // complement activation // inferred from
1417701_a	0.001099	4.01	1.56	NM_144830//X/M_0065330	<i>Tmem106a</i>	transmembrane protein 106A	
1416048_a	0.007423	3.96	7.69	NM_008496//X/M_0065395	<i>Lgals7</i>	lectin, galactose binding, soluble 7	0006915 // apoptotic process // inferred from electronic annotation
1418674_a	0.000031	3.95	1.35	NM_013644//X/M_0065307	<i>Psm110</i>	proteasome (prosome, macropain) subunit, beta type 10	0000902 // cell morphogenesis // inferred from mutant phenotype//0006508 // proteolysis // inferred from electronic annotation//0042098 // T cell proliferation // inferred from mutant
1426582_a	0.005933	3.94	-1.03	NM_172893	<i>Porp12</i>	poly (ADP-ribose) polymerase family, member 12	0008152 // metabolic process // inferred from electronic annotation
1418330_a	0.002792	3.93	1.40	NM_026929	<i>Chac1</i>	ChAc, cation transport regulator 1	0006915 // apoptotic process // inferred from electronic annotation//0006986 // response to unfolded protein // inferred from electronic annotation//0007219 // Notch signaling pathway //
1434016_a	0.008726	3.91	-1.12	NM_0012171497//NM_0012	<i>Il15ra</i>	interleukin 15 receptor, alpha chain	0007259 // JAK-STAT cascade // not recorded//0010977 // negative regulation of neuron projection development // not recorded//0031667 // response to nutrient levels // inferred from
1418616_a	0.000826	3.91	1.36	NM_145391//X/M_0065058	<i>Tapbp1</i>	TAP binding protein-like	0019885 // antigen processing and presentation of endogenous peptide antigen via MHC class I // inferred from electronic annotation
1417392_a	0.000500	3.91	1.66	NM_021272	<i>Fabp7</i>	fatty acid binding protein 7, brain	0001964 // startle response // inferred from mutant phenotype//0006810 // transport // inferred from electronic annotation//0021846 // cell proliferation in forebrain // inferred from
1421392_a	0.000408	3.89	1.16	NM_010442	<i>Hmxo1</i>	heme oxygenase (decycling) 1	0001525 // angiogenesis // not recorded//0010666 // response to hypoxia // inferred from electronic annotation//0002246 // wound healing involved in inflammatory response // not
1418806_a	0.002828	3.85	1.34	NM_010510	<i>Ifih1</i>	interferon beta 1, fibroblast	0002250 // adaptive immune response // inferred from direct assay//0002286 // T cell activation involved in immune response // not recorded//0002312 // B cell activation involved in
1417895_a	0.002906	3.85	1.51	NM_001276445//NM_0306	<i>Tlr1</i>	tol-like receptor 1	0001774 // microglial cell activation // not recorded//0002224 // toll-like receptor signaling pathway // not recorded//0002376 // immune system process // inferred from electronic
1418002_a	0.001591	3.84	1.48	NM_001013371	<i>Dtx3l</i>	deltex 3-like (Drosophila)	0006281 // DNA repair // inferred from electronic annotation//0006302 // double-strand break repair // not recorded//0006974 // cellular response to DNA damage stimulus // not
1422679_s	0.009323	3.83	1.11	NM_011352//X			

Table S7

Gene ID	p (Corr)	FC-RSV 1 d	FC-RSV 5 d	RefSeq Transcript ID	Gene Symbol	Gene Title	Gene Ontology Biological Process
1417568_a	0.004611	3.78	1.61	NM_011610	<i>Tnfrsf1b</i>	tumor necrosis factor receptor superfamily, member 1b	0006954 // inflammatory response // inferred from mutant phenotype // 0006955 // immune response // not recorded // 0007166 // cell surface receptor signaling pathway // inferred from
1448239_a	0.003041	3.77	-1.17	NM_011163 // XM_0065238	<i>El2ak2</i>	eukaryotic translation initiation factor 2-alpha kinase 2	0001186 // activation of MAPKK activity // not recorded // 0001819 // positive regulation of cytokine production // inferred from mutant phenotype // 0002376 // immune system process //
1418659_a	0.008379	3.76	1.35	NM_001271005 // NM_0103	<i>C92002504Rik // H2-</i>	RIKEN cDNA C92002504Rik // histocompatibility 2, T region locus 23 // H2-	0001916 // positive regulation of T cell mediated cytotoxicity // inferred from direct assay // 0002376 // immune system process // inferred from electronic annotation // 0002474 // antigen
1428164_a	0.003248	3.76	-1.07	NM_001141948 // NM_0011	<i>Nmi</i>	N-myc (and STAT1) interactor	
1427332_a	0.001996	3.76	-1.05	NM_001252374 // NM_0260	<i>Nt5c3</i>	5'-nucleotidase, cytosolic III	0008152 // metabolic process // inferred from electronic annotation // 0009117 // nucleotide metabolic process // inferred from electronic annotation // 0016311 // dephosphorylation // not
1417698_a	0.003702	3.76	1.56	NM_008489	<i>Lbp</i>	lipopolysaccharide binding protein	0002232 // leukocyte chemotaxis involved in inflammatory response // inferred from mutant phenotype // 0002281 // macrophage activation involved in immune response // inferred from
1419455_a	0.003655	3.75	1.26	NM_016971 // XM_0065192	<i>Sk7a8</i>	solute carrier family 7 (cationic amino acid transporter, y+ system), member	0003333 // amino acid transmembrane transport // not recorded // 0006810 // transport // inferred from electronic annotation // 0006865 // amino acid transport // not recorded // 00015695
1428707_a	0.001668	3.75	-1.07	NM_001217476 // NM_0012	<i>Pglyn2</i>	peptidoglycan recognition protein 2	0002221 // pattern recognition receptor signaling pathway // not recorded // 0002376 // immune system process // inferred from electronic annotation // 0005253 // peptidoglycan catabolic
1422759_a	0.001747	3.72	1.10	NM_001104529 // NM_0012	<i>Gpr35</i>	G protein-coupled receptor 35	0001165 // signal transduction // inferred from electronic annotation // 0007186 // G-protein coupled receptor signaling pathway // not recorded
1419426_a	0.002505	3.71	1.26	NM_011888 // XM_0041721	<i>Ct159</i>	chemokine (C-C motif) ligand 19 // predicted gene 12407 // predicted gene	0001768 // establishment of T cell polarity // not recorded // 0001771 // immunological synapse formation // inferred from direct assay // 0002407 // dendritic cell chemotaxis // not
1416564_a	0.003525	3.71	2.44	NM_001291058 // NM_0098	<i>Cd68</i>	CD68 antigen	0071310 // cellular response to organic substance // inferred from direct assay
1418004_a	0.000067	3.70	1.48	NM_001271603 // NM_0098	<i>Socs1</i>	suppressor of cytokine signaling 1	001932 // regulation of protein phosphorylation // inferred from direct assay // 0007259 // JAK-STAT cascade // inferred from direct assay // 0009958 // negative regulation of signal
1419509_a	0.007649	3.69	1.26	NM_0013173 // XM_0065007	<i>Ogfr</i>	opiod growth factor receptor	0040008 // regulation of growth // inferred from electronic annotation
1427768_a	0.001119	3.68	-1.06	NM_022415 // XM_0064982	<i>Ptges</i>	prostaglandin H synthase	001516 // prostaglandin biosynthetic process // not recorded // 0002526 // acute inflammatory response // inferred from electronic annotation // 0002544 // chronic inflammatory response
1418190_a	0.003436	3.66	1.43	NM_001204241 // NM_1531	<i>Clec4a3</i>	C-type lectin domain family 4, member a3	0006508 // proteolysis // inferred from electronic annotation
1416203_a	0.005803	3.66	4.04	NM_027112	<i>Cops2</i>	calpain, small subunit 2	0006508 // proteolysis // not recorded
1428075_a	0.005983	3.66	-1.07	NM_026913	<i>Mtld1</i>	MIT, microtubule interacting and transport, domain containing 1	0002281 // mitotic cytokinesis // not recorded // 0000920 // cytokinetic cell separation // not recorded // 0006810 // transport // inferred from electronic annotation // 0007049 // cell cycle //
1417009_a	0.000347	3.66	1.88	NM_001113474 // NM_1786	<i>Lair1</i>	leukocyte-associated Ig-like receptor 1	
1418392_a	0.002015	3.65	1.39	NM_001038604 // NM_0213	<i>Clec5a</i>	C-type lectin domain family 5, member a	0002076 // osteoblast development // inferred from direct assay // 0002376 // immune system process // inferred from electronic annotation // 0009615 // response to virus // inferred from
1418943_a	0.000614	3.65	1.32	NM_023155 // XM_0065339	<i>Cxcl16</i>	chemokine (C-X-C motif) ligand 16	0006898 // receptor-mediated endocytosis // inferred from direct assay // 0006935 // chemotaxis // inferred from electronic annotation // 0003307 // positive regulation of cell growth // not
1420464_a	0.000469	3.64	1.20	NM_001045481 // NM_0083	<i>Gm16340 // Ifi203 // LOC10086</i>	predicted gene 16340 // interferon activated gene 203 // flocculation	0030308 // negative regulation of cell growth // inferred from mutant phenotype // 0035458 // cellular response to interferon-beta // inferred from direct assay // 0040008 // cell regulation of
1417795_a	0.001453	3.64	1.54	NM_001286037 // NM_0108	<i>Ncf1</i>	neutrophil cytosolic factor 1	001878 // response to yeast // inferred from mutant phenotype // 0001909 // leukocyte mediated cytotoxicity // inferred from mutant phenotype // 0002679 // respiratory burst involved in
1436032_a	0.000942	3.64	-1.14	NM_001217105 // NM_0088	<i>Paf</i>	placental growth factor	0001525 // angiogenesis // inferred from electronic annotation // 0001658 // branching involved in uterine bud morphogenesis // inferred from direct assay // 0001666 // response to hypoxia
1416325_a	0.000053	3.62	3.19	NM_008290 // XM_0065307	<i>Hsd17b2</i>	hydroxysteroid (17-beta) dehydrogenase 2	0001701 // in utero embryonic development // inferred from mutant phenotype // 0001890 // placenta development // inferred from mutant phenotype // 0006629 // lipid metabolic process
1422889_a	0.006838	3.61	1.10	NM_008884 // NM_178087	<i>Pmi</i>	promyelocytic leukemia	0001666 // response to hypoxia // inferred from mutant phenotype // 0001666 // not recorded // 0001932 // regulation of protein phosphorylation // inferred from
1418038_a	0.000703	3.59	1.47	NM_001033435 // NM_0012	<i>Mlr1</i>	mast cell immunoglobulin like receptor 1	0033094 // negative regulation of mast cell activation // inferred from mutant phenotype // 0004303 // mast cell degranulation // inferred from mutant phenotype
1419164_a	0.002051	3.59	1.30	NM_029219 // XM_0065034	<i>Rnf19b</i>	ring finger protein 19b	0002376 // immune system process // inferred from electronic annotation // 0016567 // protein ubiquitination // inferred from electronic annotation // 0042267 // natural killer cell mediated
1417999_a	0.009795	3.59	1.48	NM_009778	<i>C3</i>	complement component 3	0001798 // positive regulation of type Ila hypersensitivity // inferred from mutant phenotype // 0001934 // positive regulation of protein phosphorylation // not recorded // 0001970 // positive
1416835_a	0.001176	3.56	2.05	NM_007534 // NM_007536	<i>Bcl2a1a // Bcl2a1b // Bcl2a1d</i>	B cell lymphoma (phymoma 2) related protein A1a // B cell	0001782 // B cell homeostasis // inferred from direct assay // 0002903 // negative regulation of B cell apoptotic process // inferred from direct assay // 0006915 // apoptotic process // inferred
1418492_a	0.003890	3.54	1.38	NM_013521	<i>Fpr1</i>	formyl peptide receptor 1	0006935 // chemotaxis // traceable author statement // 0007165 // signal transduction // inferred from electronic annotation // 0007186 // G-protein coupled receptor signaling pathway //
1423564_a	0.005252	3.54	1.07	NM_001111099 // NM_0076	<i>Cdkn1a</i>	cyclin-dependent kinase inhibitor 1A (P21)	0000079 // regulation of cyclin-dependent protein serine/threonine kinase activity // inferred from mutant phenotype // 0000082 // G1/S transition of mitotic cell cycle // not
1427964_a	0.004902	3.53	-1.06	NM_001112715 // NM_0268	<i>Ifitm1</i>	interferon induced transmembrane protein 1	0001503 // ossification // inferred from electronic annotation // 0001756 // somitogenesis // inferred from mutant phenotype // 0002376 // immune system process // inferred from electronic
1430447_a	0.002476	3.53	-1.09	NM_028679 // XM_0065142	<i>Irk3</i>	interleukin-1 receptor-associated kinase 3	0001960 // negative regulation of cytokine-mediated signaling pathway // inferred by curator // 0006468 // protein phosphorylation // inferred from direct assay // 0006468 // protein
1419932_a	0.006861	3.53	1.23	NM_133203 // XM_0065056	<i>Klra17</i>	killer cell lectin-like receptor, subfamily A, member 17	
1420465_a	0.007846	3.52	1.20	NM_001045481 // NM_0083	<i>Gm16340 // Ifi203 // LOC10086</i>	predicted gene 16340 // interferon activated gene 203 // flocculation	0030308 // negative regulation of cell growth // inferred from mutant phenotype // 0035458 // cellular response to interferon-beta // inferred from direct assay // 0040008 // regulation of
1417134_a	0.008827	3.50	1.80	NM_009660 // XM_0065320	<i>Alox15</i>	arachidonate 15-lipoxygenase	0001503 // ossification // inferred from mutant phenotype // 0002820 // negative regulation of adaptive immune response // inferred from mutant phenotype // 0006629 // lipid metabolic
1416176_a	0.002070	3.48	4.39	NM_021347 // XM_0065338	<i>Gsdma</i>	gasdermin A	0006915 // apoptotic process // not recorded
1417166_a	0.003541	3.47	1.78	NM_001289591 // NM_0012	<i>Tmem173</i>	transmembrane protein 173	0002218 // activation of innate immune response // inferred from mutant phenotype // 0002218 // activation of innate immune response // not recorded // 0002230 // positive regulation of
1417277_a	0.003665	3.47	1.74	NM_007962 // XM_0065099	<i>Mpz12</i>	myelin protein zero-like 2	0007155 // cell adhesion // inferred from electronic annotation // 0001637 // single organismal cell-cell adhesion // inferred from direct assay // 0033077 // T cell differentiation in thymus //
1418081_a	0.007255	3.46	1.45	NM_172393 // XM_0065124	<i>Aim1</i>	absent in melanoma 1	
1418532_a	0.003043	3.45	1.38	NM_00117085 // NM_0084	<i>Klra2</i>	killer cell lectin-like receptor, subfamily A, member 2	0007155 // cell adhesion // inferred from electronic annotation
1416074_a	0.006823	3.44	6.11	NM_025569 // XM_0065095	<i>Aob5</i>	ankyrin repeat and SOCS box-containing 5	0015567 // protein ubiquitination // inferred from electronic annotation // 0035556 // intracellular signal transduction // inferred from electronic annotation
1417777_a	0.000570	3.44	1.55	NM_007523 // XM_0065125	<i>Bcl2</i>	BCL2-antagonist/killer 1	0001776 // leukocyte homeostasis // inferred from genetic interaction // 0001782 // B cell homeostasis // inferred from genetic interaction // 0001782 // B cell homeostasis // inferred from
1416248_a	0.000021	3.43	3.51	NM_001146087 // NM_0011	<i>Il15f</i>	interleukin-1 family, member 5 (delta)	0001960 // negative regulation of cytokine-mediated signaling pathway // inferred from electronic annotation // 0032715 // negative regulation of interleukin-6 production // inferred from
1416121_a	0.000047	3.43	5.09	NM_007759	<i>Crabp2</i>	cellular retinoic acid binding protein II	0006810 // transport // inferred from electronic annotation // 0035115 // embryonic forelimb morphogenesis // inferred from mutant phenotype // 0004273 // retinoic acid metabolic process
1417721_a	0.008086	3.42	1.55	NM_010639	<i>Klk1</i>	kallikrein 1	0006508 // proteolysis // inferred from electronic annotation
1417806_a	0.009105	3.42	1.53	NM_183426 // XM_0065134	<i>Sbno2</i>	strawberry notch homolog 2 (Drosophila)	0002281 // macrophage activation involved in immune response // inferred from mutant phenotype // 0002281 // macrophage activation involved in immune response // not
1416253_a	0.002143	3.41	3.44	NM_001286552 // NM_0087	<i>Nrap</i>	nebulin-related anchoring protein	0030036 // actin cytoskeleton organization // traceable author statement
1428025_a	0.002987	3.41	-1.07	NM_011723 // XR_385314	<i>Xdh</i>	xanthine dehydrogenase	0001933 // negative regulation of protein phosphorylation // not recorded // 0001937 // negative regulation of endothelial cell proliferation // not recorded // 0006919 // activation of cysteine-
1425450_a	0.000355	3.41	1.00	NM_175307	<i>Fam46b</i>	family with sequence similarity 46, member 8	
1419202_a	0.009957	3.39	1.29	NM_001098799 // XM_0064	<i>Tox2</i>	TOX high mobility group box family member 2	0008585 // female gonad development // inferred from electronic annotation // 0034698 // response to gonadotropin // inferred from electronic annotation // 0045944 // positive regulation of
1423070_a	0.000755	3.39	1.09	NM_00109921 // NM_0012	<i>Ly6c1 // Ly6c2</i>	lymphocyte antigen 6 complex, locus C1 // lymphocyte antigen 6 complex,	
1417969_a	0.003887	3.37	1.49	NM_010395 // NM_010396	<i>H2-T10 // H2-T22 // H2-T9</i>	histocompatibility 2, T region locus 10 // histocompatibility 2, T region locus	0001916 // positive regulation of T cell mediated cytotoxicity // inferred from electronic annotation // 0002474 // antigen processing and presentation of peptide antigen via MHC class I // not
1417966_a	0.006562	3.36	1.49	NM_009807	<i>Casp1</i>	caspase 1	0001666 // response to hypoxia // inferred from mutant phenotype // 0001666 // response to hypoxia // not recorded // 0001774 // microglial cell activation // not recorded // 0006508 //
1421170_a	0.001996	3.34	1.17	NM_009369	<i>Tgfb1</i>	transforming growth factor, beta induced	0001525 // angiogenesis // inferred from electronic annotation // 0002062 // chondrocyte differentiation // inferred from electronic annotation // 0007155 // cell adhesion // inferred from
1424160_a	0.005557	3.33	1.05	NM_030563 // XM_0065315	<i>N4bp1</i>	NEDD4 binding protein 1	0013397 // negative regulation of protein ubiquitination // inferred from direct assay // 0032435 // negative regulation of proteasomal ubiquitin-dependent protein catabolic process // inferred
1417763_a	0.008872	3.33	1.55	NM_008842	<i>Pim1</i>	proliferation induction site 1	0006468 // protein phosphorylation // not recorded // 0008283 // cell proliferation // not recorded // 0009103 // lipopolysaccharide biosynthetic process // inferred from electronic
1417874_a	0.004410	3.29	1.51	NM_001139520 // NM_0188	<i>Sarmh3</i>	SAM domain and HD domain, 1	0002376 // immune system process // inferred from electronic annotation // 0006203 // dGTP catabolic process // not recorded // 0008152 // metabolic process // inferred from electronic
1421955_a	0.002843	3.29	1.14	NM_026960 // XM_0065213	<i>Gsdmd</i>	gasdermin D	0001666 // cellular response to extracellular stimulus // inferred from direct assay
1419122_a	0.002283	3.29	1.30	NM_001199275 // NM_0011	<i>Trmp1</i>	TRPAIP3 interacting protein 1	0002755 // MyD88-dependent toll-like receptor signaling pathway // inferred from direct assay // 0006954 // inflammatory response // inferred from electronic annotation // 0007159 //
1431659_a	0.004415	3.29	-1.42	NM_001085518 // NM_1729	<i>Gm14085 // Slic2a2</i>	predicted gene 14085 // solute carrier family 28 (sodium-coupled	0001895 // retina homeostasis // not recorded // 0006810 // transport // inferred from electronic annotation // 0015860 // purine nucleoside transmembrane transport // inferred from direct
1419686_a	0.000666	3.29	1.24	NM_009747 // XM_0065154	<i>Bdrb2</i>	bradykinin receptor, beta 2	0002438 // acute inflammatory response to antigenic stimulus // not recorded // 0006939 // smooth muscle contraction // inferred from electronic annotation // 0006950 // response to stress
1420665_a	0.004590	3.28	1.19	NM_011189	<i>Psmc1</i>	proteasome (prosome, macropain) activator subunit 1 (PA28 alpha)	0010950 // positive regulation of endopeptidase activity // inferred from physical interaction // 0019884 // antigen processing and presentation of exogenous antigen // inferred from mutant
1418538_a	0.001363	3.28	1.37	NM_010696	<i>Lcp2</i>	lymphocyte cytosolic protein 2	0045576 // mast cell activation // inferred from mutant phenotype // 0005063 // cytokine secretion // inferred from mutant phenotype
1416175_a	0.009402	3.28	4.52	NM_010079 // XM_0065255	<i>Dsg1a</i>	desmoglein 1 alpha	0007155 // cell adhesion // inferred from electronic annotation // 0007156 // homophilic cell adhesion // inferred from electronic annotation
1422128_a	0.000021	3.28	1.13	NM_146064 // XM_0065208	<i>Soot2</i>	sterol O-acetyltransferase 2	0006629 // lipid metabolic process // inferred from electronic annotation // 0008202 // steroid metabolic process // inferred from electronic annotation // 0008203 // cholesterol metabolic
1451335_a	0.000099	3.28	-1.27	NM_001042611 // NM_0012	<i>Cp</i>	ceruloplasmin	0006810 // transport // inferred from electronic annotation // 0006811 // ion transport // inferred from electronic annotation // 0006825 // copper ion transport // inferred from electronic
1429134_a	0.003290	3.27	-1.36	NM_023380	<i>Samsn1</i>	SAM domain, SH3 domain and nuclear localization signals, 1	0002820 // negative regulation of adaptive immune response // inferred from mutant phenotype // 00050732 // negative regulation of peptide-tyrosine phosphorylation // inferred from mutant
1419371_a	0.002794	3.26	1.27	NM_026907 // XM_0065338	<i>Sectm1b</i>	secreted and transmembrane 1B	
1418608_a	0.003334	3.26	1.36	NM_013807	<i>Plk3</i>	polo-like kinase 3	0000075 // cell cycle checkpoint // inferred from mutant phenotype // 0000082 // G1/S transition of mitotic cell cycle // not recorded // 0000084 // mitotic S phase // not recorded // 0000122
1421720_a	0.005121	3.26	1.14	NM_001038587 // NM_0011	<i>Adar</i>	adenosine deaminase, RNA-specific	0001701 // in utero embryonic development // inferred from mutant phenotype // 0002376 // immune system process // inferred from electronic annotation // 0006351 // transcription, DNA-
1416156_a	0.001009	3.26	4.69	NM_013505 // XM_0065255	<i>Dsc2</i>	desmocollin 2	0007155 // cell adhesion // inferred from electronic annotation // 0007156 // homophilic cell adhesion // inferred from electronic annotation // 0009267 // cellular response to starvation //
1450778_a	0.004653	3.25	-1.25	NM_021524	<i>Nampt</i>	nicotinamide phosphoribosyltransferase	0007565 // female pregnancy // inferred from electronic annotation // 0009435 // NAD biosynthetic process // inferred from direct assay // 0010470 // response to organic cyclic compound //
1429776_a	0.006010	3.25	-1.09	NM_001123371 // NM_0136	<i>Pnp1 // Pnp2</i>	purine-nucleoside phosphorylase // purine-nucleoside phosphorylase 2	0001916 // positive regulation of T cell mediated cytotoxicity // inferred from mutant phenotype // 0006139 // nucleobase-containing compound metabolic process // inferred from electronic
1418718_a	0.000931	3.25	1.35	NM_172796 // XM_0065332	<i>Sfpb</i>	schlafen 9	0006810 // transport // inferred from electronic annotation // 0007264 // small GTPase mediated signal transduction // inferred from electronic annotation // 0015031 // protein transport //
1429568_a	0.000767	3.25	-1.09	XR_105187 // XR_404705	<i>E230013L22Rik</i>	RIKEN cDNA E230013L22Rik	0007155 // cell adhesion // inferred from electronic annotation // 0007155 // cell adhesion // -- // 0007157 // heterophilic cell-cell adhesion // inferred from sequence or structural
1421026_a	0.008055	3.24	1.17	NM_177910 // XM_0065117	<i>Gmpmb</i>	GDP-mannose pyrophosphorylase B	0006790 // sulfur compound metabolic process // inferred from direct assay // 0008152 // metabolic process // not recorded
1418509_a	0.000837	3.23	1.38	NM_018751	<i>Slt1c1</i>	sulfotransferase family, cytosolic, 1C, member 1	0007073 // telomere maintenance // inferred from sequence or structural similarity // 0006351 // transcription, DNA-templated // inferred from electronic annotation // 0006355 // regulation
1429459_a	0.002906	3.22	-1.38	NM_013673 // XM_0065292	<i>Sp100</i>	nuclear antigen Sp100	0002238 // response to molecule of fungal origin // inferred from mutant phenotype // 0002376 // immune system process // inferred from electronic annotation // 0002755 // MyD88-
1424193_a	0.001916	3.22	1.05	NM_010851	<i>Myd88</i>	myeloid differentiation primary response gene 88	0007186 // G-protein coupled receptor signaling pathway // inferred from electronic annotation
1417586_a	0.003325	3.21	1.60	NM_001081746 // NM_0336	<i>Csprs // Gm15433 // Gm2666 //</i>	component of Sp100-rs // predicted pseudogene 15433 // predicted gene	0002430 // complement receptor mediated signaling pathway // not recorded // 0006915 // apoptotic process // not recorded // 0006935 // chemotaxis // inferred from electronic
1419321_a	0.005983	3.19	1.28	NM_001173550 // NM_0075	<i>Csar1</i>	complement component 5A receptor 1	0014070 // response to organic cyclic compound // inferred from electronic annotation // 0015909 // long-chain fatty acid transport // inferred from direct assay // 0019195 // lipid storage //
1417189_a	0.001060	3.19	1.77	NM_007408 // XM_0065375	<i>Plin2</i>	perilipin 2	0001811 // negative regulation of type I hypersensitivity // inferred from mutant phenotype // 0002638 // negative regulation of immunoglobulin production // inferred from mutant
1417793_a	0.005635	3.19	1.54	NM_001077189 // NM_0101	<i>Fcgr2b</i>	Fc receptor, IgG, low affinity IIB	0007275 // multicellular organismal development // inferred from electronic annotation // 0010499 // proteasomal ubiquitin-independent protein catabolic process // not recorded // 0010976
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Table S7

Gene ID	p (Corr)	FC-RSV 1 d	FC-RSV 5 d	RefSeq Transcript ID	Gene Symbol	Gene Title	Gene Ontology Biological Process
1420639_a	0.004662	3.17	1.19	NM_010371//XM_0065185	Gzmc	granzyme C	0006508 // proteolysis // not recorded//0008626 // granzyme-mediated apoptotic signaling pathway // not recorded//0019835 // cytotoxicity // inferred from electronic annotation
1417490_a	0.003199	3.16	1.63	NM_007832	Dck	deoxycytidine kinase	0006139 // nucleobase-containing compound metabolic process // inferred from electronic annotation//0006220 // pyrimidine nucleotide metabolic process // not recorded//0009157 //
1423668_a	0.002070	3.15	1.07	NM_016675//XM_0065284	Cldn2	claudin 2	0016338 // calcium-independent cell-cell adhesion // inferred from direct assay
1423680_a	0.004482	3.15	1.07	NM_001177833//NM_0011	Smax	spermine oxidase	0006598 // polyamine catabolic process // not recorded//0046208 // spermine catabolic process // inferred from direct assay//0046208 // spermine catabolic process // not
1416757_a	0.009783	3.14	2.10	NM_029806//XM_0065404	Lypd5	Ly6/Plaur domain containing 5	0006629 // lipid metabolic process // inferred from electronic annotation//0006810 // transport // inferred from electronic annotation//0006869 // lipid transport // inferred from electronic
1417590_a	0.000595	3.12	1.60	NM_001277944	Apoc2	apolipoprotein C-II	019221 // cytokine-mediated signaling pathway // inferred from electronic annotation
1417544_a	0.005716	3.12	1.61	NM_007780//XM_0065203	Cs2rb2//Cs2rb2	colony stimulating factor 2 receptor, beta, low-affinity (granulocyte-interferon-induced protein 35)	0006200 // ATP catabolic process // inferred from electronic annotation//0007141 // male meiosis I // inferred from mutant phenotype//0007275 // multicellular organismal development //
1426850_a	0.007928	3.12	-1.04	NM_027320	Ifj35	interferon-induced protein 35	0005975 // carbohydrate metabolic process // inferred from electronic annotation//0007155 // cell adhesion // inferred from electronic annotation//0007160 // cell-matrix adhesion // not
1417376_a	0.000666	3.10	1.66	NM_001155885//NM_0100	Ddx4	DEAD (Asp-Glu-Ala-Asp) box polypeptide 4	0000122 // negative regulation of transcription from RNA polymerase II promoter // not recorded//0001570 // vasculogenesis // inferred from mutant phenotype//0001656 // metanephros
1424296_a	0.009077	3.09	1.04	NM_027209	M46a6b	membrane-spanning 4-domains, subfamily A, member 6B	0000122 // negative regulation of transcription from RNA polymerase II promoter // inferred from direct assay//0000122 // negative regulation of transcription from RNA polymerase II
1416942_a	0.001128	3.09	1.91	NM_152803	Hps1	heparanase	0001916 // positive regulation of T cell mediated cytotoxicity // inferred from direct assay//0002376 // immune system process // inferred from electronic annotation//0002474 // antigen
1418213_a	0.002509	3.09	1.42	NM_144783	Wt1	Wilms tumor 1 homolog	0006915 // apoptotic process // inferred from electronic annotation//0007283 // spermatogenesis // inferred from electronic annotation//0008152 // metabolic process // inferred from
1417542_a	0.001215	3.09	1.61	NM_001177352//NM_0011	Myc	mycylomutator oncogene	0006508 // proteolysis // inferred from electronic annotation
1418760_a	0.005352	3.08	1.34	NM_001001892//NM_0103	H2-D1//H2-	histocompatibility 2, D region locus 1//histocompatibility 2, K1, K	0015991 // ATP hydrolysis coupled proton transport // inferred from electronic annotation
1423297_a	0.000755	3.07	1.08	NM_007464//XM_0065098	Birc3	histocompatibility 2, D region locus 1//histocompatibility 2, K1, K	0006508 // proteolysis // not recorded//0010716 // negative regulation of extracellular matrix disassembly // not recorded//0043542 // endothelial cell migration // not recorded
1416512_a	0.001685	3.07	2.47	NM_001177373//NM_0199	Kik11	kalikrein related-peptidase 11	0010466 // negative regulation of peptidase activity // inferred from electronic annotation
1418277_a	0.001702	3.06	1.41	NM_001136091//NM_0011	Tcirg1	T cell, immune regulator 1, ATPase, H+ transporting, lysosomal V0 protein	0055114 // oxidation-reduction process // not recorded
1457203_a	0.001865	3.05	-2.19	NM_001033922//NM_0011	Trem4	triggering receptor expressed on myeloid cells-like 4	001892 // embryonic placenta development // inferred from genetic interaction//0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 // regulation of
1417848_a	0.002108	3.03	1.52	NM_007986//XM_0064987	Fop	fibroblast activation protein	0002376 // immune system process // inferred from electronic annotation//0006508 // proteolysis // not recorded//0010716 // negative regulation of extracellular matrix disassembly // not recorded//0043542 // endothelial cell migration // not recorded
1416332_a	0.008947	3.03	3.09	NM_145369//XR_374434	Wfdc5	WAP four-disulfide core domain 5	0010466 // negative regulation of peptidase activity // inferred from electronic annotation
1416453_a	0.009491	3.03	2.67	NM_023631//XM_0064962	Aox4	aldehyde oxidase 4	0055114 // oxidation-reduction process // not recorded
1423470_a	0.004459	3.02	1.08	NM_001287738//NM_0012	Cebp	CCAAT/enhancer binding protein (C/EBP), beta	001892 // embryonic placenta development // inferred from genetic interaction//0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 // regulation of
1418317_a	0.000540	3.01	1.41	NM_001113356//NM_0231	C1ra//C1rb	complement component 1, r subcomponent A//complement component	0002376 // immune system process // inferred from electronic annotation//0006508 // proteolysis // not recorded//0006956 // complement activation // inferred from electronic
1417500_a	0.000715	3.00	1.62	NM_181407//XM_0065071	Me3	malate synthase 3, NAD(P)+-dependent, mitochondrial	0006990 // pyruvate metabolic process // not recorded//0006108 // malate metabolic process // not recorded//0055114 // oxidation-reduction process // not recorded
1418335_a	0.002565	3.00	1.40	NM_008215	Hos1	hyaluronan synthase 1	0010764 // negative regulation of fibroblast migration // not recorded//0003213 // hyaluronan biosynthetic process // inferred from direct assay//0003213 // hyaluronan biosynthetic process
1423677_a	0.000991	2.99	1.07	NM_001025313//NM_0093	Tapbp	TAP binding protein	0002397 // MHC class I protein complex assembly // inferred from electronic annotation//0002479 // antigen processing and presentation of exogenous peptide antigen via MHC class I, TAP-
1418449_a	0.003455	2.98	1.39	NM_008653//XM_0064988	Mhycp3	myosin binding protein C, cardiac	0002027 // regulation of heart rate // inferred from mutant phenotype//0003007 // heart morphogenesis // inferred from mutant phenotype//0003007 // heart morphogenesis // not
1418465_a	0.007882	2.98	1.38	NM_001025427//NM_0010	Hmgp1-rs1	high mobility group AT-hook 1//high mobility group AT-hook 1, related	0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 // regulation of transcription, DNA-templated // inferred from electronic annotation//0006366 //
1417039_a	0.002084	2.97	1.85	NM_007969	Wfdc18	WAP four-disulfide core domain 18	0010466 // negative regulation of peptidase activity // inferred from electronic annotation
1421491_a	0.001266	2.97	1.15	NM_010908//XM_0065396	Nfkbip	nuclear factor of kappa light polypeptide gene enhancer in B cells inhibitor,	0007165 // signal transduction // not recorded//0007253 // cytoplasmic sequestration of NF-kappaB // not recorded
1438944_a	0.002706	2.97	-1.56	NM_001276301//NM_0096	Ampd3	adenosine monophosphate deaminase 3	0006188 // IMP biosynthetic process // inferred from direct assay//0006188 // IMP biosynthetic process // inferred from mutant phenotype//0009117 // nucleotide metabolic process //
1419426_a	0.002055	2.96	1.26	NM_021788	Sap30	sin3 associated polypeptide	000122 // negative regulation of transcription from RNA polymerase II promoter // inferred from direct assay//0006351 // transcription, DNA-templated // inferred from electronic
1424062_a	0.001424	2.94	1.05	NM_153510	Pilra	paired immunoglobulin-like type 2 receptor alpha	0007165 // signal transduction // not recorded
1422779_a	0.000101	2.94	1.10	NM_001081024	Setd2	SET domain, bifurcated 2	0001947 // heart looping // inferred from sequence or structural similarity//0007049 // cell cycle // inferred from electronic annotation//0007059 // chromosome segregation // not
1419066_a	0.007339	2.94	1.31	NM_001136088//NM_0011	Sh3bp2	SH3-domain binding protein 2	0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 // regulation of transcription, DNA-templated // inferred from electronic annotation//0008152 //
1426678_a	0.001662	2.93	-1.03	NM_183162//NM_0065005	Helz2	helicase with zinc finger 2, transcriptional coactivator	0006953 // acute-phase response // inferred from electronic annotation
1418711_a	0.001179	2.93	1.35	NM_011316	Soa4	serum amyloid A	0007596 // blood coagulation // inferred from electronic annotation//0007599 // hemostasis // inferred from electronic annotation//0008152 // metabolic process // inferred from electronic
1449277_a	0.000545	2.93	-1.21	NM_199016//XM_0065241	Enpp4	ectonucleotide pyrophosphatase/phosphodiesterase 4	0003333 // amino acid transmembrane transport // inferred from electronic annotation//0006810 // transport // inferred from electronic annotation//0006865 // amino acid transport //
1418088_a	0.005861	2.92	1.45	NM_011404	Sk7a5	solute carrier family 7 (cationic amino acid transporter, y+ system), member	0007605 // sensory perception of sound // inferred from mutant phenotype//0003660 // regulation of cell shape // not recorded//0042742 // defense response to bacterium // inferred from
1422938_a	0.002778	2.92	1.10	NM_001198835//NM_0077	Coch	cochleate carrier family C homolog (Limulus polyphemus)	001824 // blastocyst development // inferred from mutant phenotype//0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 // regulation of
1423759_a	0.007668	2.91	1.06	NM_011461	Lod1	Spi-1 transcription factor (Spi-1/PU.1 related)	0002244 // hematopoietic progenitor cell differentiation // inferred from mutant phenotype//0017145 // stem cell division // inferred from mutant phenotype//0034058 // endosomal vesicle
1416644_a	0.000651	2.91	2.30	NM_133664	Sup1	sterile alpha motif domain containing 9-like	0001916 // positive regulation of T cell mediated cytotoxicity // inferred from mutant phenotype//0006139 // nucleobase-containing compound metabolic process // inferred from electronic
1427957_a	0.000094	2.91	-1.06	NM_010156//NM_177590	Somn9l	purine-nucleoside phosphorylase//purine-nucleoside phosphorylase 2	000122 // negative regulation of transcription from RNA polymerase II promoter // inferred from mutant phenotype//0008284 // positive regulation of cell proliferation // inferred from
1428258_a	0.006048	2.91	-1.07	NM_013632//NM_0011223	Pnp2//Pnp2	hematopoietic cell specific Lyn substrate 1	0002376 // immune system process // inferred from electronic annotation//0006468 // protein phosphorylation // inferred from electronic annotation//0007229 // integrin-mediated
1417834_a	0.005333	2.91	1.52	NM_008225	Hcl31	Gardner-Rasheed feline sarcoma viral (Fgr) oncogene homolog	0001501 // skeletal system development // not recorded//0001503 // ossification // not recorded//0001894 // tissue homeostasis // inferred from mutant phenotype//0002062 //
1419377_a	0.009068	2.90	1.27	NM_010208//XM_0065385	Fgr	collagen, type XI, alpha 2	0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 // regulation of transcription, DNA-templated // inferred from electronic annotation//0045351 //
1419482_a	0.001179	2.90	1.26	NM_009926//XM_0065235	Col11a2	interferon regulatory factor 9	0006810 // transport // inferred from electronic annotation//0006886 // intracellular protein transport // not recorded//0007032 // endosome organization // not recorded//0007154 // cell
1425921_a	0.005975	2.90	-1.01	NM_001159417//NM_0011	Irf9	sorting nexin 10	0007010 // cytoskeleton organization // non-traceable author statement
1420444_a	0.001646	2.90	1.21	NM_001127348//NM_0011	Srx10	epithelial stromal interaction 1 (breast)	0001773 // myeloid dendritic cell activation // inferred from direct assay//0045671 // negative regulation of osteoclast differentiation // inferred from mutant phenotype
1451814_a	0.001243	2.89	-1.28	NM_029495//NM_178825	Epst1	proline-serine-threonine phosphatase-interacting protein 2	0001525 // angiogenesis // inferred from electronic annotation//0006915 // apoptotic process // inferred from electronic annotation//0006931 // substrate-dependent cell migration, cell
1419154_a	0.000734	2.88	1.30	NM_013831//NM_177831	Pstpip2	paired immunoglobulin-like type 2 receptor beta 1	0042311 // vasodilation // inferred from electronic annotation
1424746_a	0.000270	2.88	1.03	NM_133209//XM_0065045	Pilrb1	tumor necrosis factor receptor superfamily, member 12a	0002244 // hematopoietic progenitor cell differentiation // inferred from mutant phenotype//0006629 // lipid metabolic process // inferred from electronic annotation//0006665 //
1423646_a	0.006725	2.88	1.07	NM_001161746//NM_0137	Tnfrsf12a	calcitonin-related polypeptide, beta	0003050 // regulation of systemic arterial blood pressure by atrial natriuretic peptide // inferred from mutant phenotype//0006184 // GTP catabolic process // inferred from electronic
1421919_a	0.008672	2.87	1.14	NM_054084//XM_0065072	Colcb	sphingomyelin phosphodiesterase 3, neutral	0001568 // blood vessel development // inferred from mutant phenotype//0009725 // response to hormone // not recorded//0030199 // collagen fibril organization // inferred from mutant
1419647_a	0.001179	2.87	1.24	NM_021491//XM_0065312	Smpd3	RAS-like, family 10, member B	0009913 // epidermal cell differentiation // not recorded//0010466 // negative regulation of peptidase activity // inferred from mutant phenotype//0010951 // negative regulation of
1417967_a	0.009666	2.87	-1.49	NM_001013386//XM_0065	Ras10b	lysyl oxidase	0031146 // SCF-dependent proteasomal ubiquitin-dependent protein catabolic process // not recorded
1460372_a	0.007016	2.86	-1.34	NM_001286181//NM_0012	Lox	serine peptidase inhibitor, Kazal type 5	0009515 // response to virus // not recorded//0010960 // intracellular transport of viral protein in host cell // not recorded//0032091 // negative regulation of protein binding // not
1416182_a	0.007475	2.85	4.31	NM_001081180//XM_0065	Spink5	F-box and WD-40 domain protein 17	0016477 // cell migration // inferred from electronic annotation//0032956 // regulation of actin cytoskeleton organization // inferred from electronic annotation
1423909_a	0.000990	2.85	1.06	NM_175401//XM_0065168	Fbw17	RIKEN cDNA 201002M122ik	0006545 // glycine biosynthetic process // inferred from electronic annotation//0006730 // one-carbon metabolic process // inferred from electronic annotation//0009165 // nucleotide
1428071_a	0.005128	2.84	-1.07	NM_053211	Cdc8b	colony stimulating factor 2 receptor, beta 2, low-affinity (granulocyte-	0006468 // protein phosphorylation // not recorded//0006915 // apoptotic process // inferred from electronic annotation//0009103 // lipopolysaccharide biosynthetic process // inferred
1417190_a	0.000489	2.84	1.77	NM_001287389//NM_0077	Cs2rb2//Cs2rb2	colony stimulating factor 2 receptor, beta 2, low-affinity (granulocyte-	0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 // regulation of transcription, DNA-templated // inferred from electronic annotation//0007283 //
1417867_a	0.009103	2.84	1.51	NM_001081291//NM_1980	Cdc8b	colony stimulating factor 2 receptor, beta 2, low-affinity (granulocyte-	0008152 // metabolic process // inferred from electronic annotation
1418244_a	0.000222	2.84	1.42	NM_010049	Dhfr	colony stimulating factor 2 receptor, beta 2, low-affinity (granulocyte-	0001501 // skeletal system development // inferred from mutant phenotype//0007040 // lysosome organization // inferred from mutant phenotype//0008152 // metabolic process //
1420535_a	0.000610	2.84	1.20	NM_001195025//NM_0287	Nuak2	colony stimulating factor 2 receptor, beta 2, low-affinity (granulocyte-	0000122 // negative regulation of transcription from RNA polymerase II promoter // inferred from direct assay//0001649 // osteoblast differentiation // inferred from mutant
1417640_a	0.005124	2.83	1.58	NM_001029929//XM_0065	Zmynd15	colony stimulating factor 2 receptor, beta 2, low-affinity (granulocyte-	0010634 // positive regulation of epithelial cell migration // not recorded//0010718 // positive regulation of epithelial to mesenchymal transition // not recorded//0070374 // positive
1422508_a	0.007469	2.83	1.12	NM_181402//XM_0065052	Parp11	colony stimulating factor 2 receptor, beta 2, low-affinity (granulocyte-	0002029 // protein polyubiquitination // not recorded//0008152 // metabolic process // inferred from electronic annotation//0016567 // protein ubiquitination // inferred from mutant
1425561_a	0.003826	2.82	-1.00	NM_007387//XM_0064985	Acp2	colony stimulating factor 2 receptor, beta 2, low-affinity (granulocyte-	0007186 // G-protein coupled receptor signaling pathway // traceable author statement//0009968 // negative regulation of signal transduction // inferred from electronic
1417308_a	0.008930	2.81	1.72	NM_013665//XM_0065012	Shox2	colony stimulating factor 2 receptor, beta 2, low-affinity (granulocyte-	0007186 // G-protein coupled receptor signaling pathway // inferred from sequence or structural similarity//0014065 // phosphatidylinositol 3-kinase signaling // inferred from sequence or
1418936_a	0.004762	2.81	1.32	NM_027450	Glipr2	colony stimulating factor 2 receptor, beta 2, low-affinity (granulocyte-	0002376 // immune system process // inferred from electronic annotation//0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 // regulation of
1419762_a	0.001132	2.80	1.23	NM_194346//XM_0065190	Rnf31	colony stimulating factor 2 receptor, beta 2, low-affinity (granulocyte-	0010951 // negative regulation of endopeptidase activity // not recorded//0019833 // cytotoxicity // inferred from direct assay//0003162 // regulation of proteolysis // not recorded
1416269_a	0.008066	2.80	3.41	NM_001159374//NM_0106	Krt32	colony stimulating factor 2 receptor, beta 2, low-affinity (granulocyte-	0010950 // positive regulation of endopeptidase activity // inferred from physical interaction//0019884 // antigen processing and presentation of exogenous antigen // inferred from mutant
1416202_a	0.008278	2.80	4.07	NM_001025610//NM_0012	M54a7	colony stimulating factor 2 receptor, beta 2, low-affinity (granulocyte-	0007165 // signal transduction // not recorded//0007268 // synaptic transmission // not recorded//0016337 // single organismal cell-cell adhesion // not recorded
1418099_a	0.000480	2.80	1.45	NM_011267	Rgs16	colony stimulating factor 2 receptor, beta 2, low-affinity (granulocyte-	0006508 // proteolysis // inferred from electronic annotation//0003163 // protein catabolic process // inferred from mutant phenotype//0003034 // regulation of cell migration // inferred
1417936_a	0.002036	2.79	1.50	NM_177320//XM_0065335	Pik3r5	colony stimulating factor 2 receptor, beta 2, low-affinity (granulocyte-	0016567 // protein ubiquitination // inferred from direct assay//0013647 // regulation of protein stability // inferred from direct assay//0035690 // cellular response to drug // inferred from
1418639_a	0.000960	2.79	1.36	NM_001252383//NM_0120	Irf5	colony stimulating factor 2 receptor, beta 2, low-affinity (granulocyte-	0008544 // epidermis development // inferred from electronic annotation
1417026_a	0.004319	2.79	1.87	NM_011452	Serpinb5b	colony stimulating factor 2 receptor, beta 2, low-affinity (granulocyte-	0006937 // regulation of muscle contraction // traceable author statement//0007029 // endoplasmic reticulum organization // inferred from mutant phenotype//0007519 // skeletal muscle
1422040_a	0.001332	2.78	1.13	XR_105147//XR_378397//	9130208014Rik	colony stimulating factor 2 receptor, beta 2, low-affinity (granulocyte-	0001816 // cytokine production // inferred from mutant phenotype//0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 // regulation of transcription,
1421002_a	0.002013	2.76	1.17	NM_001029855//NM_0012	Psmc2//Psmc2b	colony stimulating factor 2 receptor, beta 2, low-affinity (granulocyte-	0006909 // phagocytosis // inferred from genetic interaction//0006955 // immune response // inferred from mutant phenotype//0007186 // G-protein coupled receptor signaling pathway //
1416786_a	0.007493	2.75	2.09	NM_001085383//NM_0236	Anxa9	colony stimulating factor 2 receptor, beta 2, low-affinity (granulocyte-	0000165 // MAPK cascade // not recorded//0000186 // activation of MAPK activity // not recorded//0006468 // protein phosphorylation // not recorded//0006950 // response to stress //
1429874_a	0.001733	2.75	-1.39	NM_010809	Mmp3	colony stimulating factor 2 receptor, beta 2, low-affinity (granulocyte-	0001666 // response to hypoxia // not recorded//0006915 // apoptotic process // inferred from electronic annotation//0006919 // activation of cysteine-type endopeptidase activity involved
1419134_a	0.000511	2.75	1.30	XM_887064//XM_907567	LOC432459	colony stimulating factor 2 receptor, beta 2, low-affinity (granulocyte-	
1429043_a	0.001132	2.75	-1.08	NM_001033135//XM_0064	Rnf149	colony stimulating factor 2 receptor, beta 2, low-affinity (granulocyte-	
1416114_a	0.000726	2.75	5.25	NM_026335	Lce1h	colony stimulating factor 2 receptor, beta 2, low-affinity (granulocyte-	
1416006_a	0.006602	2.75	9.48	NM_009813	Csq1	colony stimulating factor 2 receptor, beta 2, low-affinity (granulocyte-	
1417900_a	0.001250	2.74	1.51	NM_009044	Rel	colony stimulating factor 2 receptor, beta 2, low-affinity (granulocyte-	
1418981_a	0.000614	2.73	1.31	NM_001163815//NM_0011	Vav1	colony stimulating factor 2 receptor, beta 2, low-affinity (granulocyte-	
1429778_a	0.000503	2.73	-1.38	NM_016693//XM_0065390	Map3k6	colony stimulating factor 2 receptor, beta 2, low-affinity (granulocyte-	

Table S7

Gene ID	p (Corr)	FC-RSV 1 d	FC-RSV 5 d	RefSeq Transcript ID	Gene Symbol	Gene Title	Gene Ontology Biological Process
1450144_a	0.004478	2.72	-1.23	NM_006655	<i>Gadd45b</i>	growth arrest and DNA-damage-inducible 45 beta	0000185 // activation of MAPKKK activity // not recorded//0000186 // activation of MAPKK activity // inferred from direct assay//0006469 // negative regulation of protein kinase activity //
1419604_a	0.002026	2.72	1.25	NM_010658	<i>Mafb</i>	v-maf musculoaponeurotic fibrosarcoma oncogene family, protein B (avian)	0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 // regulation of transcription, DNA-templated // inferred from electronic annotation//0006357 //
1418204_s	0.001874	2.71	1.43	NM_012021	<i>Pdx5</i>	peroxiredoxin 5	0006979 // response to oxidative stress // not recorded//0006979 // response to oxidative stress // inferred from sequence or structural similarity//0016480 // negative regulation of
1422506_a	0.000511	2.71	1.12	NM_001164627//NM_0011	<i>Arhgap8</i>	Rho GTPase activating protein 8	0007165 // signal transduction // inferred from electronic annotation//0002321 // positive regulation of Rho GTPase activity // not recorded//0004354 // positive regulation of GTPase activity //
1417268_a	0.002561	2.71	1.75	NM_001710332//NM_0011	<i>Clec4a2//Clec4b1</i>	C-type lectin domain family 4, member a2 //C-type lectin domain family 4, member a2, ligand polypeptide 3	0002376 // immune system process // inferred from electronic annotation//0004507 // innate immune response // inferred from electronic annotation//0001281 // positive regulation of
1416184_s	0.000917	2.70	4.26	NM_010859	<i>Myf3</i>	myosin, light polypeptide 3	0002026 // regulation of the force of heart contraction // not recorded//0006942 // regulation of striated muscle contraction // not recorded//0007519 // skeletal muscle tissue development
1416979_s	0.003814	2.70	1.89	NM_175440	<i>Prss27</i>	protease, serine 27	0006508 // proteolysis // inferred from electronic annotation
1421914_s	0.007677	2.70	1.14	NM_019432	<i>Tmem37</i>	transmembrane protein 37	0006810 // transport // inferred from electronic annotation//0006811 // ion transport // inferred from electronic annotation//0006816 // calcium ion transport // inferred from electronic
1416753_a	0.006706	2.69	2.10	NM_00104343//NM_0012	<i>Copp</i>	capping protein (actin filament), gelsolin-like	0030031 // cell projection assembly // inferred from direct assay//005193 // actin filament capping // inferred from electronic annotation
1419489_a	0.000374	2.69	1.26	NM_021618//X.M_0065212	<i>Gria3</i>	glutamate receptor, ionotropic, N-methyl D-aspartate-associated protein 1	0032469 // endoplasmic reticulum calcium ion homeostasis // inferred from direct assay//1902236 // negative regulation of intrinsic apoptotic signaling pathway in response to endoplasmic
1419288_a	0.008022	2.68	1.28	NM_019980//X.M_0065224	<i>Ltaf4//Gm9861</i>	LPS-induced TN factor //predicted gene 9861	0001817 // regulation of cytokine production // inferred from mutant phenotype//0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 // regulation of
1437250_a	0.000513	2.68	-1.53	NM_010720//X.M_0065256	<i>Lipg</i>	lipase, endothelial	0006629 // lipid metabolic process // inferred from electronic annotation//0007594 // response to nutrient // inferred from electronic annotation//0008283 // cell proliferation // not
1419332_a	0.001248	2.68	1.28	NM_016767	<i>Batf</i>	basic leucine zipper transcription factor, ATF-like	0001816 // cytokine production // inferred from mutant phenotype//0002320 // lymphoid progenitor cell differentiation // inferred from mutant phenotype//0006351 // transcription, DNA-
1420394_s	0.000955	2.68	1.21	NM_133955	<i>Rhou</i>	ras homolog gene family, member U	0000082 // G1/S transition of mitotic cell cycle // inferred from direct assay//0006184 // GTP catabolic process // inferred from mutant phenotype//0006886 // intracellular protein transport
1449353_a	0.002359	2.67	-1.22	NM_012055//X.M_0065050	<i>Asns</i>	asparagine synthetase	0001889 // liver development // inferred from electronic annotation//0006520 // cellular amino acid metabolic process // inferred from electronic annotation//0006529 // asparagine
1422617_a	0.006230	2.67	1.11	NM_013529	<i>Gpft2</i>	glutamine fructose-6-phosphate transaminase 2	0005975 // carbohydrate metabolic process // inferred from electronic annotation//0006048 // UDP-N-acetylglucosamine biosynthetic process // inferred from electronic
1435101_a	0.001026	2.66	-1.13	NM_001172117//NM_0104	<i>Hck</i>	hemopoietic cell kinase	0002376 // immune system process // inferred from electronic annotation//0006468 // protein phosphorylation // inferred from electronic annotation//0006887 // exocytosis // inferred
1427139_a	0.002653	2.66	-1.05	NM_001160018//NM_0011	<i>Tor1aip1</i>	tor1in A interacting protein 1	0032781 // positive regulation of ATPase activity // not recorded//0034504 // protein localization to nucleus // inferred from mutant phenotype//0017163 // nuclear membrane organization
1416440_a	0.003754	2.63	2.95	NM_001039042//X.M_0065	<i>Klk13</i>	kallikrein-related peptidase 13	0006508 // proteolysis // not recorded//0006508 // proteolysis // inferred from direct assay//0016485 // protein processing // inferred from direct assay
1421433_a	0.008938	2.63	1.15	NM_022411//X.M_0065326	<i>Slc13a2</i>	solute carrier family 13 (sodium-dependent dicarboxylate transporter),	0006810 // transport // inferred from electronic annotation//0006811 // ion transport // inferred from electronic annotation//0006814 // sodium ion transport // inferred from electronic
1417494_a	0.000306	2.63	1.63	NM_007806//X.M_0065306	<i>Cyba</i>	cytochrome b-245, alpha polypeptide	0001938 // positive regulation of endothelial cell proliferation // not recorded//0003106 // negative regulation of glomerular filtration by angiotensin // not recorded//0006801 // superoxide
1423248_a	0.007129	2.63	1.09	NM_009909//X.M_0064956	<i>Cxcr2</i>	chemokine (C-X-C motif) receptor 2	0002438 // acute inflammatory response to antigenic stimulus // not recorded//0002690 // positive regulation of leukocyte chemotaxis // not recorded//0006935 // chemotaxis // not
1420924_a	0.001963	2.63	1.18	NM_144810//X.M_0065293	<i>Khdcd8a</i>	kelch domain containing 8A	
1418986_a	0.006718	2.62	1.31	NM_007703//X.M_0065266	<i>Elovl3</i>	elongation of very long chain fatty acids (FEN1/Elo2, Sur4/Elo3, yeast)-like	0006629 // lipid metabolic process // inferred from electronic annotation//0006631 // fatty acid metabolic process // inferred from electronic annotation//0006633 // fatty acid biosynthetic
1418746_a	0.005561	2.62	1.34	NM_001013365	<i>Osm</i>	oscinostatin M	0006955 // immune response // inferred from electronic annotation//0007422 // peripheral nervous system development // inferred from mutant phenotype//0008284 // positive regulation of
1417846_a	0.004197	2.61	1.52	NM_027840//X.M_0065313	<i>Snz20</i>	sorting nexin 20	0001810 // transport // inferred from electronic annotation//0007154 // cell communication // inferred from electronic annotation//0015031 // protein transport // inferred from electronic
1420013_s	0.003914	2.60	1.22	NM_001077694//NM_0214	<i>Dysf</i>	dysferlin	0001778 // plasma membrane repair // inferred from direct assay//0001778 // plasma membrane repair // inferred from mutant phenotype//0006906 // vesicle fusion // inferred from
1419350_a	0.002180	2.59	1.28	XR_389711//XR_389712	<i>LOC664787</i>	Sp110 nuclear body protein-like	
1418240_a	0.001385	2.59	1.42	NM_022325	<i>Ctsz</i>	cathepsin Z	
1435644_a	0.005429	2.59	-1.49	NM_001164059//NM_0113	<i>Sell</i>	selectin, lymphocyte	0006508 // proteolysis // inferred from electronic annotation//0006441 // epithelial tube branching involved in lung morphogenesis // inferred from expression pattern
1436443_a	0.002581	2.59	-1.14	NM_001082552//NM_0092	<i>Trim21</i>	tripartite motif-containing 21	0007155 // cell adhesion // inferred from electronic annotation//0033198 // response to ATP // inferred from direct assay//0042981 // regulation of apoptotic process // not
1419598_a	0.001689	2.58	1.25	NM_001001892//NM_0103	<i>H2-D1//H2-</i>	histocompatibility 2, D region locus 1//histocompatibility 2, K1, K	0000209 // protein polyubiquitination // not recorded//0006513 // protein monoubiquitination // not recorded//0007049 // cell cycle // inferred from electronic annotation//0016567 //
1417612_a	0.001721	2.57	1.59	NM_023258	<i>Pycard</i>	PYD and CARD domain containing	0001916 // positive regulation of T cell mediated cytotoxicity // inferred from direct assay//0002376 // immune system process // inferred from electronic annotation//0002474 // antigen
1422051_a	0.005698	2.57	1.13	NM_183029	<i>Igf2bp2</i>	insulin-like growth factor 2 mRNA binding protein 2	0001773 // myeloid dendritic cell activation // not recorded//0002218 // activation of innate immune response // inferred from mutant phenotype//0002218 // activation of innate immune
1418415_s	0.004591	2.57	1.39	NM_011962//X.M_0065044	<i>Plod3</i>	procollagen-lysine, 2-oxoglutarate 5-dioxygenase 3	0006417 // regulation of translation // inferred from electronic annotation//0006810 // transport // inferred from electronic annotation//0051028 // mRNA transport // inferred from
1420407_a	0.002144	2.56	1.21	NM_001102404//NM_0011	<i>Acp5</i>	acyl-coA:cholesterol acyltransferase 1	0001701 // in utero embryonic development // inferred from mutant phenotype//0001886 // endothelial cell morphogenesis // inferred from mutant phenotype//0008104 // protein
1417821_a	0.003207	2.56	1.53	NM_011193//X.M_0065108	<i>Pstpip1</i>	acid phosphatase 5, tartrate resistant	0008152 // metabolic process // inferred from electronic annotation//0016311 // dephosphorylation // inferred from direct assay//0016311 // dephosphorylation // inferred from mutant
1416234_a	0.001529	2.56	3.72	NM_028623	<i>Cst6</i>	proline-serine-threonine phosphatase-interacting protein 1	0000910 // cytokinesis // inferred by curator//0002376 // immune system process // inferred from electronic annotation//0006897 // endocytosis // inferred from electronic
1420464_s	0.000469	2.55	1.21	NM_022324	<i>Sdf2l1</i>	cystatin E/M	0008544 // epidermis development // inferred from mutant phenotype // not recorded//0010466 // negative regulation of peptidase activity // inferred from electronic annotation//0010951 // negative
1419263_a	0.004455	2.55	1.28	NM_022324	<i>Sdf2l1</i>	stromal cell-derived factor 2-like 1	0034976 // response to endoplasmic reticulum stress // not recorded//0042981 // regulation of apoptotic process // not recorded//0017128 // cellular response to misfolded protein // not
1419263_a	0.004455	2.55	1.28	NM_028341//X.M_0065262	<i>Ttc39c</i>	tetratricopeptide repeat domain 39C	
1417327_a	0.008790	2.54	1.68	NM_007870//X.M_0065179	<i>Dnae1l3</i>	deoxyribo-nuclease 1-like 3	0000737 // DNA catabolic process, endonucleolytic // not recorded//0006308 // DNA catabolic process // inferred from electronic annotation//0006309 // apoptotic DNA fragmentation //
1460339_a	0.002906	2.54	-1.33	NM_126166//X.M_0065092	<i>Trf3</i>	tox-like receptor 3	0001774 // microglial cell activation // not recorded//0001819 // positive regulation of cytokine production // inferred from electronic annotation//0001934 // positive regulation of protein
1423246_a	0.003271	2.54	1.09	NM_133807	<i>Lnc59</i>	leucine rich repeat containing 59	
1419650_a	0.006583	2.54	1.24	NM_010266//X.M_0065266	<i>Gda</i>	guanine deaminase	0006147 // guanine catabolic process // inferred from electronic annotation
1420628_a	0.002056	2.54	1.19	NM_001290183//NM_0078	<i>Ddit3</i>	DNA-damage inducible transcript 3	0001955 // blood vessel maturation // inferred from mutant phenotype//0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 // regulation of
1434056_a	0.007394	2.53	-1.12	NM_016913//NM_023638f	<i>Porcn</i>	porcupine homolog (Drosophila)	0009100 // glycoprotein metabolic process // inferred from direct assay//0016055 // Wnt signaling pathway // inferred from electronic annotation
1417719_s	0.000159	2.53	1.56	NM_001160378//NM_0011	<i>Fam46a</i>	family with sequence similarity 46, member A	
1419075_s	0.000010	2.53	1.31	NM_013819	<i>H2-M3</i>	histocompatibility 2, M region locus 3	0001916 // positive regulation of T cell mediated cytotoxicity // inferred from direct assay//0001916 // positive regulation of T cell mediated cytotoxicity // inferred from mutant
1423070_a	0.000755	2.53	1.09	NM_009775//X.M_0065203	<i>Tspo</i>	translocator protein	0006694 // steroid biosynthetic process // not recorded//0006811 // ion transport // not recorded//0006821 // chloride transport // not recorded//0007165 // signal transduction // not
1420349_a	0.007232	2.52	1.21	NM_013759	<i>Msrb1</i>	methionine sulfoxide reductase B1	0002376 // immune system process // inferred from electronic annotation//0006979 // response to oxidative stress // inferred from electronic annotation//0030041 // actin filament
1416067_a	0.000767	2.52	6.39	NM_021508	<i>Myoz1</i>	myozenin 1	
1423594_a	0.000833	2.52	1.07	NM_025840//X.M_0014784	<i>Bzw2//Gm4354//Gm5589</i>	basic leucine zipper and W2 domains 2//predicted gene 4354//predicted	0001933 // negative regulation of protein phosphorylation // not recorded//0001933 // negative regulation of protein phosphorylation // inferred from electronic annotation//0001937 //
1419339_s	0.005179	2.52	1.28	NM_134164	<i>Syt12</i>	synaptotagmin XII	0006810 // transport // inferred from electronic annotation
1419004_s	0.001650	2.52	1.31	NM_001126182//NM_0108	<i>Naip2</i>	NLR family, apoptosis inhibitory protein 2	0002376 // immune system process // inferred from electronic annotation//0006915 // apoptotic process // inferred from electronic annotation//0006954 // inflammatory response //
1421252_a	0.002662	2.51	1.16	NM_013921//X.M_0065243	<i>Prss30</i>	protease, serine 30	0006508 // proteolysis // not recorded//0006810 // transport // inferred from electronic annotation//0006811 // ion transport // inferred from electronic annotation//0006814 // sodium
1423954_a	0.000622	2.51	1.05	NM_026405	<i>Rab32</i>	RAB32, member RAS oncogene family	0006184 // GTP catabolic process // inferred from electronic annotation//0006886 // intracellular protein transport // inferred from electronic annotation//0006913 // nucleocytoplasmic
1426276_a	0.000114	2.48	-1.02	NM_001253679//NM_0012	<i>Slc7a7</i>	solute carrier family 7 (cationic amino acid transporter, y+ system), member	0003333 // amino acid transmembrane transport // inferred from electronic annotation//0006810 // transport // inferred from electronic annotation//0006865 // amino acid transport //
1425151_a	0.005298	2.48	1.01	NM_001033310//NM_0011	<i>Cox18</i>	cytochrome c oxidase assembly protein 18	0008535 // respiratory chain complex IV assembly // not recorded//0015031 // protein transport // not recorded//0051204 // protein insertion into mitochondrial membrane // not
1431198_x	0.005185	2.48	-1.41	NM_001190974//NM_0011	<i>Axl</i>	AXL receptor tyrosine kinase	0001764 // neuron migration // inferred from genetic interaction//0001764 // neuron migration // inferred from mutant phenotype//0001779 // natural killer cell differentiation // inferred
1416750_a	0.003677	2.48	2.10	NM_00101303//X.M_0065236	<i>Emr1</i>	EGF-like module containing, mucin-like, hormone receptor-like sequence 1	0007165 // signal transduction // inferred from electronic annotation//0007166 // cell surface receptor signaling pathway // inferred from electronic annotation//0007186 // G-protein
1416309_a	0.007846	2.48	3.27	NM_000752	<i>Clqa</i>	complement component 1, q subcomponent, alpha polypeptide	0002376 // immune system process // inferred from electronic annotation//0006958 // complement activation, classical pathway // inferred from mutant phenotype//0004508 // innate
1417426_a	0.000880	2.47	1.65	NM_000793	<i>Cstb</i>	cystatin B	0008344 // adult locomotory behavior // inferred from mutant phenotype//0010466 // negative regulation of peptidase activity // not recorded//0010951 // negative regulation of
1422259_a	0.001006	2.47	1.13	NM_008398//X.M_0065132	<i>Itpa7</i>	integrin alpha 7	0007155 // cell adhesion // inferred from mutant phenotype//0007155 // cell adhesion // not recorded//0007229 // integrin-mediated signaling pathway // not recorded//0007519 //
1418264_a	0.002174	2.47	1.41	NM_001039103//NM_1339	<i>Rasa4</i>	Ras p21 protein activator 4	0007165 // signal transduction // inferred from electronic annotation//0002320 // positive regulation of Ras GTPase activity // not recorded//0035556 // intracellular signal transduction //
1421814_a	0.006025	2.46	1.14	NM_009977	<i>Cst7</i>	cystatin F (leukostyatin)	0010466 // negative regulation of peptidase activity // inferred from electronic annotation//0010951 // negative regulation of endopeptidase activity // inferred from electronic annotation
1436178_a	0.002201	2.45	-1.50	NM_172409//X.M_0064983	<i>Fmn12</i>	formin-like 2	0007010 // cytoskeleton organization // not recorded//0016043 // cellular component organization // inferred from electronic annotation//0022604 // regulation of cell morphogenesis // not
1420754_a	0.006634	2.45	1.19	NM_133500//NM_133501	<i>Ntn2</i>	netrin G2	0007275 // multicellular organismal development // inferred from electronic annotation//0007399 // nervous system development // inferred from electronic annotation//0007409 //
1429144_a	0.008593	2.45	-1.09	NM_007465//X.M_0065098	<i>Birc2</i>	baculoviral IAP repeat-containing 2	0000209 // protein polyubiquitination // not recorded//0001666 // response to hypoxia // not recorded//0001890 // placenta development // inferred from mutant phenotype//0006351 //
1433618_a	0.008034	2.44	-1.11	NM_028270	<i>Aldh5a1</i>	aldehyde dehydrogenase 1 family, member B1	0006068 // ethanol catabolic process // inferred from electronic annotation//0008152 // metabolic process // inferred from electronic annotation//0005514 // oxidation-reduction process //
1418857_a	0.001511	2.44	1.33	NM_019810	<i>Slc5o1</i>	solute carrier family 5 (sodium/glucose cotransporter), member 1	0001656 // metanephros development // inferred from mutant phenotype//0006810 // transport // inferred from electronic annotation//0006811 // ion transport // inferred from electronic
1418238_a	0.000977	2.43	1.42	NM_145530	<i>Rhov</i>	ras homolog gene family, member V	0006184 // GTP catabolic process // inferred from electronic annotation//0007165 // signal transduction // not recorded//0007264 // small GTPase mediated signal transduction // inferred
1442622_a	0.003814	2.43	-1.68	NM_001254474//NM_0083	<i>Ii15</i>	interleukin 15	0001779 // natural killer cell differentiation // inferred from genetic interaction//0001866 // NK T cell proliferation // inferred from mutant phenotype//0006954 // inflammatory response //
1421295_a	0.002257	2.43	1.16	NM_008530//X.M_0065205	<i>Ly6f</i>	lymphocyte antigen 6 complex, locus F	
1424507_a	0.005908	2.42	1.04	NM_001170853//X.M_0064	<i>Mnda//Ifi204//Ifi205//Mnd</i>	myeloid nuclear differentiation antigen like//interferon activated gene	0030308 // negative regulation of cell growth // inferred from mutant phenotype//0035458 // cellular response to interferon-beta // inferred from direct assay//0040008 // regulation of
1419125_a	0.000949	2.42	1.30	NM_001089256//NM_0530	<i>Lrp8</i>	low density lipoprotein receptor-related protein 8, apolipoprotein E	0001122 // negative regulation of transcription from RNA polymerase II promoter // inferred from mutant phenotype//0006897 // endocytosis // not recorded//0006898 // receptor-
1425008_a	0.000904	2.42	1.02	NM_010553//X.M_0064957	<i>Il18rap</i>	interleukin 18 receptor accessory protein	0007165 // signal transduction // inferred from electronic annotation//0001221 // cytokine-mediated signaling pathway // inferred from electronic annotation
1419742_a	0.002930	2.42	1.22	NM_025463//NM_139293	<i>Ece2</i>	endothelin converting enzyme 2	0006508 // proteolysis // inferred from sequence or structural similarity//0007420 // brain development // inferred from sequence or structural similarity//0007420 // brain development //
1422317_a	0.005350	2.42	1.12	NM_001177369//NM_0011	<i>NfkB2</i>	nuclear factor of kappa light polypeptide gene enhancer in B cells 2,	0002268 // follicular dendritic cell differentiation // inferred from mutant phenotype//0002467 // germinal center formation // inferred from mutant phenotype//0006351 // transcription,
1425154_a	0.000341	2.41	1.01	NM_155253	<i>Tcstv3</i>	2-cell-stage, variable group, member 3	
1418265_s	0.004423	2.41	1.41	NM_019835	<i>B4galnt5</i>	UDP-Gal:betaGalNAc beta 1,4-galactosyltransferase, polypeptide 5	0005975 // carbohydrate metabolic process // inferred from electronic annotation//0006486 // protein glycosylation // inferred from electronic annotation
1423200_a	0.009085	2.40	1.09	NM_025378	<i>Ifitm3</i>	interferon induced transmembrane protein 3	0002376 // immune system process // inferred from electronic annotation//0008285 // negative regulation of cell proliferation // inferred from direct assay//0009607 // response to biotic
1422140_a	0.000921	2.39	1.13	NM_023731	<i>Ccdc86</i>	coiled-coil domain containing 86	
1451903_a	0.009317	2.39	-1.28	NM_010755//X.M_0065205	<i>Maff</i>	v-maf musculoaponeurotic fibrosarcoma oncogene family, protein F (avian)	0001701 // in utero embryonic development // inferred from genetic interaction//0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 // regulation of
1425477_x	0.007587	2.39	1.00	NM_144549	<i>Tril1</i>	tribbles homolog 1 (Drosophila)	0006468 // protein phosphorylation // traceable author statement//0006469 // negative regulation of protein kinase activity // not recorded//0007254 // JNK cascade // not
1436791_a	0.006181	2.39	-1				

Table S7

Gene ID	p (Corr)	FC-RSV 1 d	FC-RSV 5 d	RefSeq Transcript ID	Gene Symbol	Gene Title	Gene Ontology Biological Process
1416254_a	0.009001	2.37	3.42	NM_001290786//NM_1729	<i>Muc15</i>	mucin 15	0006810 // transport // inferred from electronic annotation//0015031 // protein transport // inferred from electronic annotation//0042743 // hydrogen peroxide metabolic process // 0035556 // intracellular signal transduction // inferred from electronic annotation
1416554_a	0.006968	2.36	2.46	NM_145395//X/M_0064990	<i>Duoxa1</i>	dual oxidase maturation factor 1	
1417600_a	0.009759	2.36	1.59	NM_144804	<i>Depdc7</i>	DEF domain containing 7	000303 // response to superoxide // not recorded//0001666 // response to hypoxia // inferred from electronic annotation//0006810 // transport // inferred from electronic
1422308_a	0.000123	2.36	1.12	NM_011671//X/M_0065075	<i>Ucp2</i>	uncoupling protein 2 (mitochondrial, proton carrier)	
1419823_s	0.003673	2.36	1.23	NM_001164624//NM_1727	<i>Zfp809</i>	zinc finger protein 809	0006355 // regulation of transcription, DNA-templated // not recorded
1436953_a	0.000743	2.36	-1.15	NM_029077//X/M_0065383	<i>Trim14</i>	tripartite motif-containing 14	
1417615_a	0.004154	2.35	1.59	NM_144797	<i>Metrln</i>	metrolin, glial cell differentiation regulator-like	0002897 // negative regulation of viral transcription // not recorded//0045087 // innate immune response // not recorded//0051091 // positive regulation of sequence-specific DNA binding
1418444_a	0.001118	2.35	1.39	NM_026779//X/M_0065262	<i>Mocos</i>	molybdenum cofactor sulfase	
1419309_a	0.004359	2.35	1.28	NM_027570//X/M_0065311	<i>Ldhf</i>	lactate dehydrogenase D	0006777 // Mo-molybdopterin cofactor biosynthetic process // inferred from electronic annotation//0008152 // metabolic process // inferred from electronic annotation//0043545 // 0006754 // ATP biosynthetic process // non-traceable author statement//0055114 // oxidation-reduction process // non-traceable author statement
1423766_a	0.000726	2.35	1.06	NM_001169311//NM_1886	<i>Papd7</i>	PAP associated domain containing 7	
1421947_a	0.000702	2.35	1.14	NM_029103//X/M_0065118	<i>Manf</i>	mesencephalic astrocyte-derived neurotrophic factor	0002640 // DNA replication // inferred from electronic annotation//0006261 // DNA-dependent DNA replication // inferred from electronic annotation//0007049 // cell cycle // inferred from 0002014 // vasconstriction of artery involved in ischemic response to lowering of systemic arterial blood pressure // inferred from direct assay//0006986 // response to unfolded protein // 0001954 // positive regulation of cell-matrix adhesion // inferred from mutant phenotype//0007155 // cell adhesion // inferred from electronic annotation//0042246 // tissue regeneration //
1418749_a	0.002511	2.34	1.34	NM_013610	<i>Ninj1</i>	ninjurin 1	
1451260_a	0.004178	2.34	-1.27	NM_020568//X/M_0065247	<i>Plin4</i>	perilipin 4	0006417 // regulation of translation // inferred from electronic annotation//0007126 // meiotic nuclear division // inferred from electronic annotation//0007275 // multicellular organismal 0001659 // temperature homeostasis // inferred from genetic interaction//0002862 // negative regulation of inflammatory response to antigenic stimulus // inferred from genetic
1424292_a	0.009732	2.34	1.04	NM_177905//X/M_0065104	<i>Piwi4</i>	piwi-like RNA-mediated gene silencing 4	
1421547_a	0.004050	2.34	1.15	NM_030677	<i>Gpx2</i>	glutathione peroxidase 2	0008152 // metabolic process // inferred from electronic annotation
1423130_a	0.000749	2.33	1.09	NM_001141965//NM_0264	<i>Naa20</i>	N(alpha)-acetyltransferase 20, NatB catalytic subunit	
1425649_a	0.000132	2.33	-1.00	NM_033541//X/M_0065301	<i>Oas1c</i>	2'-5' oligoadenylate synthetase 1C	0006955 // immune response // inferred from electronic annotation//0008152 // metabolic process // inferred from electronic annotation//0051607 // defense response to virus // inferred 0002027 // regulation of heart rate // inferred from mutant phenotype//0042391 // regulation of membrane potential // inferred from genetic interaction//0060931 // sinoatrial node cell
1421635_a	0.003465	2.33	1.15	NM_001081984//NM_0223	<i>Popdc2</i>	popeye domain containing 2	
1417328_a	0.000165	2.33	1.68	NM_030017//X/M_0065163	<i>Rdh12</i>	retinol dehydrogenase 12	0007601 // visual perception // inferred from electronic annotation//0008152 // metabolic process // inferred from electronic annotation//0042572 // retinol metabolic process // not 0006096 // glycolytic process // inferred from electronic annotation//0007568 // aging // inferred from electronic annotation//0042493 // response to drug // inferred from electronic
1416192_a	0.001021	2.33	4.08	NM_001136062//NM_0012	<i>Eno3</i>	enolase 3, beta muscle	
1451106_a	0.003837	2.32	-1.26	NM_011019//X/M_0065199	<i>Osmr</i>	osteonin M receptor	0007166 // cell surface receptor signaling pathway // traceable author statement//0008284 // positive regulation of cell proliferation // not recorded//0019221 // cytokine-mediated signaling 0007229 // integrin-mediated signaling pathway // inferred from mutant phenotype//0043313 // regulation of neutrophil degranulation // inferred from mutant phenotype
1421267_a	0.007550	2.32	1.16	NM_001002842//NR_02827	<i>Pram1</i>	PM1-ARF alpha-regulated adaptor molecule 1	
1449191_a	0.000336	2.31	-1.21	NM_197986//X/M_0065065	<i>Tmem140</i>	transmembrane protein 140	0009134 // nucleoside diphosphate catabolic process // inferred from direct assay//0009143 // nucleoside triphosphate catabolic process // inferred from direct assay 0007166 // cell surface receptor signaling pathway // inferred from direct assay//0045085 // negative regulation of interleukin-2 biosynthetic process // inferred from direct assay//0045954
1451884_a	0.007800	2.31	-1.28	NM_178676	<i>Entpd3</i>	ectonucleoside triphosphate diphosphohydrolase 3	
1418703_a	0.006583	2.31	1.35	NM_008479//XR_377427	<i>Log3</i>	lymphocyte activation gene 3	0006194 // GTP catalytic process // not recorded//0007165 // signal transduction // inferred from electronic annotation//0007186 // G-protein coupled receptor signaling pathway // 0006601 // creatine biosynthetic process // not recorded//0006979 // response to oxidative stress // inferred from electronic annotation//0007584 // response to nutrient // not 0006810 // transport // inferred from electronic annotation//0006811 // ion transport // inferred from electronic annotation//0006821 // chloride transport // inferred from mutant
1417953_a	0.000036	2.30	1.49	NM_145535//X/M_0064993	<i>Sidcp2</i>	syndecan binding protein (syntenin) 2	
1417317_s	0.001713	2.30	1.71	NM_001160016//NM_0011	<i>Gnb1</i>	guanine nucleotide binding protein (G protein), beta 1	0006194 // GTP catalytic process // not recorded//0007165 // signal transduction // inferred from electronic annotation//0007186 // G-protein coupled receptor signaling pathway // 0006601 // creatine biosynthetic process // not recorded//0006979 // response to oxidative stress // inferred from electronic annotation//0007584 // response to nutrient // not 0006810 // transport // inferred from electronic annotation//0006811 // ion transport // inferred from electronic annotation//0006821 // chloride transport // inferred from mutant
1419360_a	0.000614	2.29	1.27	NM_025961	<i>Gatm</i>	glycine amidinotransferase (L-arginine:glycine amidinotransferase)	
1416834_a	0.008982	2.28	2.05	NM_178697//X/M_0065014	<i>Cka5s</i>	choline channel calcium activated 5	0001501 // skeletal system development // inferred from mutant phenotype//0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 // regulation of 0000122 // negative regulation of transcription from RNA polymerase II promoter // inferred from direct assay//0001658 // branching involved in uterine bud morphogenesis // not
1416626_a	0.001163	2.28	2.35	NM_011097//X/M_0065171	<i>Pitx1</i>	paired-like homeodomain transcription factor 1	
1419249_a	0.004006	2.28	1.29	NM_001136082//NM_0011	<i>Timeless</i>	timeless circadian clock 1	0006730 // one-carbon metabolic process // inferred from electronic annotation//0008152 // metabolic process // inferred from electronic annotation//0009058 // biosynthetic process // 0006470 // protein dephosphorylation // inferred from mutant phenotype//0006470 // protein dephosphorylation // not recorded//0008286 // insulin receptor signaling pathway // inferred 0007517 // muscle organ development // inferred from electronic annotation//0007520 // myoblast fusion // inferred from direct assay//0045026 // plasma membrane fusion // inferred 0001849 // peptide cross-linking // not recorded//0030216 // keratinocyte differentiation // not recorded//0031424 // keratinization // inferred from electronic annotation
1436038_a	0.004807	2.28	-1.14	NM_001024703//X/M_0065	<i>Mctp2</i>	multiple C2 domains, transmembrane 2	
1433581_a	0.001365	2.27	-1.11	NM_027406//X/M_0065052	<i>Alkh11</i>	aldehyde dehydrogenase 1 family, member L1	0007517 // muscle organ development // inferred from electronic annotation//0007520 // myoblast fusion // inferred from direct assay//0045026 // plasma membrane fusion // inferred 0001849 // peptide cross-linking // not recorded//0030216 // keratinocyte differentiation // not recorded//0031424 // keratinization // inferred from electronic annotation
1421972_s	0.004186	2.27	1.14	NM_011201//X/M_0064989	<i>Ptpn1</i>	protein tyrosine phosphatase, non-receptor type 1	
1419493_a	0.000591	2.27	1.26	NM_001159602//NM_0253	<i>Tmem8c</i>	transmembrane protein 8C	00016477 // cell migration // not recorded//0032312 // regulation of ARF GTPase activity // inferred from electronic annotation//0003280 // positive regulation of ARF GTPase activity // not 0000910 // cytokinesis // not recorded//0001541 // ovarian follicle development // inferred from genetic interaction//0001541 // ovarian follicle development // inferred from mutant 0008283 // cell proliferation // inferred from mutant phenotype//0023057 // negative regulation of signaling // not recorded//0031953 // negative regulation of protein autophosphorylation
1416673_a	0.003009	2.27	2.26	NM_0025726//X/M_0065321	<i>Evp1</i>	envoplakin	
1422475_a	0.000447	2.27	1.12	NM_001008232//X/M_0065	<i>Asap3</i>	ARF GAP with SH3 domain, ankyrin repeat and PH domain 3	0000910 // cytokinesis // not recorded//0001541 // ovarian follicle development // inferred from genetic interaction//0001541 // ovarian follicle development // inferred from mutant 0008283 // cell proliferation // inferred from mutant phenotype//0023057 // negative regulation of signaling // not recorded//0031953 // negative regulation of protein autophosphorylation
1424005_s	0.001568	2.26	1.05	NM_001289716//NM_0012	<i>Bcl2l1</i>	BCL2-like 1	
1419273_a	0.002428	2.26	1.28	NM_080638	<i>Mvp</i>	major vault protein	0000122 // negative regulation of transcription from RNA polymerase II promoter // inferred from genetic interaction//1900181 // negative regulation of protein localization to nucleus // 0006306 // DNA methylation // traceable author statement//0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 // regulation of transcription, DNA-
1416458_a	0.002428	2.24	2.65	NM_023655//X/M_0065106	<i>Trim29</i>	tripartite motif-containing 29	
1429466_s	0.003207	2.24	-1.38	NM_013594//X/M_0065257	<i>Mbd1</i>	methyl-CpG binding domain protein 1	0006306 // DNA methylation // traceable author statement//0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 // regulation of transcription, DNA- 0006869 // lipid transport // inferred from electronic annotation//0007165 // signal transduction // not recorded//0042157 // lipoprotein metabolic process // inferred from electronic 0006355 // transcription, DNA-templated // inferred from electronic annotation//0006355 // regulation of transcription, DNA-templated // inferred from electronic annotation//0006357 // 0000122 // negative regulation of transcription from RNA polymerase II promoter // inferred from direct assay//0000122 // negative regulation of transcription from RNA polymerase II 0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 // regulation of transcription, DNA-templated // inferred from electronic annotation//0007155 // 0032321 // positive regulation of Rho GTPase activity // inferred from electronic annotation//0035023 // regulation of Rho protein signal transduction // inferred from electronic 0001932 // regulation of protein phosphorylation // inferred from direct assay//0001932 // regulation of protein phosphorylation // inferred from genetic interaction//0001934 // positive
1418512_a	0.006660	2.24	1.38	NM_001164604//NM_0294	<i>Apol1a7a</i>	apolipoprotein L7a//apolipoprotein L7c//apolipoprotein L7c	
1450730_a	0.001932	2.24	1.25	NM_030693//X/M_0065313	<i>Af5</i>	activating transcription factor 5	0006810 // transport // inferred from electronic annotation//0006811 // ion transport // inferred from electronic annotation//0006812 // cation transport // inferred from physical 0006598 // polyamine catabolic process // inferred from direct assay//0006598 // polyamine catabolic process // not recorded//0008215 // spermine metabolic process // inferred from 0000122 // negative regulation of transcription from RNA polymerase II promoter // not recorded//0001501 // skeletal system development // inferred from genetic interaction//0002244 // 0002934 // desmosome organization // inferred from mutant phenotype//0006915 // apoptotic process // inferred from electronic annotation//0007155 // cell adhesion // inferred from 0000122 // negative regulation of transcription from RNA polymerase II promoter // not recorded//0002502 // peptide antigen assembly with MHC class I protein complex // inferred from 0002690 // positive regulation of leukocyte chemotaxis // not recorded//0006508 // proteolysis // not recorded//0007596 // blood coagulation // inferred from mutant phenotype//0007596
1419418_a	0.000445	2.23	1.26	NM_001281880//NM_0136	<i>Sema4d</i>	sema domain, immunoglobulin domain (lg), transmembrane domain (TM)	
1418086_a	0.000217	2.23	1.45	NM_134152//X/M_0065265	<i>Lpxn</i>	leupaxin	0006810 // transport // inferred from electronic annotation//0006811 // ion transport // inferred from electronic annotation//0006812 // cation transport // inferred from physical 0006598 // polyamine catabolic process // inferred from direct assay//0006598 // polyamine catabolic process // not recorded//0008215 // spermine metabolic process // inferred from 0000122 // negative regulation of transcription from RNA polymerase II promoter // not recorded//0001501 // skeletal system development // inferred from genetic interaction//0002244 // 0002934 // desmosome organization // inferred from mutant phenotype//0006915 // apoptotic process // inferred from electronic annotation//0007155 // cell adhesion // inferred from 0000122 // negative regulation of transcription from RNA polymerase II promoter // not recorded//0002502 // peptide antigen assembly with MHC class I protein complex // inferred from 0002690 // positive regulation of leukocyte chemotaxis // not recorded//0006508 // proteolysis // not recorded//0007596 // blood coagulation // inferred from mutant phenotype//0007596
1426065_a	0.001915	2.23	-1.01			RIKEN cDNA 5730411F24Rik	
1418100_a	0.005988	2.23	1.45	NM_001271358//NM_0012	<i>Arrb2</i>	arrestin, beta 2	0007165 // signal transduction // inferred from electronic annotation//0007186 // G-protein coupled receptor signaling pathway // not recorded//0007200 // phospholipase C-activating G- 0001525 // angiogenesis // inferred from direct assay//0001525 // angiogenesis // inferred from mutant phenotype//0001886 // endothelial cell morphogenesis // inferred from direct
1427091_a	0.000023	2.23	-1.05	NM_001163170	<i>Lix1</i>	Lix1-like	
1426743_a	0.008770	2.23	-1.03	NM_001164566//NM_1448	<i>Spats2l</i>	spermatogenesis associated, serine-rich 2-like	0006810 // transport // inferred from electronic annotation//0006811 // ion transport // inferred from electronic annotation//0006812 // cation transport // inferred from physical 0006598 // polyamine catabolic process // inferred from direct assay//0006598 // polyamine catabolic process // not recorded//0008215 // spermine metabolic process // inferred from 0000122 // negative regulation of transcription from RNA polymerase II promoter // not recorded//0001501 // skeletal system development // inferred from genetic interaction//0002244 // 0002934 // desmosome organization // inferred from mutant phenotype//0006915 // apoptotic process // inferred from electronic annotation//0007155 // cell adhesion // inferred from 0000122 // negative regulation of transcription from RNA polymerase II promoter // not recorded//0002502 // peptide antigen assembly with MHC class I protein complex // inferred from 0002690 // positive regulation of leukocyte chemotaxis // not recorded//0006508 // proteolysis // not recorded//0007596 // blood coagulation // inferred from mutant phenotype//0007596
1448836_s	0.005283	2.23	-1.19	NM_028287//X/M_0065128	<i>Zufsp</i>	zinc finger with UFM1-specific peptidase domain	
1421694_a	0.004004	2.23	1.15	NM_013927//X/M_0065379	<i>Cngb3</i>	cyclic nucleotide gated channel beta 3	0006810 // transport // inferred from electronic annotation//0006811 // ion transport // inferred from electronic annotation//0006812 // cation transport // inferred from physical 0006598 // polyamine catabolic process // inferred from direct assay//0006598 // polyamine catabolic process // not recorded//0008215 // spermine metabolic process // inferred from 0000122 // negative regulation of transcription from RNA polymerase II promoter // not recorded//0001501 // skeletal system development // inferred from genetic interaction//0002244 // 0002934 // desmosome organization // inferred from mutant phenotype//0006915 // apoptotic process // inferred from electronic annotation//0007155 // cell adhesion // inferred from 0000122 // negative regulation of transcription from RNA polymerase II promoter // not recorded//0002502 // peptide antigen assembly with MHC class I protein complex // inferred from 0002690 // positive regulation of leukocyte chemotaxis // not recorded//0006508 // proteolysis // not recorded//0007596 // blood coagulation // inferred from mutant phenotype//0007596
1418574_a	0.006545	2.23	1.37	NM_153783//X/M_0065361	<i>Poax</i>	polyamine oxidase (exo-N4-amino)	
1425233_a	0.000610	2.21	1.01	NM_008046//X/M_0065175	<i>Fst</i>	folistatin	0006810 // transport // inferred from electronic annotation//0006811 // ion transport // inferred from electronic annotation//0006812 // cation transport // inferred from physical 0006598 // polyamine catabolic process // inferred from direct assay//0006598 // polyamine catabolic process // not recorded//0008215 // spermine metabolic process // inferred from 0000122 // negative regulation of transcription from RNA polymerase II promoter // not recorded//0001501 // skeletal system development // inferred from genetic interaction//0002244 // 0002934 // desmosome organization // inferred from mutant phenotype//0006915 // apoptotic process // inferred from electronic annotation//0007155 // cell adhesion // inferred from 0000122 // negative regulation of transcription from RNA polymerase II promoter // not recorded//0002502 // peptide antigen assembly with MHC class I protein complex // inferred from 0002690 // positive regulation of leukocyte chemotaxis // not recorded//0006508 // proteolysis // not recorded//0007596 // blood coagulation // inferred from mutant phenotype//0007596
1416242_a	0.000749	2.21	3.54	NM_022032	<i>Perp</i>	PERP, TP53 apoptosis effector	
1419286_s	0.008606	2.21	1.28	NM_007591	<i>Calr</i>	calreticulin	0006810 // transport // inferred from electronic annotation//0006811 // ion transport // inferred from electronic annotation//0006812 // cation transport // inferred from physical 0006598 // polyamine catabolic process // inferred from direct assay//0006598 // polyamine catabolic process // not recorded//0008215 // spermine metabolic process // inferred from 0000122 // negative regulation of transcription from RNA polymerase II promoter // not recorded//0001501 // skeletal system development // inferred from genetic interaction//0002244 // 0002934 // desmosome organization // inferred from mutant phenotype//0006915 // apoptotic process // inferred from electronic annotation//0007155 // cell adhesion // inferred from 0000122 // negative regulation of transcription from RNA polymerase II promoter // not recorded//0002502 // peptide antigen assembly with MHC class I protein complex // inferred from 0002690 // positive regulation of leukocyte chemotaxis // not recorded//0006508 // proteolysis // not recorded//0007596 // blood coagulation // inferred from mutant phenotype//0007596
1418072_a	0.002174	2.21	1.46	NM_010172//X/M_0065086	<i>F7</i>	coagulation factor VII	
1422653_a	0.005825	2.21	1.11	NM_001082483//X/M_0065	<i>Efr3b</i>	EFK3 homolog B (S. cerevisiae)	0007165 // signal transduction // inferred from electronic annotation//0007186 // G-protein coupled receptor signaling pathway // not recorded//0007200 // phospholipase C-activating G- 0001525 // angiogenesis // inferred from direct assay//0001525 // angiogenesis // inferred from mutant phenotype//0001886 // endothelial cell morphogenesis // inferred from direct
1419518_a	0.001938	2.20	1.28	NM_008773//X/M_0065074	<i>P2ry2</i>	purinergic receptor P2Y, G-protein coupled 2	
1419417_a	0.009011	2.20	1.26	NM_001109991//NM_0099	<i>Col18a1</i>	collagen, type XVIII, alpha 1	0006810 // transport // inferred from electronic annotation//0007165 // signal transduction // inferred from sequence or structural similarity//0015031 // protein transport // inferred from 0007265 // Ras protein signal transduction // not recorded//0007266 // Rho protein signal transduction // not recorded//0016310 // phosphorylation // inferred from electronic annotation 0006508 // proteolysis // inferred from direct assay//0006508 // proteolysis // not recorded//0016477 // cell migration // traceable author statement//0003216 // keratinocyte 0001966 // thigmotaxis // not recorded//0002087 // regulation of respiratory gas exchange by neurological system process // inferred from genetic interaction//0007155 // cell adhesion 0006629 // lipid metabolic process // inferred from electronic annotation//0008152 // metabolic process // inferred from electronic annotation//0010891 // negative regulation of 0002376 // immune system process // inferred from electronic annotation//0016567 // protein ubiquitination // not recorded//0032728 // positive regulation of interferon-beta production 0002092 // positive regulation of receptor internalization // not recorded//0002687 // positive regulation of leukocyte migration // inferred from genetic interaction//0006954 // 0007155 // cell adhesion // not recorded
1421572_a	0.001264	2.20	1.15	NM_148927//X/M_0065411	<i>Plekh4</i>	plekstrin homology domain containing, family A [phosphoinositide binding	
1416748_a	0.003632	2.20	2.10	NM_001032326//X/M_0065	<i>Vcpkmt</i>	valosin containing protein lysine (K) methyltransferase	0018023 // peptidyl-lysine trimethylation // not recorded//0032259 // methylation // inferred from electronic annotation
1420073_s	0.005121	2.20	1.22	NM_024281//NM_133626	<i>Rrbp1</i>	ribosome binding protein 1	
1448903_a	0.007232	2.20	-1.19	NM_001081047	<i>Cnksr1</i>	connector enhancer of kinase suppressor of Ras 1	0006810 // transport // inferred from electronic annotation//0007165 // signal transduction // inferred from sequence or structural similarity//0015031 // protein transport // inferred from 0007265 // Ras protein signal transduction // not recorded//0007266 // Rho protein signal transduction // not recorded//0016310 // phosphorylation // inferred from electronic annotation 0006508 // proteolysis // inferred from direct assay//0006508 // proteolysis // not recorded//0016477 // cell migration // traceable author statement//0003216 // keratinocyte 0001966 // thigmotaxis // not recorded//0002087 // regulation of respiratory gas exchange by neurological system process // inferred from genetic interaction//0007155 // cell adhesion 0006629 // lipid metabolic process // inferred from electronic annotation//0008152 // metabolic process // inferred from electronic annotation//0010891 // negative regulation of 0002376 // immune system process // inferred from electronic annotation//0016567 // protein ubiquitination // not recorded//0032728 // positive regulation of interferon-beta production 0002092 // positive regulation of receptor internalization // not recorded//0002687 // positive regulation of leukocyte migration // inferred from genetic interaction//0006954 // 0007155 // cell adhesion // not recorded
1418652_a	0.001727	2.20	1.35	NM_0011176//X/M_0065100	<i>St14</i>	suppression of tumorigenicity 14 (colon carcinoma)	
1418898_a	0.006063	2.20	1.32	NM_198862//X/M_0065329	<i>Nlgn2</i>	neuroligin 2	0006810 // transport // inferred from electronic annotation//0007165 // signal transduction // inferred from sequence or structural similarity//0015031 // protein transport // inferred from 0007265 // Ras protein signal transduction // not recorded//0007266 // Rho protein signal transduction // not recorded//0016310 // phosphorylation // inferred from electronic annotation

Table S7

Gene ID	p (Corr)	FC-RSV 1 d	FC-RSV 5 d	RefSeq Transcript ID	Gene Symbol	Gene Title	Gene Ontology Biological Process
1416453_x	0.009491	2.16	2.81	XM_006531545//XM_0065	Ces1h	carboxylesterase 1H	0008152 // metabolic process // ---
1420931_x	0.004999	2.16	1.18	NM_001164107//NM_0011	Ripk3	receptor-interacting serine-threonine kinase 3	0001914 // regulation of T cell mediated cytotoxicity // inferred from genetic interaction//0002819 // regulation of adaptive immune response // inferred from genetic interaction//0006468
1417203_x	0.002677	2.16	1.76	NM_029612//XM_0064970	Slamf9	SLAM family member 9	
1428027_x	0.001961	2.16	-1.07	NM_001146007//NM_1756	Trim12c	tripartite motif-containing 12C	0002221 // pattern recognition receptor signaling pathway // not recorded//0016567 // protein ubiquitination // not recorded
1420912_x	0.007255	2.15	1.18	NM_133879//XM_0065384	Zbtb48	zinc finger and BTB domain containing 48	0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 // regulation of transcription, DNA-templated // inferred from electronic annotation
1423823_x	0.002862	2.15	1.06	NM_001290646//NM_0107	Lhx2	LIM homeobox protein 2	0001843 // neural tube closure // inferred from mutant phenotype//0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 // regulation of transcription, DNA-templated
1415788_x	0.002830	2.15	23.99	NM_054063	Psg28	pregnancy-specific glycoprotein 28	0007565 // female pregnancy // inferred from electronic annotation
1417516_x	0.000383	2.15	1.62	NM_009780//NM_011413/	C4a//C4b	complement component 4A (Rodgers blood group)//complement	0002376 // immune system process // inferred from electronic annotation//0006954 // inflammatory response // inferred from electronic annotation//0006956 // complement activation //
1421936_x	0.001489	2.15	1.14	NM_023142//XM_0065418	Arpc1b//Gm5637	actin related protein 2/3 complex, subunit 1B//predicted pseudogene	0030833 // regulation of actin filament polymerization // inferred from electronic annotation
1420394_x	0.000955	2.14	1.21	NM_029035//XM_0065370	Spsb1	splynyadine receptor domain and SOCS box containing 1	0015667 // protein ubiquitination // inferred from electronic annotation//0003556 // intracellular signal transduction // inferred from electronic annotation
1424654_x	0.000343	2.14	1.03	NM_001164336//NM_0011	42434	membrane-associated ring finger (3CHCA) 5	0002029 // protein polyubiquitination // not recorded//0016567 // protein ubiquitination // inferred from electronic annotation//0051865 // protein autoubiquitination // not
1454159_x	0.000315	2.14	-1.31	NM_007544//XM_0065054	Bid	BH3 interacting domain death agonist	0001836 // release of cytochrome c from mitochondria // inferred from direct assay//0001836 // release of cytochrome c from mitochondria // inferred from mutant phenotype//0001836 //
1417584_x	0.000657	2.13	1.60	NM_026985//XM_0065088	Mcemp1	mast cell expressed membrane protein 1	
1417161_x	0.007765	2.13	1.79	NM_177845//XM_0064997	Pla2g4e	phospholipase A2, group IVE	0006629 // lipid metabolic process // inferred from electronic annotation//0008152 // metabolic process // inferred from electronic annotation//0009395 // phospholipid catabolic process //
1416608_x	0.002342	2.13	2.41	NM_001033163//XM_0065	Ephx3	epoxide hydrolase 3	0008152 // metabolic process // inferred from electronic annotation
1420871_x	0.002373	2.13	1.18	NM_027852//XM_0065066	Rorres2	retinoic acid receptor responder (tazarotene induced) 2	0001523 // retinoid metabolic process // not recorded//0001701 // in utero embryonic development // inferred from electronic annotation//0001934 // positive regulation of protein
1422900_x	0.000972	2.13	1.10	NM_011611//NM_170702/	Cd40	CD40 antigen	0001934 // positive regulation of protein phosphorylation // not recorded//0002376 // immune system process // inferred from electronic annotation//0002768 // immune response-
1433733_x	0.008714	2.13	-1.12	NM_001160180//NM_0011	Tor1aip2	torsin A interacting protein 2	0007029 // endoplasmic reticulum organization // not recorded//00032781 // positive regulation of ATPase activity // not recorded
1453196_x	0.000014	2.13	-1.31	NM_020047	Tacstd2	transmembrane-associated signal transducer 2	0010633 // negative regulation of epithelial cell migration // inferred from direct assay//00050678 // regulation of epithelial cell proliferation // inferred from expression pattern//0051497 //
1423301_x	0.002420	2.12	1.08	NM_011930//XM_0065242	Ckn7	chloride channel 7	0006810 // transport // inferred from electronic annotation//0006811 // ion transport // inferred from electronic annotation//0006821 // chloride transport // inferred from electronic
1425587_x	0.003434	2.12	-1.00	NM_001121717//NM_0089	Ptpn2	protein tyrosine phosphatase, non-receptor type 2	0006470 // protein dephosphorylation // inferred from mutant phenotype//0008285 // negative regulation of cell proliferation // not recorded//0008286 // insulin receptor signaling pathway
1423684_x	0.000864	2.12	1.07	NM_001038664//NM_0012	Gngt2	guanine nucleotide binding protein (G protein), gamma transducing activity	0006184 // GTP catalytic process // not recorded//0007165 // signal transduction // inferred from electronic annotation//0007186 // G-protein coupled receptor signaling pathway //
1421596_x	0.006180	2.12	1.15	NM_030207//XM_0065148	LOC100861749//Sfj1	protein SFH1 homolog, spindle assembly associated (yeast)	0010923 // negative regulation of phosphatase activity // not recorded
1425082_x	0.001667	2.11	1.01	NM_028791	Cmt1r	cay methyltransferase 1	0006302 // double-strand break repair // inferred from electronic annotation//0006370 // 7-methylguanosine mRNA capping // not recorded//0006397 // mRNA processing // inferred from
1458206_x	0.000634	2.11	-2.39	NM_001033324//XM_0065	Zbtb16	zinc finger and BTB domain containing 16	0001501 // skeletal system development // inferred from mutant phenotype//0001823 // mesonephros development // inferred from direct assay//0006355 // regulation of transcription,
1420915_x	0.005952	2.11	1.18	NM_008551	Mpkapkp2	MAP kinase-activated protein kinase 2	0002224 // toll-like receptor signaling pathway // inferred from mutant phenotype//0006468 // protein phosphorylation // inferred from direct assay//0006950 // response to stress // not
1425326_x	0.000511	2.11	1.01	NM_001290413//NM_0094	Traf2	TNF receptor-associated factor 2	0002726 // positive regulation of T cell cytokine production // not recorded//0006461 // protein complex assembly // not recorded//0006915 // apoptotic process // inferred from electronic
1433735_x	0.002410	2.11	-1.44	NM_027560//XM_0065097	Ardc2	arrestin domain containing 2	0007165 // signal transduction // inferred from electronic annotation
1419656_x	0.005209	2.11	1.24	NM_139269//XM_0065269	Pla2g16	phospholipase A2, group XVI	0006629 // lipid metabolic process // inferred from electronic annotation//0006644 // phospholipid metabolic process // not recorded//0008654 // phospholipid biosynthetic process //
1418273_x	0.000473	2.11	1.41	NM_001045540//XM_0065	Gm12185	predicted gene 12185	0008152 // metabolic process // inferred from electronic annotation
1427371_x	0.003090	2.10	-1.05	NM_027985//XM_0065359	Mad2l2	MAD2 mitotic arrest deficient-like 2	0000122 // negative regulation of transcription from RNA polymerase II promoter // not recorded//0001558 // regulation of cell growth // not recorded//0006302 // double-strand break
1417925_x	0.008022	2.10	1.50	NM_009156	Sepw1	selenoprotein W, muscle 1	0045454 // cell redox homeostasis // inferred from electronic annotation//0055114 // oxidation-reduction process // traceable author statement
1423151_x	0.001702	2.10	1.09	NM_001083884//NM_0273	Lypd8	LY6/PLAUR domain containing 8	0016310 // phosphorylation // inferred from direct assay
1422038_x	0.003925	2.09	1.13	NM_181593	Itpkc	inositol 1,4,5-trisphosphate 3-kinase C	
1418050_x	0.001134	2.09	1.47	NM_010821//XM_0065267	Mpeg1	macrophage expressed gene 1	
1417244_x	0.000169	2.09	1.75	NM_177667//XM_0065029	Ttc22	tetratricopeptide repeat domain 22	
1424617_x	0.000220	2.09	1.03	NM_001271416//NM_0012	Ly6a	lymphocyte antigen 6 complex, locus A	
1423323_x	0.000826	2.09	1.08	NM_001146308//NM_0011	Dbnl	debrin-like	
1418168_x	0.001205	2.09	1.43	NM_001048060//NM_1980	IdnK	idnK glucokinase homolog (E. coli)	
1435634_x	0.009715	2.09	-1.14	NM_010816	Morc1	microchroma 1	
1424948_x	0.000800	2.09	1.02	NM_133954//XM_0065305	Udb1	U6 snRNA biogenesis 1	
1419832_x	0.000800	2.09	1.23	NM_001289476//NM_00119	Psmo7	proteasome (prosome, macropain) subunit, alpha type 7	
1435974_x	0.003221	2.09	-1.50	NM_008654	Ppp115a	protein phosphatase 1, regulatory (inhibitor) subunit 15A	
1449132_x	0.000369	2.09	-1.20	NM_001122675//NM_0011	Zcchc2	zinc finger, CCHC domain containing 2	
1419692_x	0.001133	2.08	1.24	NM_001159521//NM_0012	Pknk2	plexin B2	
1426392_x	0.004359	2.08	-1.02	NM_001126047//XM_0064	Sema4c	sema domain, immunoglobulin domain (Ig), transmembrane domain (TM)	
1418146_x	0.002723	2.08	1.43	NM_013558	Hspa1l	heat shock protein 1-like	
1419519_x	0.004570	2.08	1.26	NM_008348	Il10ra	interleukin 10 receptor, alpha	
1422403_x	0.001179	2.08	1.12	NM_024456//XM_0065325	Rab5c	RAB5, member RAS oncogene family	
1417825_x	0.000098	2.08	1.52	NM_177073//XM_0065079	Relt	REL transmembrane receptor	
1419942_x	0.002026	2.07	1.23	NM_010579	Elf6	eukaryotic translation initiation factor 6	
1424932_x	0.002251	2.07	1.02	NM_001025599//NM_0012	Trim26	tripartite motif-containing 26	
1460121_x	0.002089	2.07	-3.74	NM_183201//XM_0065335	Sifn5	schlafen 5	
1455447_x	0.004793	2.07	-1.32	NM_178065//XM_0065161	Arel1	apoptosis resistant E3 ubiquitin protein ligase 1	
1417990_x	0.006119	2.07	1.48	NM_001168509//NM_0011	Fjar2	free fatty acid receptor 2	
1422787_x	0.006656	2.07	1.10	NM_028584//NM_212447	Maveld3	MARVEL (membrane-associated) domain containing 3	
1423569_x	0.005188	2.06	1.07	NM_001290518//NM_0252	Sk31a2	solute carrier family 31, member 2	
1420719_x	0.001905	2.06	1.19	NM_008909	Ppl	periplakin	
1419976_x	0.006828	2.06	1.22	NM_181820	Tmc4	transmembrane channel-like gene family 4	
1423251_x	0.008933	2.06	1.09	NM_009348//XM_0065269	Tectb	tectonin beta	
1417720_x	0.007874	2.06	1.55	NM_031198//XM_0065050	Tfec	transcription factor EC	
1420814_x	0.000624	2.06	1.19	NM_030207//XM_0065148	LOC100861749//Sfj1	protein SFH1 homolog, spindle assembly associated (yeast)	
1420657_x	0.005381	2.06	1.19	NM_028351	Rspo3	R-spondin 3 homolog (Xenopus laevis)	
1424552_x	0.002410	2.06	1.03	NM_001163704//NM_0011	Fbxo6	F-box protein 6	
1449174_x	0.005757	2.05	-1.20	NM_001164197//NM_0214	Mmp19	matrix metalloproteinase 19	
1419697_x	0.005721	2.05	1.24	NM_001291799//NM_0100	Dok1	docking protein 1	
1423455_x	0.001733	2.05	1.08	NM_175118	Dusp28	dual specificity phosphatase 28	
1438928_x	0.001248	2.05	-1.16	NM_029508//XM_0065274	Pcgef5	polycystomorph ring finger 5	
1423648_x	0.002166	2.05	1.07	NM_029720//XM_0065215	Crela2	cysteine-rich with EGF-like domains 2	
1427429_x	0.000412	2.05	-1.05	NM_030694	Ifitm2	interferon induced transmembrane protein 2	
1421521_x	0.000970	2.05	1.15	NM_001098271//NM_0253	Tmem176a	transmembrane protein 176A	
1420610_x	0.008334	2.05	1.20	NM_001024716//NM_0010	Triabp	TRIO and F-actin binding protein	
1420938_x	0.006638	2.04	1.18	NM_008967//XM_0065396	Ptgir	prostaglandin I receptor (IP)	
1419004_x	0.001650	2.04	1.31	NM_019388//XM_0065217	Cd86	CD86 antigen	
1419848_x	0.000114	2.04	1.23	NM_001294138//NM_0012	Gyk	glycerol kinase	
1427762_x	0.002673	2.04	-1.06	NM_001040026//XM_0065	Sos1	SCD cytochrome oxidase deficient homolog 1 (yeast)	
1423476_x	0.001722	2.04	1.08	NM_001033433//XM_0065	Nlrp12	NLR family, pyrin domain containing 12	
1451583_x	0.005975	2.04	-1.28	NM_001164047//NM_0011	Tgfb1	TGF-beta-induced factor homeobox 1	
1420659_x	0.009475	2.04	1.19	NM_134250//XM_0065323	Havcr2	hepatitis A virus cellular receptor 2	
1423723_x	0.008191	2.04	1.07	NM_133913	Chpf2	chondroitin polymerizing factor 2	
1418155_x	0.008205	2.03	1.43	NM_028195//XM_0065214	Cytl4	cytohesin 4	
1452076_x	0.004850	2.03	-1.29	NM_001024945//NM_0232	Qsax1	quiescin Q6 sulfhydryl oxidase 1	
1416831_x	0.001826	2.03	2.06	NM_018857//XM_0065246	Msln	mesothelin	
1419268_x	0.002306	2.03	1.28	NM_001287263//NM_0090	Mst1r	macrophage stimulating 1 receptor (c-met-related tyrosine kinase)	
1417826_x	0.007853	2.03	1.52	NM_177364//XM_0065147	Sh3pdx2b	SH3 and PX domains 2B	
1435420_x	0.005387	2.03	-1.13	NM_010119	Ehd1	EH-domain containing 1	
1420591_x	0.000871	2.03	1.20	NM_133783	Ptges2	prostaglandin E synthase 2	
1436336_x	0.004311	2.03	-1.14	NM_010907	Nfkbia	nuclear factor of kappa light polypeptide gene enhancer in B cells inhibitor,	

Table S7

Gene_ID	p (Corr)	FC-RSV 1 d	FC-RSV 5 d	RefSeq Transcript ID	Gene Symbol	Gene Title	Gene Ontology Biological Process
1419209_a	0.003761	2.02	1.29	NM_001278269//NM_01318	<i>Fyb</i>	FYN binding protein	0045576 // mast cell activation // inferred from mutant phenotype
1426062_a	0.001650	2.02	-1.01	NM_172142//XM_0065399	<i>Nfkbid</i>	nuclear factor of kappa light polypeptide gene enhancer in B cells inhibitor, interferon alpha 12//interferon alpha 12//interferon alpha 15//interferon heme binding protein 2	0006954 // inflammatory response // inferred from electronic annotation//0032088 // negative regulation of NF-kappaB transcription factor activity // inferred from direct assay//0033085 //
1427194_a	0.003265	2.02	-1.05	NM_008334//NM_008336	<i>Ifna11//Ifna12//Ifna15//Ifna18</i>		0002250 // adaptive immune response // not recorded//0002286 // T cell activation involved in immune response // inferred from direct assay//0002286 // T cell activation involved in
1416614_a	0.000921	2.02	2.41	NM_019487	<i>Hebp2</i>		0109117 // negative regulation of mitochondrial membrane potential // not recorded//00010940 // positive regulation of necrotic cell death // not recorded//0035794 // positive regulation of
1426751_s	0.003575	2.02	-1.03	NM_001097617//NM_1449	<i>C1s1</i>	complement component 1, s subcomponent	0002376 // immune system process // inferred from electronic annotation//0006508 // proteolysis // not recorded//0006596 // complement activation // inferred from electronic
1421208_a	0.000158	2.02	1.16	NM_009439	<i>Psmid3</i>	proteasome (prosome, macropain) 26S subunit, non-ATPase, 3	0042176 // regulation of protein catabolic process // inferred from electronic annotation//0005790 // regulation of catabolic activity // inferred from electronic annotation
1424465_a	0.009780	2.02	1.04	NM_001161798//NM_0108	<i>Mthfr</i>	5,10-methylenetetrahydrofolate reductase	0001666 // response to hypoxia // inferred from electronic annotation//0006555 // methionine metabolic process // inferred from electronic annotation//0008152 // metabolic process //
1420644_a	0.002700	2.02	1.19	NM_009728//XM_0065405	<i>Atp10a</i>	ATPase, class V, type 10A	0006810 // transport // inferred from electronic annotation//0006812 // cation transport // inferred from electronic annotation//0006869 // lipid transport // inferred from electronic
1426774_a	0.000184	2.01	-1.23	NM_0148620//NM_0278	<i>Gypc</i>	glycophorin C	
1418747_a	0.009762	2.01	1.34	NM_016853//XM_0065149	<i>Fibp1b</i>	FK506 binding protein 1b	
1420461_a	0.001796	2.01	-1.01	NM_001141932//NM_0011	<i>Bean1</i>	brain expressed, associated with Nedd4, 1	0000413 // protein peptidyl-prolyl isomerization // inferred from direct assay//0000413 // protein peptidyl-prolyl isomerization // not recorded//0002027 // regulation of heart rate //
1426939_a	0.000819	2.01	-1.04	NM_172722//XR_387561	<i>Noa25</i>	N(Alpha)-acetyltransferase 25, N(AtB) auxiliary subunit	
1423815_s	0.005803	2.01	1.06	NM_022424//XM_0065040	<i>Fndc4</i>	fibronectin type III domain containing 4	0009306 // protein secretion // inferred from electronic annotation
1425109_a	0.007919	2.00	1.01	NM_009196	<i>Slc16a1</i>	solute carrier family 16 (monocarboxylic acid transporters), member 1	
1422553_a	0.004228	2.00	1.12	NM_009642//XM_0065359	<i>Aqtrap</i>	angiotensin II, type I receptor-associated protein	0001666 // response to hypoxia // inferred from electronic annotation//0008217 // regulation of blood pressure // inferred from mutant phenotype//0038166 // angiotensin-inferred
1417868_a	0.001305	2.00	1.51	NM_030259	<i>Rlip12</i>	Rab interacting lysosomal protein-like 2	0003382 // epithelial cell morphogenesis // inferred from mutant phenotype//0006810 // transport // inferred from electronic annotation//0006886 // intracellular protein transport //
1420920_a	0.003681	2.00	1.18	NM_001282021//NM_0012	<i>Vasp</i>	vasodilator-stimulated phosphoprotein	0001843 // neural tube closure // inferred from genetic interaction//0007411 // axon guidance // inferred from genetic interaction//0008154 // actin polymerization or depolymerization //
1419949_a	0.000531	2.00	1.23	NM_001159631//NM_0216	<i>Nek6</i>	NIMA (never in mitosis gene a)-related expressed kinase 6	0006468 // protein phosphorylation // not recorded//0006915 // apoptotic process // inferred from electronic annotation//0007049 // cell cycle // inferred from electronic
1427381_a	0.001223	2.00	-1.05	NM_001081169//XM_0065	<i>Aspg</i>	asparaginase homolog (S. cerevisiae)	0006520 // cellular amino acid metabolic process // inferred from electronic annotation//0006528 // asparagine metabolic process // not recorded//0006629 // lipid metabolic process //
1426401_a	0.002652	2.00	-1.02	NM_001024139//XM_0065	<i>Adams15</i>	a disintegrin-like and metallopeptidase (reprolysin type) with	0006508 // proteolysis // inferred from electronic annotation
1417962_s	0.002487	1.99	1.49	NM_030060//XM_0064971	<i>Botf3</i>	basic leucine zipper transcription factor, ATF-like 3	0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 // regulation of transcription, DNA-templated // inferred from electronic annotation//0009615 //
1439647_a	0.006469	1.99	-1.59	NM_001159299//NM_0012	<i>Ith4</i>	inter alpha-trypsin inhibitor, heavy chain 4	0006953 // acute-phase response // inferred from electronic annotation//0001466 // negative regulation of peptidase activity // inferred from electronic annotation//0001095 // negative
1420635_s	0.001664	1.99	1.19	NM_021308//XM_0065193	<i>Piw12</i>	piw1-like RNA-mediated gene silencing 2	0009696 // RNA 5'-end processing // inferred from direct assay//0006417 // regulation of translation // inferred from electronic annotation//0007126 // meiotic nuclear division // inferred
1436472_a	0.007952	1.99	-1.51	NM_03303//XR_385971	<i>Cda1</i>	cysteine dioxygenase 1, cytosolic	0007595 // lactation // not recorded//00010243 // response to organonitrogen compound // not recorded//0019448 // L-cysteine catabolic process // not recorded//0019452 // L-cysteine
1418054_a	0.000445	1.99	1.46	NM_011050	<i>Mopk13</i>	mitogen-activated protein kinase 13	0000165 // MAPK cascade // not recorded//0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 // regulation of transcription, DNA-templated //
1423264_a	0.001736	1.99	1.09	NM_001190804//NM_0011	<i>Dnq1b1</i>	DnaI (Hsp40) homolog, subfamily B, member 11	0004547 // protein folding // inferred from electronic annotation//00016556 // mRNA modification // inferred from direct assay//00015556 // mRNA modification // not recorded
1423833_a	0.003056	1.98	1.06	NM_001243748//NM_0197	<i>Rassf1</i>	Ras association (RalGDS/AF-6) domain family member 1	0006974 // cellular response to DNA damage stimulus // not recorded//0007049 // cell cycle // inferred from electronic annotation//0007050 // cell cycle arrest // not recorded//000165
1416349_a	0.007378	1.98	3.06	NM_009777	<i>C1qb</i>	complement component 1, q subcomponent, beta polypeptide	0002376 // immune system process // inferred from electronic annotation//0006958 // complement activation, classical pathway // inferred from electronic annotation//00045087 // Innate
1416267_a	0.002056	1.98	3.42	NM_027163	<i>Il1f8</i>	interleukin 1 family, member 8	0001813 // positive regulation of cytokine production // inferred from direct assay//0006954 // inflammatory response // inferred from electronic annotation//0006955 // immune response
1419579_a	0.002130	1.98	1.25	NM_007798	<i>Ctsb</i>	cathepsin B	0006508 // proteolysis // not recorded//0030574 // collagen catabolic process // not recorded//0046697 // decidualization // inferred from genetic interaction//0005790 // regulation of
1419980_a	0.000213	1.98	1.22	NM_013623//XM_0065376	<i>Orm3</i>	orosomucoid 3	0002682 // regulation of immune system process // inferred from electronic annotation//0006810 // transport // inferred from electronic annotation
1426555_a	0.001511	1.98	-1.03	NM_144554//NM_175093	<i>Trib3</i>	tribbles homolog 3 (Drosophila)	0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 // regulation of transcription, DNA-templated // inferred from electronic annotation//0006468 //
1419272_a	0.000512	1.98	1.28	NM_007695//XM_0065291	<i>Chil1</i>	chitinase-like 1	0005975 // carbohydrate metabolic process // inferred from electronic annotation//0006032 // chitin catabolic process // inferred from electronic annotation//0006915 // apoptotic process
1421594_a	0.001865	1.97	1.15	NM_008533//XM_0065175	<i>Cd180</i>	CD180 antigen	0002322 // B cell proliferation involved in immune response // inferred from mutant phenotype//0002376 // immune system process // inferred from electronic annotation//0006954 //
1423857_a	0.002677	1.97	1.06	NM_007807//XM_0065275	<i>Cybb</i>	cytochrome b-245, beta polypeptide	0006801 // superoxide metabolic process // not recorded//0006810 // transport // inferred from electronic annotation//0006811 // ion transport // inferred from electronic
1451540_a	0.004622	1.97	-1.27	NM_0080639//XM_0065053	<i>Timp4</i>	tissue inhibitor of metalloproteinase 4	0007417 // central nervous system development // inferred from electronic annotation//0009725 // response to hormone // inferred from electronic annotation//00010466 // negative
1420607_a	0.009784	1.97	1.20	NM_001163440//NM_0011	<i>Mov10</i>	Maloney leukemia virus 10	0008152 // metabolic process // inferred from electronic annotation//00031047 // gene silencing by RNA // inferred from electronic annotation//00035279 // mRNA cleavage involved in gene
1418917_a	0.003886	1.97	1.32	NM_172442//XM_0065268	<i>Dtx4</i>	deltex 4 homolog (Drosophila)	0007219 // Notch signaling pathway // inferred from electronic annotation//00016567 // protein ubiquitination // inferred from electronic annotation
1416635_a	0.003951	1.97	2.32	NM_001290706//NM_0254	<i>Tmem54</i>	transmembrane protein 54	
1421052_a	0.000570	1.97	1.17	NM_010792//XM_0065133	<i>Mett11</i>	methyltransferase like 1	0006400 // tRNA modification // not recorded//0008033 // tRNA processing // inferred from electronic annotation//0030488 // tRNA methylation // not recorded//0032259 // methylation
1416241_a	0.006583	1.97	3.55	NM_026509	<i>Muc</i>	mucin-related coiled-coil protein	0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 // regulation of transcription, DNA-templated // inferred from electronic annotation//0007266 //
1417060_a	0.000239	1.96	1.84	NM_00126765//NM_0132	<i>Birc3</i>	cathepsin S	0002250 // adaptive immune response // inferred from electronic annotation//0006508 // proteolysis // inferred from direct assay//0006508 // proteolysis // not recorded//0030574 //
1422705_a	0.003536	1.96	1.11	NM_053015//XM_0065292	<i>Mplp1</i>	melanophilin	0006695 // protein targeting // inferred from mutant phenotype//0006886 // intracellular protein transport // inferred from electronic annotation//0030318 // melanocyte differentiation //
1431763_a	0.003419	1.96	-1.10	NM_001110305//NM_0011	<i>Keap1</i>	kelch-like ECH-associated protein 1	0001701 // in utero embryonic development // inferred from mutant phenotype//0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 // regulation of
1425609_a	0.000456	1.96	-1.00	NM_001252939//NM_0137	<i>Cars</i>	cysteinyl-RNA synthetase	0006412 // translation // inferred from electronic annotation//0006418 // tRNA aminoacylation for protein translation // inferred from electronic annotation//0004623 // cysteinyl-tRNA
1423140_a	0.005341	1.96	1.09	NM_010114//NM_010116	<i>Klk1822//Klk1b9</i>	kallikrein 1-related peptidase b22//kallikrein 1-related peptidase b9	0006508 // proteolysis // inferred from direct assay//0001638 // zymogen activation // inferred from direct assay
1435008_a	0.002218	1.96	-1.47	NM_145626//NM_181732	<i>Aida</i>	acid interactor, dorsalization associated	0007025 // multicellular organismal development // inferred from electronic annotation//0009953 // dorsal/ventral pattern formation // not recorded//0030178 // negative regulation of
1425699_a	0.001733	1.96	-1.00	NM_027869//XM_0065148	<i>Pnpt1</i>	polyribonucleotide nucleotidyltransferase 1	0000957 // mitochondrial RNA catabolic process // not recorded//0000958 // mitochondrial mRNA catabolic process // inferred from mutant phenotype//0000958 // mitochondrial mRNA
1424809_a	0.001119	1.96	-1.02	NM_001190473//NM_0011	<i>Dapk3</i>	death-associated protein kinase 3	0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 // regulation of transcription, DNA-templated // inferred from electronic annotation//0006468 //
1427150_a	0.009027	1.96	-1.05	NM_199299//XM_0065344	<i>Jade2</i>	jade family PHF finger 2	0043966 // histone H3 acetylation // not recorded//0043981 // histone H4-K5 acetylation // not recorded//0043982 // histone H4-K8 acetylation // not recorded//0043983 // histone H4-K12
1419898_s	0.000229	1.96	1.23	NM_011122	<i>Plod1</i>	procollagen-lysine, 2-oxoglutarate 5-dioxygenase 1	0001666 // response to hypoxia // inferred from electronic annotation//0008544 // epidermis development // not recorded//00017185 // peptidyl-lysine hydroxylation // not
1417567_a	0.004673	1.95	1.61	NM_011075//XM_0065035	<i>Abcb1b</i>	ATP-binding cassette, sub-family B (MDR/TAP), member 1B	0001666 // response to hypoxia // inferred from electronic annotation//0006200 // ATP catabolic process // not recorded//0006810 // transport // not recorded//0006855 // drug
1429054_a	0.009703	1.95	-1.08	NM_025821//XM_0065223	<i>Corhsp1</i>	calcium regulated heat stable protein 1	0006355 // regulation of transcription, DNA-templated // inferred from electronic annotation//0043488 // regulation of mRNA stability // inferred from mutant phenotype
1419407_a	0.000126	1.94	1.27	NM_025531//XM_0065000	<i>Simo2</i>	slowmo homolog 2 (Drosophila)	0015914 // phospholipid transport // not recorded
1423110_a	0.001142	1.94	1.09	NM_009272	<i>Srm</i>	spermidine synthase	0006596 // polyamine biosynthetic process // inferred from electronic annotation//0008152 // metabolic process // inferred from electronic annotation//0008295 // spermidine biosynthetic
1426287_a	0.003669	1.94	-1.02	NM_028838//XM_0065123	<i>Lrrc2</i>	leucine rich repeat containing 2	
1421027_a	0.001000	1.94	1.17	NM_019752	<i>Htra2</i>	Htra serine peptidase 2	0006508 // proteolysis // not recorded//0006672 // ceramide metabolic process // inferred from electronic annotation//0006915 // apoptotic process // inferred from electronic
1433706_a	0.001670	1.94	-1.11	NM_175382	<i>Fam72a</i>	family with sequence similarity 72, member A	0031552 // negative regulation of brain-derived neurotrophic factor-activated receptor activity // not recorded//0043065 // positive regulation of apoptotic process // not recorded
1421850_a	0.000050	1.94	1.14	NM_025021	<i>Ocmstap</i>	osteoclast stimulatory transmembrane protein	0031245 // cell differentiation // inferred from electronic annotation//0034241 // positive regulation of macrophage fusion // inferred from genetic interaction//0045672 // positive
1421824_a	0.000158	1.94	1.14	NM_146217//XM_0065309	<i>Aors1//Exoc6</i>	alanyl-RNA synthetase//exosome component 6	0001942 // hair follicle development // inferred from mutant phenotype//0006364 // RNA processing // inferred from electronic annotation//0006400 // tRNA modification // inferred from
1425226_x	0.000184	1.93	1.01	NM_009373	<i>Tgm2</i>	transglutaminase 2, C polypeptide	0001974 // blood vessel remodeling // not recorded//0007186 // G-protein coupled receptor signaling pathway // traceable author statements//0007200 // phospholipase C-activating G-
1416592_a	0.000181	1.93	2.42	NM_001032298//NM_0010	<i>Bglap1//Bglap2//Bglap3</i>	bone gamma-carboxylglutamate protein//bone gamma-carboxylglutamate	0030500 // regulation of bone mineralization // inferred from electronic annotation//0031016 // pancreas development // inferred from mutant phenotype//0031214 // biomineral tissue
1420183_a	0.000023	1.93	1.22	NM_001037539//NM_0011	<i>Prkx2</i>	prokinectin 2	0001525 // angiogenesis // not recorded//0003349 // epicardium-derived cardiac endothelial cell differentiation // traceable author statements//0006935 // chemotaxis // not
1429490_a	0.009108	1.93	-1.09	NM_138952//XM_0065376	<i>Ripk2</i>	receptor (TNFRSF)-interacting serine-threonine kinase 2	0001961 // positive regulation of cytokine-mediated signaling pathway // inferred from mutant phenotype//0002250 // adaptive immune response // inferred from mutant
1423452_a	0.005879	1.93	1.08	NM_133801//XM_0065251	<i>Gt2f1</i>	general transcription factor IIF, polypeptide 1	0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 // regulation of transcription, DNA-templated // inferred from electronic annotation//0006367 //
1435335_a	0.004848	1.92	-1.13	NM_001271616//NM_0080	<i>Fgfbp1</i>	fibroblast growth factor binding protein 1	0007267 // cell-cell signaling // not recorded//0008284 // positive regulation of cell proliferation // inferred from genetic interaction//0045743 // positive regulation of fibroblast growth
1449628_s	0.005512	1.92	-1.22	NM_031380//XM_0065143	<i>Fst3</i>	folistatin-like 3	0001503 // ossification // inferred from electronic annotation//0001822 // kidney development // inferred from electronic annotation//0002244 // hematopoietic progenitor cell
1419214_a	0.001589	1.92	1.29	NM_0103030//XM_0065334	<i>Slc9a3r1</i>	solute carrier family 9 (sodium/hydrogen exchanger), member 3 regulator 1	0003096 // renal sodium ion transport // inferred from mutant phenotype//0007191 // adenylate cyclase-activating dopamine receptor signaling pathway // inferred from mutant
1420074_a	0.001893	1.92	1.22	NM_001291128//NM_0012	<i>Nnat</i>	neuronal	0007275 // multicellular organismal development // inferred from electronic annotation//0007420 // brain development // inferred from electronic annotation//0009749 // response to
1420854_a	0.002322	1.92	1.18	NM_175207//XM_0065162	<i>Ankrd9</i>	ankyrin repeat domain 9	0008152 // metabolic process // inferred from electronic annotation
1422411_s	0.000219	1.92	1.12	NM_001146161//NM_0087	<i>Slc11a2</i>	solute carrier family 11 (proton-coupled divalent metal ion transporters),	0000041 // transition metal ion transport // not recorded//0001666 // response to hypoxia // inferred from electronic annotation//0003032 // detection of oxygen // inferred from electronic
1419613_a	0.009810	1.92	1.25	NM_001101340//NM_0011	<i>Psmg4</i>	proteasome (prosome, macropain) assembly chaperone 4	
1428766_a	0.003143	1.92	-1.08	NM_001163346//NM_0200	<i>Cdc42ep4</i>	CD42 activating protein (Rho GTPase binding) 4	0007266 // Rho protein signal transduction // inferred from direct assay//0008360 // regulation of cell shape // not recorded//0031274 // positive regulation of pseudopodium assembly //
1425067_a	0.005265	1.92	1.01	NM_001271411//NM_0012	<i>Nfiam1</i>	Nfai2 factor molecule with ITAM motif 1	0007165 // signal transduction // not recorded//0007165 // signal transduction // inferred from sequence or structural similarity//0030183 // B cell differentiation // inferred from mutant
1421571_a	0.000023	1.91	1.15	NM_001293728//NM_0116	<i>Tu1f1</i>	tufelin 1	0032114 // biomineral tissue development // inferred from electronic annotation
1423537_a	0.001001	1.91	1.08	NM_028064//NM_005214	<i>Slc39a9</i>	slc39 family member 9 (zinc transporter), member 4	0006810 // transport // inferred from electronic annotation//0006811 // ion transport // inferred from electronic annotation//0006829 // zinc ion transport // inferred from direct
1426794_a	0.000445	1.91	-1.03	NM_010757//XM_0065046	<i>Mafk</i>	v-maf musculoaponeurotic fibrosarcoma oncogene family, protein K (avian)	0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 // regulation of transcription, DNA-templated // inferred from direct assay//0007399 // nervous
1418735_a	0.000016	1.91	1.35	NM_001289531//NM_0231	<i>Cndp2</i>	CNDP dipeptidase 2 (metallopeptidase M20 family)	0006508 // proteolysis // inferred from direct assay//0006508 // proteolysis // not recorded//0008152 // metabolic process // inferred from electronic annotation
1418753_a	0.004010	1.91	1.34	NM_010877//XM_0065292	<i>Nc2</i>	neurophil cytosolic factor 2	0006742 // NADP catabolic process // not recorded//0006801 // superoxide metabolic process // not recorded//0007568 // aging // inferred from electronic annotation//0009749 //
1424976_a	0.003093	1.91	1.02	NM_007381	<i>Acadl</i>	acyl-Coenzyme A dehydrogenase, long-chain	0001659 // temperature homeostasis // inferred from mutant phenotype//0006629 // lipid metabolic process // inferred from electronic annotation//0006631 // fatty acid metabolic process
1419376_a	0.009468	1.91	1.27	NM_016720	<i>Neu3</i>	neuraminidase 3	0005975 // carbohydrate metabolic process // not recorded//0006629 // lipid metabolic process // inferred from electronic annotation//0006689 // ganglioside catabolic process // not
1436241_s	0.005918	1.91	-1.14	NM_181848//XM_0064975	<i>Optn</i>	optineurin	0000042 // protein targeting to Golgi // not recorded//0007030 // Golgi organization // not recorded//0008284 // positive regulation of cell proliferation // not recorded//0034613 // cellular
1426223_a	0.001277	1.90	-1.02	NM_010758//XM_0065323	<i>Mafg</i>	v-maf musculoaponeurotic fibrosarcoma oncogene family, protein G (avian)	0000122 // negative regulation of transcription from RNA polymerase II promoter // inferred from electronic annotation//0000122 // negative regulation of transcription from RNA polymerase
1416556_a	0.002911	1.90	2.45	NM_008156	<i>Gpld1</i>		

Table S7

Gene ID	p (Corr)	FC-RSV 1 d	FC-RSV 5 d	RefSeq Transcript ID	Gene Symbol	Gene Title	Gene Ontology Biological Process
1417189_a	0.001060	1.90	1.77	NM_001001999//NM_0103	Gp1bb//Sept5	glycoprotein Ib, beta polypeptide//septin 5	0007049 // cell cycle // inferred from electronic annotation//0007155 // cell adhesion // inferred from sequence or structural similarity//0007596 // blood coagulation // inferred from
1420476_a	0.003063	1.90	1.20	NM_172488//XM_0065187	Lcc1	laccase (multicopper oxidoreductase) domain containing 1	
1427096_x	0.001616	1.90	-1.05	NM_008334//NM_008336	Ifna11//Ifna12//Ifna15//Ifna	interferon alpha 11//interferon alpha 12//interferon alpha 15//interferon	0002250 // adaptive immune response // not recorded//0002286 // T cell activation involved in immune response // inferred from direct assay//0002286 // T cell activation involved in
1425182_x	0.006369	1.90	1.01	NM_007413	Adora2b	adenosine A2b receptor	0001973 // adenosine receptor signaling pathway // not recorded//0002882 // positive regulation of chronic inflammatory response to non-antigenic stimulus // inferred from mutant
1417191_a	0.002359	1.89	1.76	NM_016749//XM_0065297	Mybph	myosin binding protein H	0007155 // cell adhesion // inferred from electronic annotation
1417700_a	0.005396	1.89	1.56	NM_015789//XM_0065409	Dkl1	dyckin-like 1	0045600 // positive regulation of fat cell differentiation // inferred from direct assay
1451852_a	0.006508	1.89	-1.28	NM_019549	Plek	pleckstrin	0002244 // hematopoietic progenitor cell differentiation // inferred from electronic annotation//0002576 // platelet degranulation // inferred from electronic annotation//0006904 // vesicle
1416624_a	0.002311	1.89	2.35	NM_054074	Defb6	defensin beta 6	0006952 // defense response // inferred from electronic annotation//0042742 // defense response to bacterium // inferred from electronic annotation//00050829 // defense response to
1415640_a	0.006311	1.89	1.24	NM_010166//NM_210071	Eya3	eyes absent 3 homolog (Drosophila)	0006281 // DNA repair // inferred from electronic annotation//0006302 // double-strand break repair // not recorded//0006351 // transcription, DNA-templated // inferred from electronic
1423656_a	0.006752	1.89	1.07	NM_00116420//NM_0011	Tmem176b	transmembrane protein 176b	0030154 // cell differentiation // inferred from electronic annotation//2001439 // negative regulation of dendritic cell differentiation // inferred from mutant phenotype
1427469_a	0.003103	1.89	-1.05	NM_173036//XM_0065311	Gpr97	G protein-coupled receptor 97	0007165 // signal transduction // inferred from electronic annotation//0007166 // cell surface receptor signaling pathway // inferred from electronic annotation//0007186 // G-protein
1425644_a	0.007777	1.89	-1.00	NM_023587//XM_0065225	Ptpib	protein tyrosine phosphatase-like (proline instead of catalytic arginine),	0006629 // lipid metabolic process // inferred from electronic annotation//0006631 // fatty acid metabolic process // inferred from electronic annotation//0006633 // fatty acid biosynthetic
1424657_a	0.004323	1.88	1.03	NM_001039720//NR_10804	9030619P08Rik	lymphocyte antigen 6 complex pseudogene	
1423154_a	0.003595	1.88	1.09	NM_001110498//NM_0105	Ifnar2	interferon (alpha and beta) receptor 2	0006357 // regulation of transcription from RNA polymerase II promoter // inferred from direct assay//0008283 // cell proliferation // inferred from direct assay//0035455 // response to
1424972_a	0.001068	1.88	1.02	NM_008519//XM_0065186	Ltb4r1	leukotriene B4 receptor 1	0006954 // inflammatory response // inferred from electronic annotation//0007165 // signal transduction // inferred from direct assay//0007186 // G-protein coupled receptor signaling
1416857_a	0.000719	1.88	2.03	NM_001093749//NM_1769	Mpz13	myelin protein zero-like 3	0007155 // cell adhesion // inferred from electronic annotation//0030198 // extracellular matrix organization // inferred from mutant phenotype//0042633 // hair cycle // inferred from
1418074_a	0.007878	1.88	1.46	NM_177613//XM_0065134	Cdc34	cell division cycle 34	0000209 // protein polyubiquitination // not recorded//0006513 // protein monoubiquitination // inferred from sequence or structural similarity//0007049 // cell cycle // inferred from
1417739_a	0.007191	1.88	1.55	NM_001142965	9630041G16Rik//Frrs1	RIKEN cDNA 9630041G16 gene//ferric-chelate reductase 1 like	
1419799_a	0.000827	1.87	1.23	NM_119928//XM_0065410	Kik4	kalikrein related-peptidase 4 (protease, enamel matrix, prostate)	0006508 // proteolysis // inferred from electronic annotation//0022617 // extracellular matrix disassembly // inferred from mutant phenotype//0030163 // protein catabolic process //
1419158_a	0.007641	1.87	1.30	NM_133982	Rpp25	ribonuclease P/MRP 25 subunit	0008033 // RNA processing // inferred from electronic annotation//0009050 // RNA phosphodiester bond hydrolysis // inferred from electronic annotation//0009502 // RNA phosphodiester
1437921_x	0.001527	1.87	-1.54	NM_133990	Il13ro1	interleukin 13 receptor, alpha 1	0002639 // positive regulation of immunoglobulin production // inferred from electronic annotation//0019221 // cytokine-mediated signaling pathway // inferred from electronic
1423442_a	0.005848	1.87	1.08	NM_001163747//NM_0284	Tmem192	transmembrane protein 192	
1425394_a	0.002684	1.87	1.00	NM_009671//XM_0065320	Ankyf1	ankyrin repeat and FYVE domain containing 1	0006897 // endocytosis // non-traceable author statement
1434987_a	0.007318	1.87	-1.13	NM_001135149//NM_0011	Slc39a8	solute carrier family 39 (metal ion transporter), member 8	0006810 // transport // inferred from electronic annotation//0006811 // ion transport // inferred from electronic annotation//0006829 // zinc ion transport // not recorded//0030001 //
1421842_a	0.006549	1.87	-1.14	NM_026738//XM_0065169	1110007C09Rik	RIKEN cDNA 1110007C09 gene	0042981 // regulation of apoptotic process // inferred from electronic annotation
1418624_a	0.001243	1.87	1.36	NM_009399//XM_0065293	Tnfrsf11a	tumor necrosis factor receptor superfamily, member 11a, NFKB activator	0001503 // ossification // inferred from mutant phenotype//0002250 // adaptive immune response // not recorded//0007275 // multicellular organismal development // inferred from
1434513_a	0.003687	1.86	-1.13	NM_019786	Tbk1	TANK-binding kinase 1	0002218 // activation of innate immune response // inferred from mutant phenotype//0002376 // immune system process // inferred from electronic annotation//0006468 // protein
1423459_a	0.005333	1.86	1.08	NM_001195023//NM_1994	Nplca4	nuclear protein localization 4 homolog (S. cerevisiae)	0007030 // Golgi organization // not recorded//0030433 // ER-associated ubiquitin-dependent protein catabolic process // inferred from sequence or structural similarity//0043161 //
1428657_a	0.002056	1.86	-1.08	NM_028472	Bmper	BMP-binding endothelial regulator	0001657 // ureteric bud development // inferred from expression pattern//0002043 // blood vessel endothelial cell proliferation involved in sprouting angiogenesis // not recorded//0010594
1418511_a	0.000053	1.86	1.38	NM_138310//XM_0065073	Apobir	apolipoprotein B receptor	0006629 // lipid metabolic process // inferred from electronic annotation//0006641 // triglyceride metabolic process // inferred from direct assay//0006810 // transport // inferred from
1435193_a	0.002564	1.86	-1.13	NM_145495//XM_0065317	Rin1	Ras and Rab interactor 1	0006897 // endocytosis // inferred from electronic annotation//0007165 // signal transduction // inferred from electronic annotation//0007613 // memory // inferred from mutant
1423292_a	0.002589	1.86	1.08	NM_008334//NM_008336	Ifna11//Ifna12//Ifna15//Ifna	interferon alpha 11//interferon alpha 12//interferon alpha 15//interferon	0002250 // adaptive immune response // not recorded//0002286 // T cell activation involved in immune response // inferred from direct assay//0002286 // T cell activation involved in
1421448_a	0.002359	1.86	1.15	NM_00105196//NM_0011	Tje3	transcription factor E3	0002376 // immune system process // inferred from electronic annotation//0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 // regulation of
1434792_a	0.002862	1.86	-1.46	NM_001199043//NM_0012	Lgals8	lectrin, galactose binding, soluble 8	0002317 // plasma cell differentiation // inferred from direct assay//0031295 // T cell costimulation // inferred from direct assay//0006816 // calcium ion transport // inferred from electronic
1432198_a	0.009636	1.86	-1.42	NM_153566	Yrdc	yrdc domain containing (E.coli)	0051051 // negative regulation of transport // not recorded
1418535_a	0.004128	1.86	1.37	NM_001161428//NM_0194	Unc93b1	unc-93 homolog B1 (C. elegans)	0002224 // toll-like receptor signaling pathway // inferred from mutant phenotype//0002376 // immune system process // inferred from electronic annotation//0006886 // intracellular
1420922_a	0.008086	1.86	1.18	NM_198411//XM_0065162	Inf2	inverted form, FH2 and WH2 domain containing	0016043 // cellular component organization // inferred from electronic annotation//0030036 // actin cytoskeleton organization // inferred from electronic annotation//0002535 // regulation
1418560_a	0.002697	1.86	1.37	NM_153570	Noc4l	nuclear complex associated 4 homolog (S. cerevisiae)	0042254 // ribosome biogenesis // inferred from electronic annotation
1420465_x	0.007846	1.86	1.20	NM_011521	Sdc4	syndecan 4	0001657 // ureteric bud development // inferred from electronic annotation//0007165 // signal transduction // not recorded//0045860 // positive regulation of protein kinase activity // not
1440901_a	0.001616	1.85	-1.63	NM_013599//XM_0064988	Mmp9	matrix metalloproteinase 9	0001501 // skeletal system development // inferred from genetic interaction//0001501 // skeletal system development // inferred from mutant phenotype//0001503 // ossification //
1419584_a	0.000023	1.85	1.25	NM_00107741//NM_0080	Gma	glucosidase, beta, acid	0005975 // carbohydrate metabolic process // inferred from electronic annotation//0006629 // lipid metabolic process // inferred from electronic annotation//0006665 // sphingolipid
1418894_x	0.001504	1.85	1.32	NM_001120456//NM_0136	Sema6b	sema domain, transmembrane domain (TM), and cytoplasmic domain,	0007275 // multicellular organismal development // inferred from electronic annotation//0007399 // nervous system development // inferred from electronic annotation//0030154 // cell
1426195_a	0.008783	1.85	-1.01	NM_023362	Chmp4b	charged multivesicular body protein 4b	0006620 // posttranslational protein targeting to membrane // not recorded//0006810 // transport // inferred from electronic annotation//0015031 // protein transport // inferred from
1417942_a	0.000921	1.85	1.50	NM_001136471//NM_1722	Ccdc9	coiled-coil domain containing 9	
1423997_a	0.005114	1.85	1.05	NM_001093754//NM_0012	Denn2d2	DENN/MADD domain containing 2D	0002313 // regulation of Rab GTPase activity // not recorded//0032851 // positive regulation of Rab GTPase activity // inferred from sequence or structural similarity//0032851 // positive
1422617_a	0.006230	1.85	1.11	NM_009137	Ccl22	chemokine (C-C motif) ligand 22	0006935 // chemotaxis // inferred from electronic annotation//0006954 // inflammatory response // inferred from electronic annotation//0006955 // immune response // inferred from
1417825_a	0.000098	1.85	1.53	NM_013834//XM_0065090	Sfrp1	secreted frizzled-related protein 1	0001649 // osteoblast differentiation // inferred from electronic annotation//0001657 // ureteric bud development // inferred from expression pattern//0001756 // somitogenesis // inferred
1425861_x	0.000473	1.84	-1.01	NM_001177901//NM_1753	Zfp513	zinc finger protein 513	0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 // regulation of transcription, DNA-templated // inferred from electronic annotation//0006041 //
1449277_a	0.000545	1.84	-1.21	NM_001177730//NM_0138	Nr1h3	nuclear receptor subfamily 1, group H, member 3	0000122 // negative regulation of transcription from RNA polymerase II promoter // inferred from direct assay//0006351 // transcription, DNA-templated // inferred from electronic
1418014_a	0.009350	1.84	1.48	NR_028589//NR_028590//	Gm14005	predicted gene 14005	
1417307_a	0.000620	1.84	1.72	NM_178595//XR_374104	Pth1	peptidyl-tRNA hydrolase 1 homolog (S. cerevisiae)	0008152 // metabolic process // inferred from electronic annotation
1421752_a	0.000837	1.84	1.14	NM_008950	Psmc5	protease (prosome, macropain) 26S subunit, ATPase 5	0006200 // ATP catabolic process // not recorded//0006281 // DNA repair // inferred from electronic annotation//0006310 // DNA recombination // inferred from electronic
1421542_a	0.003758	1.84	1.15	NM_0111660	Txn1	thioredoxin 1	0000122 // negative regulation of transcription from RNA polymerase II promoter // inferred from genetic interaction//0006351 // transcription, DNA-templated // inferred from electronic
1417533_a	0.001606	1.84	1.62	NM_001109657//NM_0012	Gas7	growth arrest specific 7	0007275 // multicellular organismal development // inferred from electronic annotation//0007399 // nervous system development // inferred from electronic annotation//0003600 //
1418206_a	0.001409	1.84	1.42	NM_053214	Myo1f	myosin IF	0002446 // neutrophil mediated immunity // inferred from mutant phenotype//0007162 // negative regulation of cell adhesion // inferred from mutant phenotype//0008152 // metabolic
1425525_a	0.008022	1.84	-1.00	NM_001045529//XM_0065	Morc3	microorchidia 3	0006468 // protein phosphorylation // not recorded//0007569 // cell aging // not recorded//0007991 // post-embryonic development // inferred from mutant phenotype//0018105 //
1421618_a	0.007605	1.84	1.15	NM_001141981//NM_0011	Rbm43	RNA binding motif protein 43	
1442461_a	0.007151	1.84	-1.68	NM_008343	Igf1rp3	insulin-like growth factor binding protein 3	0001558 // regulation of cell growth // inferred from genetic interaction//0001649 // osteoblast differentiation // inferred from expression pattern//0001933 // negative regulation of protein
1422135_a	0.002911	1.84	1.13	NM_145501//XR_386524	Phk2a	phosphatidylinositol 4-kinase type 2 alpha	0002554 // basophil degranulation // not recorded//0006661 // phosphatidylinositol biosynthetic process // not recorded//0016310 // phosphorylation // inferred from electronic
1428082_a	0.002906	1.84	-1.07	NM_0111330	Ccl11	chemokine (C-C motif) ligand 11	0001938 // positive regulation of endothelial cell proliferation // not recorded//0002544 // chronic inflammatory response // inferred from electronic annotation//0002551 // mast cell
1420338_a	0.009676	1.84	1.21	NM_009663	Aloxap	arachidonate 5-lipoxygenase activating protein	0002540 // leukotriene production involved in inflammatory response // inferred from mutant phenotype//0002675 // positive regulation of acute inflammatory response // not
1423037_a	0.000260	1.83	1.10	NM_001033136//XM_0065	Rmdn3	regulator of microtubule dynamics 3	0006874 // cellular calcium ion homeostasis // not recorded//0006915 // apoptotic process // inferred from electronic annotation//0030154 // cell differentiation // inferred from electronic
1419764_a	0.004014	1.83	1.23	NM_011141	Pou3f1	POU domain, class 3, transcription factor 1	0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 // regulation of transcription, DNA-templated // inferred from electronic annotation//0006366 //
1424397_a	0.009810	1.83	1.04	NM_028617//XM_0065097	Mvb12a	multivesicular body subunit 12A	0006810 // transport // inferred from electronic annotation//0015033 // protein transport // inferred from electronic annotation//0042058 // regulation of epidermal growth factor receptor
1417673_a	0.000161	1.83	1.57	NM_024246//XM_0065021	Tmem79	transmembrane protein 79	0002070 // epithelial cell maturation // inferred from mutant phenotype//0031069 // hair follicle morphogenesis // inferred from mutant phenotype//0042335 // cuticle development //
1416978_a	0.001237	1.83	1.89	NM_001168274//NM_0289	Gsdmc2//Gsdmc4	gasterdin C2//gasterdin C4	0006576 // intestinal epithelial cell development // inferred from expression pattern
1421426_a	0.000610	1.83	1.15	NM_011186	Psmb5	proteasome (prosome, macropain) subunit, beta type 5	0006508 // proteolysis // inferred from electronic annotation//0006979 // response to oxidative stress // inferred from direct assay//0043161 // proteasome-mediated ubiquitin-dependent
1419678_a	0.009613	1.83	1.24	NM_138677//XM_0065057	Edem1	ER degradation enhancer, mannosidase alpha-like 1	0006986 // response to unfolded protein // inferred from electronic annotation//0030433 // ER-associated ubiquitin-dependent protein catabolic process // inferred from direct assay
1435800_a	0.009566	1.83	-1.14	NM_002105052//NM_0012	Jdp2	jun dimerization protein 2	0000122 // negative regulation of transcription from RNA polymerase II promoter // inferred from direct assay//0000122 // negative regulation of transcription from RNA polymerase II
1423373_a	0.005179	1.83	1.08	NM_030743//XM_0065004	Rnf114	ring finger protein 114	0007275 // multicellular organismal development // inferred from electronic annotation//0007283 // spermatogenesis // inferred from electronic annotation//0016567 // protein
1419630_a	0.002751	1.83	1.25	NM_025878//XM_0065248	Mpr18b	mitochondrial ribosomal protein S18b	0006412 // translation // inferred from electronic annotation
1417501_a	0.000417	1.83	1.62	NM_173008//XM_0065400	Ssc5d	scavenger receptor cysteine rich domain containing (5 domains)	0002376 // immune system process // inferred from electronic annotation//0006898 // receptor-mediated endocytosis // inferred from direct assay//0006952 // defense response // inferred
1423847_a	0.002930	1.82	1.06	NM_001289568//NM_0012	Soss6	spindle assembly 6 homolog (C. elegans)	0007049 // cell cycle // inferred from electronic annotation//0007099 // centriole replication // not recorded//0051298 // centrosome duplication // not recorded
1419404_x	0.002862	1.82	1.27	NM_001081274//NM_0258	Pgd	phosphogluconate dehydrogenase	0006098 // pentose-phosphate shunt // inferred from electronic annotation//0009051 // pentose-phosphate shunt, oxidative branch // not recorded//0019322 // pentose biosynthetic
1421299_a	0.009528	1.82	1.16	NM_031181//XM_0065413	Slglecte	sialic acid binding Ig-like lectin E	0007155 // cell adhesion // inferred from direct assay//0035556 // intracellular signal transduction // inferred from physical interaction
1419480_a	0.000637	1.82	1.26	NM_010909//XM_0065327	Nfkb1	nuclear factor of kappa light polypeptide gene enhancer in B cells inhibitor	0007249 // I-kappaB kinase/NF-kappaB signaling // inferred from direct assay//0031665 // negative regulation of lipopolysaccharide-mediated signaling pathway // not recorded//0032088 //
1421307_a	0.000355	1.82	1.16	NM_145402//XM_0065387	Tmem51	transmembrane protein 51	
1423090_x	0.006331	1.82	1.09	NM_013586	Lnc3	lysyl oxidase-like 3	001837 // epithelial to mesenchymal transition // not recorded//0006898 // receptor-mediated endocytosis // inferred from electronic annotation//0045892 // negative regulation of
1420798_x	0.007879	1.81	1.19	NM_001172100//NM_0011	Rnh1	ribonuclease/angiogenesis inhibitor 1	0043086 // negative regulation of catalytic activity // not recorded//0004765 // regulation of angiogenesis // not recorded
1421642_a	0.005329	1.81	1.15	NM_009068//XM_0065166	Ripk1	receptor (TNFRSF)-interacting serine-threonine kinase 1	001934 // positive regulation of protein phosphorylation // not recorded//0006468 // protein phosphorylation // inferred from electronic annotation//0006915 // apoptotic process // not
1424569_a	0.009475	1.81	1.03	NM_010431//XM_0065154	Hif1a	hypoxia inducible factor 1, alpha subunit	0001525 // angiogenesis // inferred from mutant phenotype//0001568 // blood vessel development // inferred from mutant phenotype//0001666 // response to hypoxia // inferred from
1424215_a	0.007896	1.81	-1.12	NM_011835//XM_0065127	Katn1	katanin p60 (ATPase-containing) subunit A1	0001578 // microtubule bundle formation // inferred from genetic interaction//0001764 // neuron migration // inferred from mutant phenotype//0006200 // ATP catabolic process //
1429104_a	0.006143	1.81	-1.09	NM_001004185//Serpin1a1c//Serpi	Whamm	WAS protein homolog associated with actin, golgi membranes and	0007015 // actin filament organization // inferred from electronic annotation
1422224_a	0.002257	1.81	1.13	NM_009244//NM_009245	Serpin1b1//Serpin1a1c//Serpi	serine (or cysteine) peptidase inhibitor, clade A, member 1B//serine (or	0001701 // in utero embryonic development // inferred from mutant phenotype//0006487 // protein N-linked glycosylation // inferred from direct assay//0006953 // acute-phase response //
1422719_x	0.007375	1.81	1.11	NM_026111//NM_207677	Dedd2	death effector domain-containing DNA binding protein 2	0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 // regulation of transcription, DNA-templated // inferred from electronic annotation//0006915 //
1421152_a	0.004033	1.81	1.17	NM_008510	Xcl1	chemokine (C motif) ligand 1	0001916 // positive regulation of T cell mediated cytotoxicity // not recorded//0002690 // positive regulation of leukocyte chemotaxis // inferred from direct assay//0002725 // negative
1422639_a	0.000600	1.81	1.11	NM_145968//NM_147155	Tagap1	T cell activation Rho GTPase activating protein//T cell activation GTPase	0007165 // signal transduction // inferred from electronic annotation//0043547 // positive regulation of GTPase activity // inferred from electronic annotation
1426257_a	0.005079	1.81	-1.02	NM_008334//NM_008336	Ifna11//Ifna12//Ifna15//Ifna		

Table S7

Gene ID	p (Corr)	FC-RSV 1 d	FC-RSV 5 d	RefSeq Transcript ID	Gene Symbol	Gene Title	Gene Ontology Biological Process
1421256_a	0.002166	1.81	1.16	NM_027873	Ubiad1	UBA1 prenyltransferase domain containing 1	0001885 // endothelial cell development // inferred from sequence or structural similarity//0006744 // ubiquinone biosynthetic process // not recorded//0009234 // menaquinone
1425576_a	0.008334	1.81	-1.00	NM_001166372//NM_0011	42430	membrane-associated ring finger (3CHCA) 1	0002029 // protein polyubiquitination // inferred from direct assay//0000209 // protein polyubiquitination // not recorded//0002376 // immune system process // inferred from electronic
1450444_a	0.003272	1.81	-1.24	NM_007865//X/M_0065235	Dil1	delta-like 1 (Drosophila)	001701 // in utero embryonic development // not traceable author statement//0001756 // somitogenesis // inferred from genetic interaction//0001757 // somite specification // inferred
1422684_a	0.000751	1.80	1.11	NM_021297	Tlr4	toll-like receptor 4	0000187 // activation of MAPK activity // inferred from mutant phenotype//0001774 // microglial cell activation // not recorded//0000218 // activation of innate immune response // inferred
1418273_a	0.000279	1.80	1.41	NM_008175	Gm	granulin	0000398 // mRNA splicing, via spliceosome // not recorded//0000398 // mRNA splicing, via spliceosome // ---//0001835 // blastocyst hatching // inferred from direct assay//0006369 //
1418157_a	0.009343	1.80	1.43	NM_01080944//X/M_0064	Atp8b4	ATPase, class I, type 8B, member 4	0006812 // cation transport // inferred from electronic annotation//0008152 // metabolic process // inferred from electronic annotation//0015914 // phospholipid transport // inferred from
1429537_a	0.006333	1.80	-1.38	NM_008871//X/M_0065090	Plat	plasminogen activator, tissue	0001666 // response to hypoxia // inferred from mutant phenotype//0006508 // proteolysis // inferred from direct assay//0006508 // proteolysis // not recorded//0014909 // smooth
1425583_a	0.007252	1.80	-1.00	NM_001285423//NM_0169	Esdl//GmZ904	esterase D/formylglutathione hydrolase//predicted pseudogene Z904	0006508 // proteolysis // inferred from electronic annotation//0046294 // formaldehyde catabolic process // inferred from electronic annotation
1415607_a	0.001591	1.80	1.25	NM_001109748//NM_0168	Tomm40	translocase of outer mitochondrial membrane 40 homolog (yeast)	0006626 // protein targeting to mitochondrion // not recorded//0006810 // transport // inferred from electronic annotation//0006811 // ion transport // inferred from electronic
1420429_a	0.003833	1.80	1.21	NM_130886//X/M_0065323	Card14	caspase recruitment domain family, member 14	0001934 // positive regulation of protein phosphorylation // not recorded//0006915 // apoptotic process // inferred from electronic annotation//0003209 // tumor necrosis factor-mediated
1420495_a	0.005146	1.80	1.20	NM_028421//X/M_028864	Zc3hov1	protein CCHC type, antiviral 1	0002376 // immune system process // inferred from electronic annotation//0008152 // metabolic process // inferred from electronic annotation//0009615 // response to virus // not
1418326_a	0.004128	1.80	1.40	NM_009151//X/M_0065302	Seleplg	selectin, platelet (p-selectin) ligand	0007155 // cell adhesion // inferred from electronic annotation//0005090 // leukocyte tethering or rolling // inferred from mutant phenotype//0005092 // leukocyte adhesive activation //
1418912_a	0.000676	1.80	1.32	NM_001003911//X/M_0065	Adams7	a disintegrin-like and metallopeptidase (reprolysin type) with src-like adaptor	0006508 // proteolysis // inferred from direct assay//0032331 // negative regulation of chondrocyte differentiation // not recorded//0051603 // proteolysis involved in cellular protein
1433880_a	0.006039	1.80	-1.12	NM_001029841//NM_0091	Sla	hook homolog 2 (Drosophila)	0006810 // transport // inferred from electronic annotation//0007032 // endosome organization // not recorded//0007040 // lysosome organization // not recorded//0008333 // endosome
1421828_a	0.002432	1.80	1.14	NM_001167991//NM_1332	Hook2	hook homolog 2 (Drosophila)	0018108 // peptidyl-tyrosine phosphorylation // not recorded//0030334 // regulation of cell migration // not recorded
1426053_a	0.000230	1.80	-1.01	NM_001163464//NM_0256	Abi3	ABI gene family, member 3	0006909 // phagocytosis // not recorded
1424123_a	0.002052	1.80	1.05	NM_001290660//NM_0254	Cd302	CD302 antigen	0007178 // transmembrane receptor protein serine/threonine kinase signaling pathway // inferred from electronic annotation
1416998_a	0.005121	1.79	1.88	NM_027366//X/M_0065248	Ly6g6e	lymphocyte antigen 6 complex, locus G6e	0005975 // carbohydrate metabolic process // inferred from electronic annotation//0006006 // glucose metabolic process // inferred from electronic annotation//0010510 // regulation of
1431359_a	0.006500	1.79	-1.10	NM_145630	Pdk3	pyruvate dehydrogenase kinase, isoenzyme 3	0006508 // proteolysis // not recorded//0006915 // apoptotic process // not recorded//0007519 // skeletal muscle tissue development // inferred from mutant phenotype//0010952 //
1452353_a	0.000743	1.79	-1.29	NM_001289704//NM_0012	Cflar	CASP8 and FADD-like apoptosis regulator	0007155 // cell adhesion // inferred from electronic annotation
1417279_a	0.004443	1.79	1.74	NM_001252472//NM_0012	Cd84	CD84 antigen	0042102 // positive regulation of T cell proliferation // inferred from direct assay//0042130 // negative regulation of T cell proliferation // inferred from direct assay
1420350_a	0.000112	1.79	1.21	NM_021396	Pcdcl1lg2	programmed cell death 1 ligand 2	0002376 // immune system process // inferred from electronic annotation//0006508 // proteolysis // inferred from direct assay//0006508 // proteolysis // not recorded//0006509 //
1448846_a	0.004422	1.79	-1.19	NM_030711//X/M_0065174	Erap1	endoplasmic reticulum aminopeptidase 1	0003866 // cortical actin cytoskeleton organization // inferred from mutant phenotype//0001898 // negative regulation of protein kinase B signaling // inferred from mutant
1423250_a	0.003143	1.78	1.09	NM_028444	Pkcd6a2	protein kinase C, delta binding protein	0006810 // transport // inferred from electronic annotation//0043029 // T cell homeostasis // inferred from genetic interaction//0045586 // regulation of T cell differentiation // inferred
1416826_a	0.007473	1.78	1.93	NM_021053	Slc46a2	solute carrier family 4, member 2	0001666 // response to hypoxia // inferred from electronic annotation//0006000 // fructose metabolic process // not recorded//0006096 // glycolytic process // not recorded//0006754 //
1420951_a	0.007878	1.78	1.18	NM_026485//X/M_0065213	Traab	TraB domain containing	0002537 // nitric oxide production involved in inflammatory response // inferred from mutant phenotype//0003333 // amino acid transmembrane transport // not recorded//0006809 //
1417231_a	0.000404	1.78	1.75	NM_001177307//NM_0011	Aldoa	aldolase A, fructose-bisphosphate	0006810 // transport // inferred from electronic annotation//0015031 // protein transport // inferred from electronic annotation
1421807_a	0.007347	1.78	1.14	NM_001044740//NM_0075	Slc7a2	solute carrier family 7 (cationic amino acid transporter, y+ system), member 2	0006810 // transport // inferred from electronic annotation//0005085 // transmembrane transport // inferred from electronic annotation
1429954_a	0.000090	1.77	-1.39	NM_001252503//NM_0012	Afpgh	afthophilin	0006508 // proteolysis // inferred from electronic annotation//0006810 // transport // inferred from electronic annotation//0015031 // protein transport // inferred from electronic
1420823_a	0.005211	1.77	1.19	NM_0013406//X/M_0065046	Slc12a9	solute carrier family 12 (potassium/chloride transporters), member 9	0006741 // NADP biosynthetic process // inferred from electronic annotation//0008152 // metabolic process // inferred from electronic annotation//0016310 // phosphorylation // inferred
1421162_a	0.000827	1.77	1.17	NM_001167680//NM_1725	Rhbf2	rhomboïd 5 homolog 2 (Drosophila)	0006412 // translation // inferred from electronic annotation//0006418 // tRNA aminoacylation for protein translation // inferred from electronic annotation//0006420 // arginyl-RNA
1433803_a	0.000408	1.77	-1.12	NM_001159637//NM_1386	Nadk	NAD kinase	0006914 // autophagy // inferred from electronic annotation//0007155 // cell adhesion // inferred from electronic annotation//0007566 // embryo implantation // inferred from direct
1422592_a	0.002360	1.77	1.11	NM_025936	Rors	arginyl-RNA synthetase	0030041 // actin filament polymerization // inferred from mutant phenotype//0030041 // actin filament polymerization // not recorded//0031175 // neuron projection development //
1448712_a	0.009603	1.77	-1.19	NM_029478//X/M_0065344	Vmp1	vacuole membrane protein 1	0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 // regulation of transcription, DNA-templated // inferred from electronic annotation//0006357 //
1427412_s	0.003838	1.77	-1.05	NM_001253817//NM_0012	Tmem184b	transmembrane protein 184b	0006468 // protein phosphorylation // inferred from direct assay//0008360 // regulation of cell shape // not recorded//0010976 // positive regulation of neuron projection development //
1427313_a	0.002746	1.77	-1.05	NM_174850	Mical2	MICAL-like 2	0003333 // amino acid transmembrane transport // not recorded//0005975 // carbohydrate metabolic process // inferred from electronic annotation//0006810 // transport // inferred from
1426672_a	0.005297	1.77	-1.03	NM_011869//X/M_0065333	Med24	mediator complex subunit 24	0002262 // myeloid cell homeostasis // inferred from mutant phenotype//0006508 // proteolysis // inferred from mutant phenotype//0006509 // membrane protein ectodomain proteolysis
1421052_a	0.000570	1.77	1.17	NM_010194//X/M_0065406	Fes	feline sarcoma oncogene	0006021 // inositol biosynthetic process // inferred from electronic annotation//0006629 // lipid metabolic process // inferred from electronic annotation//0008654 // phospholipid
1450290_a	0.009426	1.77	-1.24	NM_001161413//NM_0085	Slc3a2	solute carrier family 3 (activators of dibasic and neutral amino acid	0016567 // protein ubiquitination // inferred from electronic annotation//0003556 // intracellular signal transduction // inferred from electronic annotation
1452348_s	0.001411	1.76	-1.29	NM_021607//X/M_0064969	Ncstn	nicastrin	0003333 // amino acid transmembrane transport // inferred from sequence or structural similarity//0006810 // transport // inferred from electronic annotation//000865 // amino acid
1423944_a	0.000237	1.76	1.06	NM_001033711//NM_0010	Evi2a//Evi2b	ectoprotein viral integration site 2a//Evi2a-Evi2b readthrough//ecotropic	0007155 // cell adhesion // inferred from electronic annotation
1427346_a	0.002360	1.76	-1.05	NM_183170	Mpv17	MPV17 mitochondrial membrane protein-like 2	0007165 // signal transduction // inferred from electronic annotation//0007186 // G-protein coupled receptor signaling pathway // inferred from electronic annotation//0002198 // cerebral
1424826_s	0.000751	1.76	1.02	NM_023627	Ispn1	myo-inositol 1-phosphate synthase A1	0001503 // ossification // inferred from electronic annotation//0007275 // multicellular organismal development // inferred from electronic annotation//0003036 // actin cytoskeleton
1439019_a	0.005782	1.76	-1.57	NM_001267724//NM_1782	Abi13	ankyrin repeat and SOCS box-containing 13	0006184 // GTP catalytic process // not recorded//0006810 // transport // inferred from electronic annotation//0006886 // intracellular protein transport // inferred from electronic
1423176_a	0.006025	1.76	1.09	NM_145384//XR_390734	Pqgic2	PQ loop repeat containing 2	0001764 // neuron migration // inferred from mutant phenotype//0007155 // cell adhesion // not recorded//0007229 // integrin-mediated signaling pathway // inferred from electronic
1418022_a	0.002543	1.76	1.47	NM_001111058//NM_0212	Cd33	CD33 antigen	0045116 // protein neddylation // inferred from mutant phenotype//0045116 // protein neddylation // not recorded
1430306_a	0.005680	1.76	-1.09	NM_001177556//NM_0011	Gng12	guanine nucleotide binding protein (G protein), gamma 12	0051292 // nuclear pore complex assembly // not recorded
1423171_a	0.001008	1.76	1.09	NM_001114087//NM_0011	Pdlim7	PDB2 and LIM domain 7	0032747 // positive regulation of interleukin-23 production // not recorded//0071345 // cellular response to cytokine stimulus // not recorded//0072537 // fibroblast activation // not
1419208_a	0.001272	1.76	1.29	NM_023126//X/M_0065095	Rab8a	RAB8, member RAS oncogene family	0006886 // intracellular protein transport // inferred from electronic annotation//0006887 // exocytosis // inferred from direct assay//0006887 // exocytosis // not recorded//0016192 //
1424783_a	0.004054	1.76	1.02	NM_013565//X/M_0065323	Itpa3	integrin alpha 3	0000272 // intrasaccharide catabolic process // inferred from electronic annotation//0005975 // carbohydrate metabolic process // inferred from electronic annotation//0006030 // chitin
1425445_a	0.002724	1.76	1.00	NM_026454//X/M_0065298	Ube2f	ubiquitin-conjugating enzyme E2F (putative)	0006508 // proteolysis // inferred from direct assay//0007229 // integrin-mediated signaling pathway // inferred from electronic annotation//0010573 // vascular endothelial growth factor
1427592_a	0.006653	1.75	-1.06	NM_027513//X/M_0065065	Nup205	nucleoporin 205	0000165 // MAPK cascade // not recorded//0000302 // response to reactive oxygen species // inferred from electronic annotation//0001525 // angiogenesis // not recorded//0001556 //
1448809_a	0.000849	1.75	-1.19	NM_008359//X/M_0065056	Il17ra	interleukin 17 receptor A	0007155 // cell adhesion // inferred from electronic annotation
1416737_a	0.009763	1.75	2.12	NM_001393//X/M_0065389	Sytl1	synaptotagmin-like 1	0007165 // signal transduction // inferred from electronic annotation//0007186 // G-protein coupled receptor signaling pathway // inferred from electronic annotation//0002198 // cerebral
1417219_s	0.002568	1.75	1.76	NM_001284524//NM_0012	Chit1	chitinase 1 (chitrolysinase)	0001503 // ossification // inferred from electronic annotation//0007275 // multicellular organismal development // inferred from electronic annotation//0003036 // actin cytoskeleton
1448857_a	0.008200	1.75	-1.19	NM_001081401//NM_1778	Adams3	a disintegrin-like and metallopeptidase (reprolysin type) with PTK2 protein tyrosine kinase 2 beta	0006184 // GTP catalytic process // not recorded//0006810 // transport // inferred from electronic annotation//0006886 // intracellular protein transport // inferred from electronic
1421065_a	0.001604	1.75	1.17	NM_001162365//NM_0011	Ptk2b	PTK2 protein tyrosine kinase 2 beta	0001764 // neuron migration // inferred from mutant phenotype//0007155 // cell adhesion // not recorded//0007229 // integrin-mediated signaling pathway // inferred from electronic
1452066_a	0.004686	1.75	-1.29	NM_001105245//NM_0011	Pcdh19	protocadherin 19	0045116 // protein neddylation // inferred from mutant phenotype//0045116 // protein neddylation // not recorded
1422703_a	0.001828	1.75	1.11	NM_009163//X/M_0065134	Sgpl1	sphingosine phosphatase lyase 1	0007155 // cell adhesion // inferred from electronic annotation//0007156 // homophilic cell adhesion // inferred from electronic annotation
1421922_a	0.009375	1.74	1.14	NM_019924//X/M_0065272	Rps80a4	ribosomal protein S6 kinase, polypeptide 4	0001553 // luteinization // inferred from mutant phenotype//0001570 // vasculogenesis // inferred from mutant phenotype//0001822 // kidney development // inferred from mutant
1424269_a	0.001097	1.74	1.04	NM_019822//X/M_0065006	Adm1	adhesion regulating molecule 1	0006355 // regulation of transcription, DNA-templated // not recorded//0006468 // protein phosphorylation // not recorded//0006950 // response to stress // inferred from electronic
1422962_a	0.002036	1.74	1.10	NM_145927//X/M_0065154	Fntb	frnesyltransferase, CAX box, beta	0001541 // ovarian follicle development // inferred from mutant phenotype//0006368 // transcription elongation from RNA polymerase II promoter // not recorded//0007286 // spermatid
1452414_s	0.004089	1.74	-1.29	NM_001252543//NM_0012	Sec23b	SEC23B (S. cerevisiae)	0007275 // multicellular organismal development // inferred from electronic annotation//0008152 // metabolic process // inferred from mutant phenotype//0008284 // positive regulation of
1419412_a	0.002257	1.74	1.26	NM_001081162//X/M_0064	Slc4a11	solute carrier family 4, sodium bicarbonate transporter-like, member 11	0006810 // transport // inferred from electronic annotation//0006886 // intracellular protein transport // inferred from electronic annotation//0006888 // ER to Golgi vesicle-mediated
1423104_a	0.000839	1.74	1.09	NM_011898	Spry4	sprouty homolog 4 (Drosophila)	0006810 // transport // inferred from electronic annotation//0006811 // ion transport // inferred from electronic annotation//0006814 // sodium ion transport // not recorded//0006820 //
1417802_a	0.000273	1.74	1.53	NM_001162924//NM_0197	Pkp3	plakophilin 3	0007275 // multicellular organismal development // inferred from electronic annotation//0009966 // regulation of signal transduction // inferred from electronic annotation//00043407 //
1424309_a	0.001874	1.74	1.04	NM_001252568//NM_0012	Lrrc8a//Phyhd1	leucine rich repeat containing 8A//phytanoyl-CoA dioxygenase domain	0002159 // desmosome assembly // not recorded//0007155 // cell adhesion // inferred from electronic annotation//00016337 // single organismal cell-cell adhesion // inferred from electronic
1424783_a	0.004054	1.74	1.02	NM_001164709//NM_0287	Syvn1	synovial apoptosis inhibitor 1, synovial	0002329 // pre-B cell differentiation // inferred from mutant phenotype//0006810 // transport // inferred from electronic annotation//0006811 // ion transport // inferred from electronic
1425140_a	0.004802	1.74	1.01	NM_001008072//NM_0010	Dab2	disabled 2, mitogen-responsive phosphoprotein	0001701 // in utero embryonic development // inferred from mutant phenotype//0006986 // response to unfolded protein // not recorded//0007275 // multicellular organismal
1424131_a	0.000900	1.73	1.05	NM_0011175//X/M_0065156	Lgmn	legumain	0009094 // cell morphogenesis involved in differentiation // inferred from mutant phenotype//0001701 // in utero embryonic development // inferred from mutant phenotype//0001921 //
1418064_a	0.002995	1.73	1.46	NM_183168//X/M_0065076	P2ry6	pyrimidinergic receptor P2Y, G-protein coupled, 6	0001101 // response to acid // inferred from mutant phenotype//0003014 // renal system process // inferred from mutant phenotype//0006508 // proteolysis // inferred from direct
1421876_a	0.007033	1.73	1.14	NM_001291859//NM_0074	Rhoc	ras homolog gene family, member C	0007165 // signal transduction // inferred from electronic annotation//0007186 // G-protein coupled receptor signaling pathway // inferred from direct assay//0014911 // positive regulation
1417689_a	0.002514	1.73	1.57	NM_207105	H2-Ab1	histocompatibility 2, class II antigen A, beta 1	0009010 // cytokinesis // not recorded//0006184 // GTP catalytic process // inferred from electronic annotation//0007165 // signal transduction // not recorded//0007264 // small GTPase
1449531_a	0.004253	1.73	-1.22	NM_172863//X/M_0065014	Zfp697	zinc finger protein 697	0002344 // B cell affinity maturation // inferred from direct assay//0002376 // immune system process // inferred from electronic annotation//0002381 // immunoglobulin production
1423115_a	0.004093	1.72	1.09	NM_027828	Fhm110c	family with sequence similarity 110, member C	0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 // regulation of transcription, DNA-templated // inferred from electronic annotation
1420722_a	0.007446	1.72	1.19	NM_00108635//NM_1832	Shk35	serine/threonine kinase 35	0003335 // positive regulation of cell migration // not recorded//0005189 // positive regulation of protein kinase B signaling // not recorded//0006491 // regulation of cell projection assembly
1422341_s	0.002257	1.72	1.12	NM_001081041	Ptpn23	protein tyrosine phosphatase, non-receptor type 23	0006468 // protein phosphorylation // inferred from electronic annotation//0016310 // phosphorylation // inferred from electronic annotation
1416453_x	0.009491	1.72	2.74	NM_001013373//X/M_0065	Tmprss13	transmembrane protease, serine 13	0006470 // protein dephosphorylation // inferred from electronic annotation//0006810 // transport // inferred from electronic annotation//0015031 // protein transport // inferred from
1455152_a	0.003796	1.72	-1.32	NM_175176//X/M_0065012	Erich3	glutamate rich 3	0006508 // proteolysis // inferred from electronic annotation//0006898 // receptor-mediated endocytosis // inferred from electronic annotation
1424754_a	0.000714	1.72	1.03	NM_145516//X/M_0065270	Slc25a2b	solute carrier family 25, member 28	0006810 // transport // inferred from electronic annotation//0006811 // ion transport // inferred from electronic annotation//0005072 // iron ion homeostasis // inferred from electronic
1436622_a	0.003143	1.72	-1.52	NM_009150	Selenbp2	selenium binding protein 1	0006810 // transport // inferred from electronic annotation//0005031 // protein transport // inferred from electronic annotation//0005087 // brown fat cell differentiation // inferred from
1458141_a	0.002218	1.72	-2.38	NM_130171	F3	coagulation factor III	0001938 // positive regulation of endothelial cell proliferation // not recorded//0002541 // activation of plasma proteins involved in acute inflammatory response // not recorded//0006919 //
1426502_s	0.003595	1.72	-1.02	NM_010470//NR_027485	Psmad2	proteasome (prosome, macropain) 26S subunit, non-ATPase, 2	0042176 // regulation of protein catabolic process // inferred from electronic annotation//0005079 // regulation of catalytic activity // inferred from electronic annotation
1420929_a	0.006564	1.72	1.18	NM_001162950//NM_0168	Hif3a	hypoxia inducible factor 3, alpha subunit	0001666 // response to hypoxia // inferred from direct assay//0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 // regulation of transcription, DNA-
1425995_s	0.						

Table S7

Gene ID	p (Corr)	FC-RSV 1 d	FC-RSV 5 d	RefSeq Transcript ID	Gene Symbol	Gene Title	Gene Ontology Biological Process
1422661_a	0.000114	1.71	1.11	NM_011956// <i>/XM_0065243</i>	<i>Nubp2</i>	nucleotide binding protein 2	0016226 // iron-sulfur cluster assembly // inferred from electronic annotation
1425293_a	0.009343	1.71	1.01	NM_018758// <i>/XM_0065139</i>	<i>ApoB3</i>	amyloid beta (A4) precursor protein-binding, family A, member 3	0001701 // in utero embryonic development // inferred from genetic interaction//0006810 // transport // inferred from electronic annotation//0007268 // synaptic transmission // inferred
1424311_a	0.003090	1.71	1.04	NM_145934// <i>/NR_102313//</i>	<i>Stap2</i>	signal transducing adaptor family member 2	
1426256_a	0.004007	1.71	-1.02	NM_178751// <i>/XM_0065044</i>	<i>Orai2</i>	ORAI calcium release-activated calcium modulator 2	
1425008_a	0.000852	1.71	1.02	NM_001127324// <i>/NM_0079</i>	<i>Erc1</i>	exon repair cross-complementing rodent repair deficiency,	0000720 // pyrimidine dimer repair by nucleotide-excision repair // inferred from mutant phenotype//0000737 // DNA catabolic process, endonucleolytic // not recorded//0001302 //
1426571_a	0.000496	1.71	-1.03	NM_145537// <i>/XM_0064985</i>	<i>Edem2</i>	ER degradation enhancer, mannosidase alpha-like 2	0008152 // metabolic process // inferred from electronic annotation
1416209_a	0.001026	1.71	3.93	NM_001168274// <i>/NM_0313</i>	<i>Gsdmc1//Gsdmc2</i>	gasdermin C//gasdermin C2	0060576 // intestinal epithelial cell development // inferred from expression pattern
1434038_a	0.002862	1.71	-1.12	NM_010120// <i>/XM_0065256</i>	<i>Efl1a//88287469//Gm4027</i>	eskermyc1 translation initiation factor 1A//expressed sequence	0006412 // translation // inferred from electronic annotation//0006413 // translational initiation // inferred from electronic annotation
1423706_a	0.004574	1.70	-1.07	NM_148678	<i>Gors</i>	glycyl-tRNA synthetase	0006412 // translation // inferred from electronic annotation//0006418 // tRNA aminoacylation for protein translation // inferred from electronic annotation//0006426 // glycol-tRNA
1423824_a	0.001500	1.70	1.06	NM_011421	<i>Smpd1</i>	sphingomyelin phosphodiesterase 1, acid lysosomal	0006685 // sphingomyelin catabolic process // inferred from electronic annotation//0008152 // metabolic process // inferred from electronic annotation//0023021 // termination of signal
1427327_a	0.001604	1.70	-1.05	NM_011299// <i>/XM_0065231</i>	<i>Rpska2</i>	ribosomal protein S6 kinase, polypeptide 2	0001556 // oocyte maturation // inferred from direct assay//0002035 // brain renin-angiotensin system // inferred from direct assay//0006468 // protein phosphorylation // inferred from
1419907_s	0.009355	1.70	1.23	NM_001136066// <i>/NM_0104</i>	<i>Hmox2</i>	heme oxygenase (decycling) 2	0001666 // response to hypoxia // not recorded//0006788 // heme oxidation // inferred from electronic annotation//0006979 // response to oxidative stress // not recorded//0005114 //
1437285_s	0.005374	1.70	-1.53	NM_001048146// <i>/NM_0012</i>	<i>Azi2</i>	5-azacytidine induced gene 2	0000278 // mitotic cell cycle // inferred from mutant phenotype//0001816 // cytokine production // inferred from mutant phenotype//0007249 // l-kappaB kinase/NF-kappaB signaling //
1422132_a	0.002674	1.70	1.13	NM_001163540// <i>/NM_0011</i>	<i>Plec//Parp10</i>	plectin//poly (ADP-ribose) polymerase family, member 10	0007584 // response to nutrient // not recorded//00031581 // hemidesmosome assembly // not recorded//0046417 // chorismate metabolic process // inferred from electronic
1418775_a	0.003494	1.70	1.34	NM_01010971// <i>/NM_0011</i>	<i>Gm10177//Gm11575//Sec61</i>	predicted gene 10177//predicted gene 11575//SEC61, gamma subunit	0006605 // protein targeting // inferred from electronic annotation//0006810 // transport // inferred from electronic annotation//0006886 // intracellular protein transport // inferred from
1423166_a	0.006466	1.70	1.09	NM_007914// <i>/XM_0064986</i>	<i>Ehf</i>	ets homologous factor	0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 // regulation of transcription, DNA-templated // inferred from electronic annotation//0006357 //
1423167_a	0.004221	1.70	1.09	NM_009304	<i>Syngt2</i>	synaptogyrin 2	0006605 // protein targeting // not recorded
1449379_a	0.001963	1.69	-1.22	NM_001136067// <i>/NM_0011</i>	<i>Ikbkg</i>	inhibitor of kappaB kinase gamma	0001782 // B cell homeostasis // inferred from mutant phenotype//0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 // regulation of transcription,
1448357_a	0.002452	1.69	-1.18	NM_001103156// <i>/NM_0011</i>	<i>Steap2</i>	3a transmembrane epithelial antigen of prostate 2	0006810 // transport // inferred from electronic annotation//0006811 // ion transport // inferred from electronic annotation//0006893 // Golgi to plasma membrane transport // not
1423031_a	0.009475	1.69	1.10	NM_011693	<i>Vcam1</i>	vascular cell adhesion molecule 1	0001666 // response to hypoxia // inferred from electronic annotation//0005256 // acute inflammatory response // inferred from electronic annotation//0002544 // chronic inflammatory
1448926_a	0.002101	1.69	-1.20	NM_175308	<i>Mob3c</i>	MOB kinase activator 3C	0016310 // phosphorylation // inferred from electronic annotation
1447937_a	0.006613	1.68	-1.84	NM_013562	<i>Ifrd1</i>	interferon-related developmental regulator 1	0007275 // multicellular organismal development // inferred from electronic annotation//0007527 // adult somatic muscle development // inferred from mutant phenotype//00030154 // cell
1418073_a	0.001963	1.68	1.46	NM_172709// <i>/NM_178139</i>	<i>Otap1</i>	otopetrin 1	0009590 // detection of gravity // inferred from mutant phenotype//00031214 // biomaterial tissue development // inferred from electronic annotation//0042472 // inner ear morphogenesis
1424997_a	0.005333	1.68	1.02	NM_009341// <i>/NM_011553//</i>	<i>Tcp10a//Tcp10b//Tcp10c</i>	T-complex protein 10a//T-complex protein 10b//T-complex protein 10c	
1424874_a	0.008548	1.68	1.02	NM_001005507// <i>/NM_0011</i>	<i>Smg7</i>	Smg-7 homolog, nonsense mediated mRNA decay factor (C. elegans)	0001184 // nuclear-transcribed mRNA catabolic process, nonsense-mediated decay // inferred from electronic annotation
1431175_a	0.004279	1.68	-1.41	NM_001033405// <i>/XM_0065</i>	<i>Trem2</i>	triggering receptor expressed on myeloid cells-like 2	0042110 // T cell activation // not recorded
1435013_a	0.008016	1.68	-1.13	NM_001082923// <i>/NM_0081</i>	<i>Gpx3</i>	glutathione peroxidase 3	0006749 // glutathione metabolic process // not recorded//0006979 // response to oxidative stress // inferred from electronic annotation//0042744 // hydrogen peroxide catabolic process //
1455143_a	0.003296	1.68	-1.32	NM_011157// <i>/NM_0065133</i>	<i>Sgn</i>	serglycin	0006915 // apoptotic process // inferred from electronic annotation//0008626 // granzyme-mediated apoptotic signaling pathway // inferred from sequence or structural similarity//0008626
1426603_a	0.009733	1.68	-1.03	NM_010736	<i>Ltrb</i>	lymphotxin B receptor	0006915 // apoptotic process // inferred from electronic annotation//0043011 // myeloid dendritic cell differentiation // inferred from mutant phenotype//0043123 // positive regulation of i-
1427414_a	0.008639	1.68	-1.05	NM_001162533// <i>/NM_0258</i>	<i>Sh3d21</i>	SH3 domain containing 21	
1418563_a	0.004496	1.68	1.37	NM_001290822// <i>/NM_0103</i>	<i>Pdpr</i>	podoplanin	0000902 // cell morphogenesis // inferred from direct assay//0001946 // lymphangiogenesis // inferred from mutant phenotype//0006693 // prostaglandin metabolic process // inferred
1429422_a	0.001651	1.68	-1.37	NM_029614// <i>/XM_0065082</i>	<i>Prss23</i>	protease, serine 23	0006508 // proteolysis // inferred from electronic annotation
1418248_a	0.000369	1.68	1.42	NM_001205081// <i>/NM_1725</i>	<i>Trim47</i>	tripartite motif-containing 47	
1425463_a	0.007989	1.68	1.00	NM_001040403// <i>/NM_0012</i>	<i>Flot2</i>	flotillin 2	0007155 // cell adhesion // inferred from electronic annotation
1420887_a	0.000301	1.68	1.18	NM_008163	<i>Grb2</i>	growth factor receptor bound protein 2	0007265 // Ras protein signal transduction // traceable author statement//0007568 // aging // not recorded//0008286 // insulin receptor signaling pathway // not recorded//0008543 //
1425452_s	0.004727	1.68	1.00	NM_026637// <i>/XM_0065053</i>	<i>Ggct</i>	gamma-glutamyl cyclotransferase	0001836 // release of cytochrome c from mitochondria // not recorded//0006750 // glutathione biosynthetic process // inferred from electronic annotation
1422591_a	0.006469	1.68	1.11	NM_001080979// <i>/NM_0115</i>	<i>Tead4</i>	TEA domain family member 4	0001701 // in utero embryonic development // inferred from mutant phenotype//0001708 // cell fate specification // inferred from mutant phenotype//0001825 // blastocyst formation //
1423316_a	0.000837	1.67	1.08	NM_019566	<i>Rhog</i>	ras homolog gene family, member G	0006184 // GTP catalytic process // not recorded//0006886 // intracellular protein transport // inferred from electronic annotation//0006913 // nucleocytoplasmic transport // inferred from
1418275_a	0.004859	1.67	1.41	NM_023596// <i>/XM_0065141</i>	<i>Sic29a3</i>	solute carrier family 29 (nucleoside transporters), member 3	0006810 // transport // inferred from electronic annotation//0001585 // nucleoside transport // not recorded//1901642 // nucleoside transmembrane transport // not recorded
1422156_a	0.001702	1.67	1.13	NM_011609	<i>Tnfrsf10a</i>	tumor necrosis factor receptor superfamily, member 1a	0001666 // response to hypoxia // inferred from electronic annotation//0006693 // prostaglandin metabolic process // traceable author statement//0006915 // apoptotic process // inferred
1419619_a	0.008723	1.67	1.25	NM_018825// <i>/XM_0065044</i>	<i>Sh2b2</i>	SH2B adaptor protein 2	0001922 // B-1 B cell homeostasis // inferred from mutant phenotype//0007399 // nervous system development // not recorded//0008286 // insulin receptor signaling pathway // inferred
1420464_s	0.000469	1.67	1.21	NM_080510// <i>/XM_0065001</i>	<i>Trim69</i>	tripartite motif-containing 69	0006915 // apoptotic process // inferred from electronic annotation//0016567 // protein ubiquitination // not recorded
1460370_a	0.007232	1.67	-1.34	NM_008086// <i>/XM_0065098</i>	<i>Casp12</i>	caspase 12	0006508 // proteolysis // not recorded//0006508 // proteolysis // inferred from reviewed computational analysis//0006915 // apoptotic process // inferred from direct assay//00016540 //
1426098_a	0.009281	1.67	-1.01	NM_001168516// <i>/NM_0011</i>	<i>Zdhc24</i>	zinc finger, DHHC domain containing 24	0008152 // metabolic process // inferred from electronic annotation
1418977_a	0.001301	1.67	1.31	NM_023182	<i>Ctrl</i>	chymotrypsin-like	0006508 // proteolysis // inferred from direct assay//0006508 // proteolysis // not recorded
1451316_a	0.007232	1.66	-1.27	NM_023220// <i>/XM_0065000</i>	<i>Spp12a</i>	signal peptide peptidase like 2A	0006508 // proteolysis // inferred from electronic annotation//0006509 // membrane protein ectodomain proteolysis // not recorded//00031293 // membrane protein intracellular domain
1416547_a	0.003380	1.66	2.46	NM_001168256// <i>/NM_0011</i>	<i>Tmem40</i>	transmembrane protein 40	
1418402_a	0.009552	1.66	1.39	NM_170758// <i>/XM_0065330</i>	<i>Cd300a</i>	CD300a antigen	0002376 // immune system process // inferred from electronic annotation//0002552 // serotonin secretion by mast cell // inferred from direct assay//0006898 // receptor-mediated
1422403_a	0.001179	1.66	1.12	NM_008012	<i>Akr108</i>	aldo-keto reductase family 1, member B8	0016488 // farnesyl catabolic process // not recorded//0044597 // daunorubicin metabolic process // not recorded//0044598 // doxorubicin metabolic process // not recorded//00055114 //
1430912_a	0.004591	1.66	-1.10	NM_009932	<i>Col4a2</i>	collagen, type IV, alpha 2	0001525 // angiogenesis // inferred from electronic annotation//0006351 // transcription, DNA-templated // inferred from direct assay//00016525 // negative regulation of angiogenesis // not
1425142_a	0.005193	1.66	1.01	NM_001080126// <i>/NM_0012</i>	<i>Casp8</i>	caspase 8	0001525 // angiogenesis // inferred from mutant phenotype//0001841 // neural tube formation // inferred from mutant phenotype//0006508 // proteolysis // inferred from genetic
1424762_a	0.005015	1.66	1.03	NM_001003917// <i>/NM_0012</i>	<i>Atg9a</i>	autophagy related 9A	0000045 // autophagic vacuole assembly // not recorded//0000422 // mitochondrion degradation // ---//0006810 // transport // inferred from electronic annotation//0006914 // autophagy
1425742_a	0.007364	1.66	-1.01	NM_001163434// <i>/NM_0223</i>	<i>Hspa5</i>	heat shock protein 5	0000902 // cell morphogenesis // inferred from electronic annotation//0006983 // ER overload response // inferred from direct assay//0006987 // activation of signaling protein activity
1423976_a	0.001961	1.66	1.05	NM_011966// <i>/XM_0065111</i>	<i>Psmo4</i>	proteasome (prosome, macropain) subunit, alpha type 4	0006508 // proteolysis // inferred from electronic annotation//0006511 // ubiquitin-dependent protein catabolic process // inferred from electronic annotation//00051603 // proteolysis
1421918_a	0.000813	1.66	1.14	NM_001025561// <i>/NM_0010</i>	<i>Pus1</i>	puseudouridine synthase 1	0001522 // pseudouridine synthesis // inferred from electronic annotation//0008033 // tRNA processing // inferred from electronic annotation//0009451 // RNA modification // inferred from
1419583_a	0.002322	1.66	1.25	NM_138747	<i>Nop2</i>	NOP2 nuclear protein	0006364 // rRNA processing // inferred from electronic annotation//0032259 // methylation // inferred from electronic annotation
1419409_a	0.000016	1.66	1.27	NM_172371// <i>/XM_0065341</i>	<i>Sic16a13</i>	solute carrier family 16 (monocarboxylic acid transporters), member 13	0006810 // transport // inferred from electronic annotation//0005508 // transmembrane transport // inferred from electronic annotation
1434768_a	0.005912	1.66	1.13	NM_011486// <i>/NM_13659//</i>	<i>Sto3</i>	signal transducer and activator of transcription 3	0001659 // temperature homeostasis // inferred from mutant phenotype//0001754 // eye photoreceptor cell differentiation // inferred from mutant phenotype//0006351 // transcription,
1421076_a	0.008614	1.66	1.17	NM_0012390// <i>/XM_0065312</i>	<i>So11</i>	sal-like 1 (Drosophila)	0000122 // negative regulation of transcription from RNA polymerase II promoter // inferred from direct assay//0000122 // negative regulation of transcription from RNA polymerase II
1410508_a	0.008085	1.66	1.31	NM_026827// <i>/NM_028389//</i>	<i>Tmem219</i>	transmembrane protein 219	0006915 // apoptotic process // inferred from electronic annotation
1426807_a	0.007350	1.66	-1.03	NM_001161365// <i>/NM_1776</i>	<i>Rin3</i>	Ras and Rab interactor 3	0007165 // signal transduction // inferred from electronic annotation//0002313 // regulation of Rab GTPase activity // not recorded//00023851 // positive regulation of Rab GTPase activity //
1422156_a	0.001702	1.66	1.13	NM_018749// <i>/XM_0065211</i>	<i>Elf3d</i>	ekaryotic translation initiation factor 3, subunit D	0001731 // formation of translation preinitiation complex // inferred from electronic annotation//0001732 // formation of translation initiation complex // inferred from direct
1428505_s	0.002388	1.66	-1.08	NM_001190852// <i>/NM_0011</i>	<i>Pdlim5</i>	PDZ and LIM domain 5	0001963 // regulation of synapse assembly // not recorded//0006101 // regulation of dendritic spine morphogenesis // not recorded
1418543_s	0.007879	1.66	1.37	NM_053103	<i>Entpd7</i>	ectonucleoside triphosphate diphosphohydrolase 7	0009191 // ribonucleoside diphosphate catabolic process // not recorded//0009203 // ribonucleoside triphosphate catabolic process // not recorded//0006784 // heme a biosynthetic process
1418673_a	0.001527	1.65	1.35	NM_010573	<i>Irx1</i>	Iroquois related homeobox 1 (Drosophila)	0001656 // metanephros development // inferred from expression pattern//0006355 // regulation of transcription, DNA-templated // inferred from electronic annotation//00072086 //
1453472_a	0.000967	1.65	-1.31	NM_009878// <i>/XM_0065099</i>	<i>Cdkn2d</i>	cyclin-dependent kinase inhibitor 2D (p19, inhibits CDK4)	0000079 // regulation of cyclin-dependent protein serine/threonine kinase activity // not recorded//0000082 // G1/S transition of mitotic cell cycle // not recorded//0007031 // DNA synthesis
1423725_a	0.004399	1.65	1.06	NM_001205286// <i>/NM_0012</i>	<i>Tmem39a</i>	transmembrane protein 39a	
1422842_a	0.001953	1.65	1.10	NM_001162939// <i>/NM_0265</i>	<i>Aen</i>	apoptosis enhancing nuclease	0006915 // apoptotic process // inferred from electronic annotation//0006974 // cellular response to DNA damage stimulus // inferred from electronic annotation//0008152 // metabolic
1423090_x	0.006331	1.65	1.09	NM_029934// <i>/XM_0065404</i>	<i>Mboat7</i>	membrane bound O-acetyltransferase domain containing 7	0006629 // lipid metabolic process // inferred from electronic annotation//0008654 // phospholipid biosynthetic process // inferred from electronic annotation//0021591 // ventricular
1417319_a	0.006280	1.65	1.69	NM_175731	<i>Acer1</i>	alkaline ceramidase 1	0006629 // lipid metabolic process // inferred from electronic annotation//0006665 // sphingolipid metabolic process // inferred from direct assay//0006672 // ceramide metabolic process //
1424017_a	0.004038	1.65	1.05	NM_001085440// <i>/NM_1754</i>	<i>Smcr8</i>	Smith-Magenis syndrome chromosome region, candidate 8 homolog	
1418655_a	0.007501	1.64	1.35	NM_001291212// <i>/NM_0012</i>	<i>Myo18a</i>	myosin XVIIIa	0007030 // Golgi organization // not recorded//0008152 // metabolic process // inferred from electronic annotation//0016477 // cell migration // not recorded//00031032 // actomyosin
1421574_a	0.003902	1.64	1.15	NM_001004180// <i>/XM_0065</i>	<i>Fam222a</i>	family with sequence similarity 222, member A	
1424233_a	0.001901	1.64	1.05	NM_134100	<i>Mfsd5</i>	major facilitator superfamily domain containing 5	0006810 // transport // inferred from electronic annotation//0006811 // ion transport // inferred from electronic annotation//0005508 // transmembrane transport // inferred from
1422403_a	0.002342	1.64	1.12	NM_025465// <i>/XM_0065097</i>	<i>Tma16</i>	translation machinery associated 16 homolog (S. cerevisiae)	
1424165_a	0.008082	1.64	1.05	NM_011163 // <i>/XM_0065206</i>	<i>Mtpa11</i>	mitogen-activated protein kinase 11	0000165 // MAPK cascade // not recorded//0000165 // MAPK cascade // inferred from sequence or structural similarity//0006351 // transcription, DNA-templated // inferred from electronic
1418045_a	0.008224	1.64	1.47	XM_006516441// <i>/XM_0065</i>	<i>Gm2701//LOC102631912</i>	predicted gene 2701//NADH dehydrogenase [ubiquinone] 1 beta ring finger and FYVE like domain containing protein	
1424783_a	0.004054	1.64	1.03	NM_001007465// <i>/NM_0011</i>	<i>Rjfi</i>	ring finger and FYVE like domain containing protein	
1418381_a	0.001702	1.64	1.39	NM_026753	<i>Fam96b</i>	family with sequence similarity 96, member B	0006511 // ubiquitin-dependent protein catabolic process // not recorded//0006886 // intracellular protein transport // inferred from direct assay//0006915 // apoptotic process // inferred
1425011_x	0.000739	1.64	1.02	NM_001077709// <i>/NM_0082</i>	<i>Sic39a7</i>	solute carrier family 39 (zinc transporter), member 7	0007059 // chromosome segregation // not recorded
1420020_a	0.005623	1.64	1.22	NM_019502// <i>/XM_0065073</i>	<i>Timm10b</i>	translocase of inner mitochondrial membrane 10B	0006810 // transport // inferred from electronic annotation//0006811 // ion transport // inferred from electronic annotation//0006829 // zinc ion transport // inferred from electronic
1434660_a	0.002478	1.64	-1.46	NM_133662	<i>Ier3</i>	immediate early response 3	0006810 // transport // inferred from electronic annotation//0007018 // microtubule-based movement // inferred from electronic annotation//0008152 // metabolic process // inferred from
1427173_a	0.002053	1.64	-1.05	NM_001077496// <i>/NM_1460</i>	<i>Evi2a-evi2b//Evi2b//Evi2a</i>	Evi2a-Evi2b readthrough//ecotropic viral integration site 2b//ecotropic	0001562 // response to protozoan // inferred from mutant phenotype//0003085 // negative regulation of systemic arterial blood pressure // inferred from mutant phenotype//0006282 //
1427174_a	0.009317	1.64	-1.05	NM_001077496// <i>/NM_1460</i>	<i>Evi2a-evi2b//Evi2b//Evi2a</i>	Evi2a-Evi2b readthrough//ecotropic viral integration site 2b//ecotropic	
1421441_a	0.005387	1.64	-1.15	NM_001037722// <i>/NM_0096</i>	<i>Adam15</i>	a disintegrin and metalloproteinase domain 15 (metagridin)	0001525 // angiogenesis // inferred from electronic annotation//0006508 // proteolysis // not recorded//0007

Table S7

Gene ID	p (Corr)	FC-RSV 1 d	FC-RSV 5 d	RefSeq Transcript ID	Gene Symbol	Gene Title	Gene Ontology Biological Process
1420416_a	0.001456	1.63	1.21	NM_178639//NM_005068	Sfxn5	sideroflexin 5	0006810 // transport // inferred from electronic annotation//0006811 // ion transport // inferred from electronic annotation//0006812 // cation transport // inferred from electronic
1431554_a	0.000462	1.63	-1.10	NR_027919	Bambi-ps1	BMP and activin membrane-bound inhibitor, pseudogene (Xenopus laevis)	
1424875_a	0.004672	1.63	1.02	NM_001291186//NM_1980	Abr	active BCR-related gene	0007165 // signal transduction // inferred from electronic annotation//0007420 // brain development // inferred from genetic interaction//0003036 // actin cytoskeleton organization //
1423401_a	0.008856	1.63	1.08	NM_01083938//NM_0266	Rnaset2a//Rnaset2b	ribonuclease T2a//ribonuclease T2b	0006401 // RNA catabolic process // inferred from sequence or structural similarity//0009305 // nucleic acid phosphodiester bond hydrolysis // inferred from electronic annotation//00090501
1423408_a	0.008662	1.63	1.08	NM_01083938//NM_0266	Rnaset2a//Rnaset2b	ribonuclease T2a//ribonuclease T2b	0006401 // RNA catabolic process // inferred from sequence or structural similarity//0009305 // nucleic acid phosphodiester bond hydrolysis // inferred from electronic annotation//00090501
1427450_a	0.001915	1.63	-1.05	NM_172279//NM_0065398	Mark4	MAP/microtubule affinity-regulating kinase 4	0000226 // microtubule cytoskeleton organization // not recorded//0001578 // microtubule bundle formation // inferred from electronic annotation//0001578 // microtubule bundle
1448979_a	0.006187	1.63	-1.20	NM_025310	FtsJ	FtsJ homolog 3 (E. coli)	0000453 // enzyme-directed rRNA 2'-O-methylation // inferred from electronic annotation//0001510 // RNA methylation // inferred from electronic annotation//0006364 // rRNA processing
1421908_a	0.002262	1.63	1.14	NM_001204979//NM_0113	Sars	seryl-aminooacyl-RNA synthetase	0006412 // translation // inferred from electronic annotation//0006418 // tRNA aminoacylation for protein translation // inferred from electronic annotation//0006434 // seryl-tRNA
1423567_a	0.003403	1.63	1.07	NM_026673//NM_0195	Gtpbp2	GTP binding protein 2	0006184 // GTP catabolic process // inferred from electronic annotation
1420760_s	0.005241	1.63	1.19	NM_026673//NM_0065273	Nudt22	nucleic (nucleoside diphosphate linked moiety X)-type motif 22	0008152 // metabolic process // inferred from electronic annotation
1417346_a	0.002347	1.63	1.67	NM_020594//NR_027827	Chd3os	chromodomain helicase DNA binding protein 3, opposite strand	
1448411_a	0.003301	1.63	-1.18	NM_028770//NM_0065214	Krt80	keratin 80	
1424732_a	0.001963	1.63	1.03	NM_010239//NR_073181	Fth1	ferritin heavy chain 1	0006826 // iron ion transport // inferred from electronic annotation//0006879 // cellular iron ion homeostasis // inferred from electronic annotation//0006880 // intracellular sequestering of
1451527_a	0.000370	1.63	-1.27	NM_001135100//NM_0296	IL34	interleukin 34	0001934 // positive regulation of protein phosphorylation // not recorded//0001934 // positive regulation of protein phosphorylation // inferred from sequence or structural
1450798_a	0.001170	1.62	-1.25	NM_139064	Tnfrp2	TNFAIP3 interacting protein 2	0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 // regulation of transcription, DNA-templated // inferred from electronic annotation//0006915 //
1421679_a	0.002598	1.62	1.15	NM_030244	Ier5l	immediate early response 5-like	
1426285_a	0.000087	1.62	-1.02	NM_025380	Eef1e1	eukaryotic translation elongation factor 1 epsilon 1	0006281 // DNA repair // non-traceable author statement//0006412 // translation // inferred from electronic annotation//0006414 // translational elongation // inferred from electronic
1428140_a	0.003768	1.62	-1.07	NM_145523	Gca	grancalcin	0006508 // proteolysis // not recorded//0006810 // transport // inferred from electronic annotation//0006811 // ion transport // inferred from electronic annotation//0006813 // potassium
1417814_a	0.001961	1.62	1.53	NM_028725//NM_0065314	Sdr42e1	short chain dehydrogenase/reductase family 42E, member 1	0006694 // steroid biosynthetic process // inferred from electronic annotation//0008152 // metabolic process // inferred from electronic annotation//0009058 // biosynthetic process //
1424360_a	0.000603	1.62	1.04	NM_001136078//NM_0088	Pitpnm1	phosphatidylinositol transfer protein, membrane-associated 1	0006810 // transport // inferred from electronic annotation//0015031 // protein transport // inferred from electronic annotation
1422738_a	0.007615	1.62	1.11	NM_178643	C23005212Rik	RIKEN cDNA C23005212 gene	0006281 // DNA repair // inferred from electronic annotation//0006974 // cellular response to DNA damage stimulus // inferred from electronic annotation
1423918_a	0.007765	1.62	1.06	NM_019873//NM_0065246	Fkbp1	FK506 binding protein-like	0000413 // protein peptidyl-prolyl isomerization // not recorded//0018208 // peptidyl-proline modification // not recorded//0006077 // chaperone-mediated protein folding // --
1422939_a	0.005380	1.62	1.10	NM_133757//NM_0065343	Pgs1	phosphatidylglycerophosphate synthase 1	0006629 // lipid metabolic process // inferred from electronic annotation//0006655 // phosphatidylglycerol biosynthetic process // inferred from sequence or structural similarity//0006655 //
1449591_a	0.001982	1.62	-1.22	NM_198007//NM_0065129	Ascc3	activating signal integrator 1 complex subunit 3	0006200 // ATP catabolic process // not recorded//0006281 // DNA repair // inferred from electronic annotation//0006307 // DNA dealkylation involved in DNA repair // not
1424820_a	0.009745	1.62	-1.02	NM_019418	Trsfj54	tumor necrosis factor (ligand) superfamily, member 14	0006955 // immune response // inferred from electronic annotation//0008588 // release of cytoplasmic sequestered NF-kappaB // not recorded//00010820 // positive regulation of T cell
1424564_a	0.000751	1.62	1.03	NM_022992	Atfip6s	ADP-ribosylation factor-like 6 interacting protein 5	0008631 // intrinsic apoptotic signaling pathway in response to oxidative stress // not recorded//0010917 // negative regulation of mitochondrial membrane potential // not
1429291_a	0.000642	1.61	-1.09	NM_001163590//NM_0011	Sx11	syntaxin 11	0001913 // T cell mediated cytotoxicity // inferred from mutant phenotype//0006810 // transport // inferred from electronic annotation//0006886 // intracellular protein transport //
1451929_a	0.004153	1.61	-1.28	NM_0011636//NM_0065110	Plscr1	phospholipid scramblase 1	0006366 // transcription from RNA polymerase II promoter // not recorded//0006659 // phosphatidylserine biosynthetic process // inferred from direct assay//0006915 // apoptotic process
1420210_a	0.007587	1.61	1.22	NM_199447//NM_0065265	Rrp12	ribosomal RNA processing 12 homolog (S. cerevisiae)	
1421355_a	0.000188	1.61	1.16	NM_028275//NM_0065196	1700112E06Rik	RIKEN cDNA 1700112E06 gene	0030154 // cell differentiation // inferred from electronic annotation//0030318 // melanocyte differentiation // not recorded
1416997_a	0.000751	1.61	1.88	NM_172589	Lhfp1e2	lipoma HMGIC fusion partner-like 2	
1423441_a	0.002388	1.61	1.08	NM_021547//NM_0065338	Stard3	START domain containing 3	0006694 // steroid biosynthetic process // inferred from electronic annotation//0006701 // progesterone biosynthetic process // inferred from mutant phenotype//0006810 // transport //
1426310_a	0.006771	1.61	-1.02	NM_011103//NM_0065186	Prkcd	protein kinase C, delta	0006468 // protein phosphorylation // inferred from direct assay//0006468 // protein phosphorylation // not recorded//0006915 // apoptotic process // not recorded//0006979 // response
1420332_a	0.000024	1.61	1.21	NM_009735	B2m	beta-2 microglobulin	0001916 // positive regulation of T cell mediated cytotoxicity // inferred from mutant phenotype//0002237 // response to molecule of bacterial origin // inferred from mutant
1419896_a	0.003528	1.61	1.23	NM_006982	5730471H19Rik	RIKEN cDNA 5730471H19 gene	019058 // viral life cycle // inferred from electronic annotation
1426793_a	0.000739	1.61	-1.03	NM_028053//NM_0065380	Tmem38b	transmembrane protein 38b	0006810 // transport // inferred from electronic annotation//0006811 // ion transport // inferred from electronic annotation//0006813 // potassium ion transport // inferred from electronic
1420728_a	0.002002	1.60	1.19	NM_019914//NM_0065018	Mllt11	myeloid/lymphoid or mixed-lineage leukemia (trithorax) homolog, protein disulfide isomerase associated 6	003065 // positive regulation of apoptotic process // not recorded//004893 // positive regulation of transcription, DNA-templated // not recorded//0051901 // positive regulation of
1431995_a	0.000407	1.60	-1.10	NM_027959	Pdia6	protein disulfide isomerase associated 6	0006457 // protein folding // not recorded//0006662 // glycerol ether metabolic process // inferred from electronic annotation//0030168 // platelet activation // inferred from sequence or
1423730_a	0.004699	1.60	1.06	NM_008062//NM_019468	G6pd2//G6pdx	glucose 6-phosphate dehydrogenase 2//glucose 6-phosphate	0001816 // cytokine production // inferred from mutant phenotype//0001816 // cytokine production // not recorded//0001998 // angiogenesis mediated vasoconstriction involved in
1426259_a	0.004521	1.60	-1.02	NM_019501//NM_0064981	Pds1	perylene (solanesyl) diphosphate synthase, subunit 1	0006744 // ubiquinone biosynthetic process // inferred from direct assay//0006744 // ubiquinone biosynthetic process // not recorded//0008152 // metabolic process // inferred from direct
1420380_a	0.000636	1.60	1.21	NM_016698//NM_0065304	Rnf10	ring finger protein 10	0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 // regulation of transcription, DNA-templated // inferred from electronic annotation//00010626 //
1460711_a	0.000736	1.60	-1.34	NM_00109632	Rnf39	ring finger protein 39	
1422485_a	0.006743	1.60	1.12	NM_00108117//NM_0065	Lama5	laminin, alpha 5	0001658 // branching involved in ureteric bud morphogenesis // inferred from mutant phenotype//0001738 // morphogenesis of a polarized epithelium // inferred from mutant
1448461_a	0.000782	1.60	-1.18	NM_153393//NM_0065332	Col2a1	collagen, type XXII, alpha 1	0072007 // protein homotrimerization // not recorded
1419082_a	0.000702	1.60	1.30	NM_007485//NM_0065316	Rhod	ras homolog gene family, member D	0007264 // small GTPase mediated signal transduction // inferred from electronic annotation
1427633_a	0.006558	1.60	-1.06	NM_030889//NM_0065042	Sorcs2	soritin-related VPS10 domain containing receptor 2	0006810 // transport // inferred from electronic annotation
1426674_a	0.007473	1.60	-1.03	NM_018820//NM_0065402	Sertad1	SERTA domain containing 1	0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 // regulation of transcription, DNA-templated // inferred from electronic annotation//0030308 //
1422401_a	0.000101	1.60	1.12	NM_183034	Plekha1	pleckstrin homology domain containing, family M (with RUN domain)	0035556 // intracellular signal transduction // inferred from electronic annotation
1434691_a	0.007423	1.60	-1.13	NM_001253804//NM_0091	Sk12a4	solute carrier family 12, member 4	0006810 // transport // inferred from electronic annotation//0006811 // ion transport // inferred from electronic annotation//0006813 // potassium ion transport // inferred from electronic
1419554_a	0.002415	1.60	1.25	NM_080437//NM_0065116	Celsr3	cadherin, EGF LAG seven-pass G-type receptor 3 (flamingo) homolog, CD80 antigen	0001764 // neuron migration // inferred from mutant phenotype//0007155 // cell adhesion // inferred from electronic annotation//0007156 // homophilic cell adhesion // inferred from
1420970_a	0.002623	1.60	1.17	NM_009855//NM_0065217	Cd80	CD80 antigen	0031295 // T cell costimulation // inferred from direct assay//0042102 // positive regulation of T cell proliferation // inferred from genetic interaction//0042102 // positive regulation of T cell
1416453_a	0.009491	1.60	2.70	NM_001168274//NM_0313	Gsdmc2//Gsdmc4	gasdermin C2//gasdermin C2//gasdermin C4	0060576 // intestinal epithelial cell development // inferred from expression pattern
1426661_a	0.005333	1.60	-1.03	NM_033074	Tors	threonyl-tRNA synthetase	0006412 // translation // inferred from electronic annotation//0006418 // tRNA aminoacylation for protein translation // inferred from electronic annotation//0006435 // threonyl-tRNA
1416906_a	0.001051	1.60	1.95	NM_007582	Cacng1	calcium channel, voltage-dependent, gamma subunit 1	0006810 // transport // inferred from electronic annotation//0006811 // ion transport // inferred from electronic annotation//0006816 // calcium ion transport // inferred from electronic
1428086_a	0.000787	1.60	-1.07	NM_001159502//NM_0204	Ddx24	DEAD (Asp-Glu-Ala-Asp) box polypeptide 24	0006200 // ATP catabolic process // inferred from electronic annotation//0008152 // metabolic process // inferred from electronic annotation
1424420_a	0.008513	1.60	1.04	NM_001112744//NM_0065	Arhgef16	Rho guanine nucleotide exchange factor (GEF) 16	0032863 // activation of Rac GTPase activity // not recorded//0032864 // activation of Cdc42 GTPase activity // not recorded//0035023 // regulation of Rho protein signal transduction //
1422718_a	0.004517	1.59	1.11	NM_001159328//NM_0082	Hgs	HGF-regulated tyrosine kinase substrate	0006810 // transport // inferred from electronic annotation//0006886 // intracellular protein transport // inferred from electronic annotation//0008333 // endosome to lysosome transport //
1427188_a	0.007552	1.59	-1.05	NM_001291215//NM_0012	Phf23	PHD finger protein 23	
1427145_a	0.009001	1.59	-1.05	NM_008943//NM_0065156	Pxen1	presenilin 1	0000045 // autophagic vacuole assembly // inferred from mutant phenotype//0000122 // negative regulation of transcription from RNA polymerase II promoter // inferred from mutant
1423808_a	0.002944	1.59	1.06	NM_011968//NM_0065158	Psmo6	proteasome (prosome, macropain) subunit, alpha type 6	0006508 // proteolysis // inferred from electronic annotation//0006511 // ubiquitin-dependent protein catabolic process // inferred from electronic annotation//0007519 // skeletal muscle
1418609_a	0.005311	1.59	1.36	NM_026384	Dgat2	diacylglycerol O-acyltransferase 2	0006071 // glycerol metabolic process // inferred from electronic annotation//0006629 // lipid metabolic process // inferred from electronic annotation//0019432 // triglyceride biosynthetic
1420404_a	0.000130	1.59	1.22	NM_144905//NM_0065378	6330416G13Rik	RIKEN cDNA 6330416G13 gene	
1424608_a	0.000718	1.59	1.03	NM_134000//NM_0065124	Traf3ip2	TRAF3 interacting protein 2	0001783 // B cell apoptotic process // inferred from mutant phenotype//0006959 // humoral immune response // inferred from mutant phenotype//0043123 // positive regulation of I-
1418273_a	0.000330	1.59	1.41	NM_153795//NM_0065265	Fermt3	fermitin family homolog 3 (Drosophila)	0007155 // cell adhesion // inferred from electronic annotation//0007159 // leukocyte cell-cell adhesion // inferred from mutant phenotype//0007159 // leukocyte cell-cell adhesion //
1450321_a	0.004406	1.59	-1.24	NM_175094	Pdhx	pyruvate dehydrogenase complex, component X	0008152 // metabolic process // inferred from electronic annotation
1423773_a	0.008630	1.59	1.06	NM_001099631	Sh2d5	SH2 domain containing 5	
1451437_a	0.006646	1.58	-1.27	NM_001033272//NM_0065	Spata13	spermatogenesis associated 13	0016477 // cell migration // not recorded//0030032 // lamellipodium assembly // not recorded//0030334 // regulation of cell migration // not recorded//0032314 // regulation of Rac
1422411_s	0.000158	1.58	-1.12	NM_198632//NM_0065311	Trim67	tripartite motif-containing 67	0010976 // positive regulation of neuron projection development // inferred from direct assay//0010976 // positive regulation of neuron projection development // inferred from mutant
1427758_a	0.001651	1.58	-1.06	NM_001177810//NM_0011	Rapgef3	Rap guanine nucleotide exchange factor (GEF) 3	0001525 // angiogenesis // inferred from electronic annotation//0001932 // regulation of protein phosphorylation // inferred from electronic annotation//0007264 // small GTPase mediated
1419315_a	0.000454	1.58	1.28	NM_183263//NM_0065339	Rnm1l	RNA methyltransferase like 1	0001510 // RNA methylation // inferred from electronic annotation//0006396 // RNA processing // inferred from electronic annotation//0032259 // methylation // inferred from electronic
1426885_a	0.001138	1.58	-1.04	NM_016881//NM_0065223	Pmm2	phosphomannomutase 2	0008152 // metabolic process // inferred from electronic annotation//0009298 // GDP-mannose biosynthetic process // inferred from electronic annotation//0019307 // mannose
1419725_a	0.005146	1.58	1.23	NM_145403//NM_0065101	Tmprs4	transmembrane protease, serine 4	0006508 // proteolysis // inferred from electronic annotation//0006888 // receptor-mediated endocytosis // inferred from electronic annotation
1419463_a	0.000404	1.58	1.26	NM_001114595//NM_0011	Ehbp11	EH domain binding protein 1-like 1	
1426565_a	0.004380	1.58	-1.03	NM_009776//NM_0064986	Serpin1	serine (or cysteine) peptidase inhibitor, clade G, member 1	0001869 // negative regulation of complement activation, lectin pathway // not recorded//0002376 // immune system process // inferred from electronic annotation//0006958 //
1422736_a	0.000138	1.58	1.11	NM_021328//NM_0065193	Bn3	bridging integrator 3	0000917 // barrier septum assembly // inferred from electronic annotation//0007049 // cell cycle // inferred from electronic annotation//0008004 // protein localization // inferred from
1426464_a	0.000637	1.58	-1.02	NM_134615//NM_006538	Yors	tyrosyl-tRNA synthetase	0006412 // translation // inferred from electronic annotation//0006418 // tRNA aminoacylation for protein translation // inferred from electronic annotation//0006437 // tyrosyl-tRNA
1429321_a	0.002322	1.58	-1.09	NM_001290454//NM_0233	Ubap1	ubiquitin-associated protein 1	0006810 // transport // inferred from electronic annotation//0015031 // protein transport // inferred from electronic annotation//0043162 // ubiquitin-dependent protein catabolic process
1417027_a	0.006068	1.58	1.87	NM_027097//NM_0065411	Klk12	kallikrein-related peptidase 12	0006508 // proteolysis // not recorded
1453004_a	0.008639	1.58	-1.30	NM_008153//NM_0065301	Cmk1r1	chemokine-like receptor 1	0006935 // chemotaxis // not recorded//0007165 // signal transduction // inferred from electronic annotation//0007186 // G-protein coupled receptor signaling pathway // not
1424698_s	0.008715	1.58	1.03	NM_026115	Hat1	histone aminotransferase 1	0006335 // DNA replication-dependent nucleosome assembly // not recorded//0006336 // DNA replication-independent nucleosome assembly // not recorded//0006348 // chromatin
1426369_a	0.001624	1.58	-1.02	NM_134095//NM_0065210	Des1	desmoylating isopeptidase 1	0006508 // proteolysis // inferred from electronic annotation
1420818_a	0.007363	1.58	1.19	NM_026111	Pqct1	glutaminyl-peptide cyclotransferase-like	0006508 // proteolysis // inferred from electronic annotation//0017186 // peptidyl-pyrogutamic acid biosynthetic process, using glutaminyl-peptide cyclotransferase // not recorded
1426525_a	0.001006	1.58	-1.02	NM_172856//NM_0064994	Cers6	ceramide synthase 6	0006355 // regulation of transcription, DNA-templated // inferred from electronic annotation//0006629 // inferred from metabolic process // inferred from electronic annotation//0030148 //
1425591_a	0.001146	1.58	-1.00	NM_001167578//NM_0093	Tcp10a//Tc10b//Tc10c	t-complex protein 10a//t-complex protein 10b//t-complex protein 10c	
1421976_a	0.000404	1.58	1.14	NM_001253353//NM_0012	Fam214b	family with sequence similarity 214, member B	
1417015_a	0.001119	1.57	1.87	NM_134158//NM_0065321	AF251705	cDNA sequence AF251705	0002376 // immune system process // inferred from electronic annotation//00050715 // positive regulation of cytokine secretion // inferred from direct assay
1423957_a	0.006759	1.57	1.05	NM_001039194//NM_0012	Ajfm2	apoptosis-inducing factor, mitochondrion-associated 2	0008637 // apoptotic mitochondrial process // not recorded//0030261 // chromosome condensation // inferred from sequence or structural similarity//0030261 // chromosome
1424036_a	0.008593	1.57	1.05	NM_001033140	Sdhaf1	succinate dehydrogenase complex assembly factor 1	0034553 // mitochondrial respiratory chain complex II assembly // not recorded

Table S7

Gene ID	p (Corr)	FC-RSV 1 d	FC-RSV 5 d	RefSeq Transcript ID	Gene Symbol	Gene Title	Gene Ontology Biological Process
1439116_a	0.008197	1.57	-1.16	NM_001162993//NM_0281	<i>Ccdc71l</i>	coiled-coil domain containing 71 like	
1420688_a	0.001435	1.57	1.19	NM_007918	<i>Eif4ebp1</i>	eukaryotic translation initiation factor 4E binding protein 1	0000082 // G1/S transition of mitotic cell cycle // not recorded//0002931 // response to ischemia // inferred from electronic annotation//0006417 // regulation of translation // inferred from 1902042 // negative regulation of extrinsic apoptotic signaling pathway via death domain receptors // inferred from direct assay//0090502 // RNA phosphodiester bond hydrolysis,
1420465_s	0.007846	1.57	1.20	NM_024290//XM_0065086	<i>Tnfrsf23//Tnfrsf22</i>	tumor necrosis factor receptor superfamily, member 23//tumor necrosis	
1417616_a	0.007365	1.57	1.59	NM_001144855//XM_0065	<i>Pgfia4</i>	protein tyrosine phosphatase, receptor type, f polypeptide (PTPFR),	
1417801_a	0.004761	1.57	1.54	NM_013901//XM_0065015	<i>Skc39a1</i>	solute carrier family 39 (zinc transporter), member 1	0006810 // transport // inferred from electronic annotation//0006811 // ion transport // inferred from electronic annotation//0006829 // zinc ion transport // inferred from direct
1423280_a	0.000415	1.57	1.08	NM_001159724//NM_0089	<i>Pvr12</i>	poliovirus receptor-related 2	0001675 // acrosome assembly // inferred from mutant phenotype//0002860 // positive regulation of natural killer cell mediated cytotoxicity directed against tumor cell target // not
1418078_a	0.001699	1.57	1.45	NM_023040//NM_121443/	<i>Gfer</i>	growth factor, env1 (S. cerevisiae)-like (augmenter of liver regeneration)	0005514 // oxidation-reduction process // not recorded
1421821_a	0.001188	1.57	1.14	NM_008406//XM_0065185	<i>Ith1</i>	inter-alpha trypsin inhibitor, heavy chain 1	0010466 // negative regulation of peptidase activity // inferred from electronic annotation//0010951 // negative regulation of endopeptidase activity // inferred from electronic
1425089_a	0.001555	1.56	1.01	NM_008368//XM_0065204	<i>Il2rb</i>	interleukin 2 receptor, beta chain	0012221 // cytokine-mediated signaling pathway // not recorded//0030101 // natural killer cell activation // not recorded//0038110 // interleukin-2-mediated signaling pathway // not
1425913_a	0.000021	1.56	-1.01	NM_138953	<i>E12</i>	elongation factor RNA polymerase II 2	0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 // regulation of transcription, DNA-templated // inferred from electronic annotation//0006368 //
1418757_a	0.006786	1.56	1.34	NM_026958	<i>Sirp</i>	SRA stem-loop interacting RNA binding protein	0000961 // negative regulation of mitochondrial RNA catabolic process // inferred from genetic interaction//0006351 // transcription, DNA-templated // inferred from electronic
1427346_a	0.002360	1.56	-1.05	NM_010500	<i>Ier5</i>	immediate early response 5	
1424497_a	0.003954	1.56	1.04	NM_178616	<i>Psmc11</i>	proteasome (prosome, macropain) 26S subunit, non-ATPase, 11	0006511 // ubiquitin-dependent protein catabolic process // not recorded//0043248 // proteasome assembly // not recorded//0048863 // stem cell differentiation // not recorded
1419162_s	0.004050	1.56	1.30	NM_001004435//NM_0010	<i>Pik3r6</i>	phosphoinositide 3-kinase, regulatory subunit 6	0001525 // angiogenesis // inferred from electronic annotation//0007186 // G-protein coupled receptor signaling pathway // inferred from direct assay//0043406 // positive regulation of
1417069_a	0.006633	1.56	1.83	NM_018754	<i>Sfn</i>	stratifin	0000079 // regulation of cyclin-dependent protein serine/threonine kinase activity // inferred from direct assay//0001836 // release of cytochrome c from mitochondria // not
1426629_a	0.009263	1.56	-1.03	NM_025840//XM_0065151	<i>Bzw2//Gm4354//Gm5589</i>	basic leucine zipper and W2 domains 2//predicted gene 4354//predicted	0007275 // multicellular organismal development // inferred from electronic annotation//0007399 // nervous system development // inferred from electronic annotation//0016070 // RNA
1421925_a	0.009951	1.56	1.14	NM_145515//XM_0064971	<i>Mark1</i>	MAP/microtubule affinity-regulating kinase 1	0000226 // microtubule cytoskeleton organization // not recorded//0001764 // neuron migration // not recorded//0006468 // protein phosphorylation // not recorded//0007010 //
1420858_a	0.009046	1.56	1.18	NM_133772//XM_0065097	<i>Ssbp4</i>	single stranded DNA binding protein 4	
1423340_a	0.008069	1.56	1.08	NM_001290565//NM_1535	<i>Syne4</i>	spectrin repeat containing, nuclear envelope family member 4	0045198 // establishment of epithelial cell apical/basal polarity // inferred from mutant phenotype
1420848_a	0.002930	1.56	1.18	NM_011820//XM_0065136	<i>Ggt5</i>	gamma-glutamyltransferase 5	0006508 // proteolysis // inferred from electronic annotation//0006749 // glutathione metabolic process // inferred from electronic annotation//0006750 // glutathione biosynthetic process
1424169_a	0.003248	1.56	1.05	NM_007771//XM_0065131	<i>Cry1</i>	cryptochrome 1 (photolyase-like)	0000122 // negative regulation of transcription from RNA polymerase II promoter // not recorded//0006094 // gluconeogenesis // inferred from mutant phenotype//0006281 // DNA repair //
1421476_a	0.005014	1.55	1.15	NM_025317	<i>Mrlp54</i>	mitochondrial ribosomal protein L54	
1424694_a	0.007303	1.55	1.03	NM_011178	<i>Prtn3</i>	proteainase 3	0006508 // proteolysis // inferred from electronic annotation//0030574 // collagen catabolic process // inferred from electronic annotation//0050765 // negative regulation of phagocytosis //
1450492_a	0.008743	1.55	-1.24	NM_178798//XM_0065311	<i>Sk766</i>	solute carrier family 7 (cationic amino acid transporter, y+ system), member	0003333 // amino acid transmembrane transport // inferred from electronic annotation//0006810 // transport // inferred from electronic annotation//0006865 // amino acid transport //
1427097_a	0.001963	1.55	-1.05	NM_001037711//NM_0012	<i>Cgn</i>	cingulin	0000226 // microtubule cytoskeleton organization // inferred from mutant phenotype//0003382 // epithelial cell morphogenesis // inferred from mutant phenotype//0008152 // metabolic
1449303_a	0.005541	1.55	-1.21	NM_030250	<i>Nus1</i>	nuclear uncondensed prenyl pyrophosphate synthase 1 homolog (S. cerevisiae)	0001525 // angiogenesis // inferred from electronic annotation//0006486 // protein glycosylation // inferred from electronic annotation//0007275 // multicellular organismal development //
1427359_a	0.006659	1.55	-1.05	NM_026942//NR_028146//	<i>Stom1</i>	stomatin-like 1	
1425746_a	0.003434	1.55	-1.01	NM_198163//XM_0065305	<i>Rob35</i>	RAB35, member RAS oncogene family	0009010 // cytokinesis // not recorded//0006184 // GTP catabolic process // inferred from electronic annotation//0006810 // transport // inferred from electronic annotation//0006886 //
1418083_a	0.007908	1.55	1.45	NM_01163489//NM_0011	<i>Sema04</i>	sema domain, immunoglobulin domain (Ig), transmembrane domain (TM)	0001525 // angiogenesis // inferred from electronic annotation//0002292 // T cell differentiation involved in immune response // inferred from mutant phenotype//0002376 // immune
1418587_a	0.003500	1.55	1.36	NM_023901//NM_029805	<i>Tsc22d4</i>	TSC22 domain family, member 4	0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 // regulation of transcription, DNA-templated // inferred from electronic annotation//0006970 //
1428312_a	0.009675	1.55	-1.08	NM_145619//XM_0065117	<i>Parp3</i>	poly (ADP-ribose) polymerase family, member 3	0000723 // telomere maintenance // not recorded//0006302 // double-strand break repair // inferred from genetic interaction//0006302 // double-strand break repair // not
1419979_s	0.007869	1.55	1.22	NM_026464//XR_386010	<i>Wdr55</i>	WD repeat domain 55	0006364 // rRNA processing // inferred from mutant phenotype
1420174_s	0.005717	1.55	1.22	NM_008512	<i>Lrp1</i>	low density lipoprotein receptor-related protein 1	0006897 // endocytosis // inferred from electronic annotation//0006898 // receptor-mediated endocytosis // inferred from direct assay//0006898 // receptor-mediated endocytosis // not
1423094_a	0.002238	1.55	-1.10	NM_008947	<i>Psmc1</i>	protease (prosome, macropain) 26S subunit, ATPase 1	0006281 // DNA repair // inferred from electronic annotation//0006310 // DNA recombination // inferred from electronic annotation//0030163 // protein catabolic process // inferred from
1416453_x	0.009491	1.55	2.75	NM_024230//XM_0065001	<i>Smtm1</i>	smoothelin-like 1	0014823 // response to activity // inferred from mutant phenotype//0018105 // peptidyl-serine phosphorylation // inferred from direct assay//0042493 // response to drug // inferred from
1450990_a	0.000544	1.55	-1.25	NM_001110794//NM_0096	<i>Anxa7</i>	annexin A7	0006874 // cellular calcium ion homeostasis // inferred from mutant phenotype//0006914 // autophagy // not recorded//0007599 // hemostasis // inferred from mutant
1423670_a	0.001684	1.55	1.07	NM_001159551//NM_0011	<i>H13</i>	histocompatibility 13	0006508 // proteolysis // inferred from electronic annotation//0033619 // membrane protein proteolysis // not recorded
1428085_a	0.003575	1.55	-1.07	NM_029929//XM_0065305	<i>Vps33a</i>	vacuolar protein sorting 33A (yeast)	0006810 // transport // inferred from electronic annotation//0006904 // vesicle docking involved in exocytosis // inferred from electronic annotation//0015031 // protein transport //
1423446_a	0.007257	1.55	1.08	NM_172521	<i>Nutn1</i>	NUT midline carcinoma, family member 1	
1420637_a	0.000551	1.55	1.19	NM_176860//XM_0065106	<i>Ubash3b</i>	ubiquitin associated and SH3 domain containing, B	0006469 // negative regulation of protein kinase activity // inferred from mutant phenotype//0035335 // peptidyl-tyrosine dephosphorylation // inferred from mutant phenotype//0051279 //
1436887_x	0.006230	1.54	-1.15	NM_001001738//XM_0065	<i>Itpr1</i>	inositol 1,4,5-trisphosphate receptor interacting protein	0006469 // negative regulation of protein kinase activity // inferred from direct assay//1902042 // negative regulation of extrinsic apoptotic signaling pathway via death domain receptors //
1420017_a	0.000566	1.54	1.22	NM_144522	<i>Tbc1d10b</i>	TBC1 domain family, member 20b	0032313 // regulation of Rab GTPase activity // not recorded//0032851 // positive regulation of Rab GTPase activity // not recorded
1421140_a	0.003322	1.54	1.17	NM_012000//XM_0065088	<i>Cnr8</i>	ceroid-lipofuscinosis, neuronal 8	001306 // age-dependent response to oxidative stress // inferred from mutant phenotype//0006644 // phospholipid metabolic process // inferred from mutant phenotype//0006644 //
1448262_a	0.001829	1.54	-1.17	NM_001287180//NM_0097	<i>Atf4</i>	activating transcription factor 4	0006094 // gluconeogenesis // inferred from direct assay//0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 // regulation of transcription, DNA-
1422143_a	0.003494	1.54	1.13	NM_001127355//NM_0011	<i>Eif2b4</i>	eukaryotic translation initiation factor 2B, subunit 4 delta	0001541 // ovarian follicle development // not recorded//0006412 // translation // inferred from electronic annotation//0006413 // translational initiation // not recorded//0006417 //
1416453_x	0.009491	1.54	2.67	NM_023463	<i>Ly6g6c</i>	lymphocyte antigen 6 complex, locus G6C	
1452474_a	0.005380	1.54	-1.29	NM_135573//XR_377439	<i>Fkbp14</i>	FK506 binding protein 14	0000413 // protein peptidyl-prolyl isomerization // not recorded//0006457 // protein folding // inferred from electronic annotation//0018208 // peptidyl-proline modification // not
1425186_a	0.007864	1.54	1.01	NM_001190768//NM_0011	<i>Ddx19b//Ddx19a</i>	DEAD (Asp-Glu-Ala-Asp) box polypeptide 19b//DEAD (Asp-Glu-Ala-Asp)	0008152 // metabolic process // inferred from electronic annotation//0006810 // transport // inferred from electronic annotation//0010043 // response to zinc // inferred from electronic
1418386_a	0.002342	1.54	1.39	NM_026631	<i>Nhp2</i>	NHP2 ribonucleoprotein	0006364 // rRNA processing // inferred from electronic annotation//0031118 // rRNA pseudouridine synthesis // inferred from sequence or structural similarity//0042254 // ribosome
1424256_a	0.008379	1.54	1.04	NM_001003913//NM_0011	<i>Mars</i>	methionine-tRNA synthetase	0006412 // translation // inferred from electronic annotation//0006418 // tRNA aminoacylation for protein translation // inferred from electronic annotation//0006431 // methionyl-tRNA
1427053_a	0.001435	1.54	-1.04	NM_001160319	<i>Ubr4</i>	ubiquitin protein ligase E3 component n-recogin 4	0016567 // protein ubiquitination // inferred from electronic annotation//0042787 // protein ubiquitination involved in ubiquitin-dependent protein catabolic process // not recorded
1424692_a	0.008219	1.54	1.03	NM_001136085//NM_0012	<i>Uba1</i>	ubiquitin-like modifier activating enzyme 1	0006464 // cellular protein modification process // inferred from electronic annotation//0016567 // protein ubiquitination // inferred from electronic annotation//0016567 // protein
1428114_a	0.003091	1.53	-1.07	NM_001081427//NM_1340	<i>Flnb</i>	filamin, beta	0007519 // skeletal muscle tissue development // inferred from direct assay
1420361_a	0.007026	1.53	1.21	NM_146251//XM_0064980	<i>Pnpla7</i>	patatin-like phospholipase domain containing 7	0006629 // lipid metabolic process // inferred from electronic annotation//0008152 // metabolic process // inferred from electronic annotation
1448480_a	0.001795	1.53	-1.18	NM_007611//XM_0065266	<i>Casp7</i>	caspase 7	0001836 // release of cytochrome c from mitochondria // inferred from genetic interaction//0006508 // proteolysis // inferred from direct assay//0006508 // proteolysis // not
1431931_a	0.006745	1.53	-1.42	NM_172625	<i>Ino80c</i>	INO80 complex subunit C	0006281 // DNA repair // inferred from electronic annotation//0006310 // DNA recombination // inferred from electronic annotation//0006351 // transcription, DNA-templated // inferred
1427717_a	0.009858	1.53	-1.06	NM_001110192//NM_0011	<i>Inpp5d</i>	inositol polyphosphate-5-phosphatase D	0002376 // immune system process // inferred from electronic annotation//0006915 // apoptotic process // inferred from electronic annotation//0008285 // negative regulation of cell
1421956_a	0.000388	1.53	1.14	NM_016740//XM_0030863	<i>Gm12854//Gm5068//S100o1</i>	predicted gene 12854//predicted gene 5068//S100 calcium binding	0007283 // spermatogenesis // inferred from mutant phenotype//0042127 // regulation of cell proliferation // inferred from electronic annotation
1430612_a	0.000775	1.53	-1.40	NM_145458//NM_178279/	<i>Pxk</i>	PX domain containing serine/threonine kinase	0006468 // protein phosphorylation // inferred from electronic annotation//0006954 // inflammatory response // not recorded//0007154 // cell communication // inferred from electronic
1419914_s	0.001313	1.53	1.23	NM_025774	<i>Pkrp1</i>	Pkr interacting protein 1 (IL11 inducible)	0003014 // renal system process // not recorded//000649 // negative regulation of protein kinase activity // inferred from direct assay//0042326 // negative regulation of phosphorylation //
1419078_a	0.001982	1.53	1.30	NM_010226	<i>Foxs1</i>	forkhead box S1	0000122 // negative regulation of transcription from RNA polymerase II promoter // not recorded//0001503 // ossification // not recorded//0001568 // blood vessel development // inferred
1418840_a	0.000751	1.53	1.33	NM_145970//XM_0065308	<i>Cc2d1a</i>	coiled-coil and C2 domain containing 1A	0000122 // negative regulation of transcription from RNA polymerase II promoter // inferred from direct assay//0006351 // transcription, DNA-templated // inferred from electronic
1424771_a	0.000920	1.53	1.03	NM_026325//NR_028418/	<i>Tmem179b</i>	transmembrane protein 179B	
1451764_a	0.000593	1.52	-1.28	NM_019657	<i>Hsd17b12</i>	hydroxysteroid (17-beta) dehydrogenase 12	0006629 // lipid metabolic process // inferred from electronic annotation//0006633 // fatty acid biosynthetic process // inferred from electronic annotation//0006694 // steroid biosynthetic
1423112_a	0.000374	1.52	1.09	NM_001290801//NM_1738	<i>Mga1a</i>	mannoside acetylglucosaminyltransferase 4, isoenzyme A	0005975 // carbohydrate metabolic process // inferred from electronic annotation//0006486 // protein glycosylation // inferred from electronic annotation
1420811_a	0.003043	1.52	1.19	NM_133972//XM_0065097	<i>Arm6c</i>	armadillo repeat containing 6	0002244 // hematopoietic progenitor cell differentiation // inferred from genetic interaction
1418110_a	0.000204	1.52	1.44	NM_027206//XM_0065020	<i>Tnfrsf8/2</i>	tumor necrosis factor, alpha-induced protein 8-like 2	0002376 // immune system process // inferred from electronic annotation//0045087 // innate immune response // inferred from electronic annotation//0050728 // negative regulation of
1438467_a	0.001733	1.52	-1.16	NM_007423	<i>Alp</i>	alpha feto protein	001542 // ovulation from ovarian follicle // inferred from mutant phenotype//0006810 // transport // inferred from electronic annotation//0019953 // sexual reproduction // inferred from
1421156_a	0.003201	1.52	1.17	NM_001081114//XM_0065	<i>Ctip3</i>	CAP-GLY domain containing linker protein 3	0001934 // positive regulation of protein phosphorylation // inferred from direct assay//0010828 // positive regulation of glucose transport // inferred from mutant phenotype//0018230 //
1431843_a	0.001865	1.52	-1.10	NM_001161769//NM_0011	<i>Lmo4</i>	LIM domain only 4	0001843 // neural tube closure // inferred from mutant phenotype//0003281 // ventricular septum development // inferred from mutant phenotype//0006351 // transcription, DNA-
1449347_a	0.002168	1.52	-1.22	NM_001291865//NM_0091	<i>Soi1</i>	spermidine/spermine N1-acetyl transferase 1	0001525 // angiogenesis // inferred from electronic annotation//0006595 // polyamine metabolic process // not recorded//0006598 // polyamine catabolic process // not
1420835_a	0.006268	1.51	1.18	NM_007321//NM_175413/	<i>Lrrc39</i>	leucine rich repeat containing 39	
1418809_a	0.002052	1.51	1.33	NM_001243043//NM_0012	<i>Ap1b1</i>	adaptor protein complex AP-1, beta 1 subunit	0006810 // transport // inferred from electronic annotation//0006886 // intracellular protein transport // traceable author statement//0006897 // endocytosis // inferred from electronic
1422542_a	0.000436	1.51	1.12	NM_013481	<i>Bop1</i>	block of proliferation 1	0000448 // cleavage in ITS2 between 5.8S rRNA and LSU-RNA of tricornicrion rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA) // inferred from mutant phenotype//0000463 // maturation of
1422062_a	0.000730	1.51	1.13	NM_021313//XM_0064961	<i>Rn725</i>	ring finger protein 25	0016567 // protein ubiquitination // inferred from direct assay//00051092 // positive regulation of NF-kappaB transcription factor activity // not recorded
1426501_a	0.000600	1.51	-1.02	NM_025894	<i>Psmc12</i>	proteasome (prosome, macropain) 26S subunit, non-ATPase, 12	
1420804_s	0.002166	1.51	1.19	NM_001081135//XM_0065	<i>Prrg3</i>	proline rich G1a (G-carboxyglutamic acid) 3 (transmembrane)	
1426979_a	0.001748	1.51	-1.04	NM_175675	<i>Sk35f6</i>	solute carrier family 35, member F6	0006810 // transport // inferred from electronic annotation//0008284 // positive regulation of cell proliferation // not recorded//0008643 // carbohydrate transport // inferred from
1423625_s	0.005734	1.51	1.07	NM_013840//XM_0065276	<i>Uxt</i>	ubiquitously expressed transcript	0000122 // negative regulation of transcription from RNA polymerase II promoter // not recorded//0000226 // microtubule cytoskeleton organization // not recorded//0000226 //
1424807_a	0.001761	1.51	1.02	NM_007602//XM_0065072	<i>Capn5</i>	calpain 5	0006508 // proteolysis // not recorded
1419917_s	0.009684	1.51	1.23	NM_001085378//XM_0065	<i>Mylh7b</i>	myosin, heavy chain 7B, cardiac muscle, beta	0008152 // metabolic process // inferred from electronic annotation//0016192 // vesicle-mediated transport // inferred from electronic annotation
1434239_a	0.007384	1.51	-1.12	NM_007961//XM_0065055	<i>Etv6</i>	ets variant 6	0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 // regulation of transcription, DNA-templated // inferred from direct assay//0006357 // regulation
1420514_a	0.005171	1.51	1.20	NM_024478	<i>Grpel1</i>	GrpE-like 1, mitochondrial	0006457 // protein folding // inferred from electronic annotation//0050790 // regulation of catalytic activity // inferred from electronic annotation
1421843_a	0.003399	1.50	1.14	NM_177611//XM_0064978	<i>Psd4</i>	pleckstrin and Sec7 domain containing 4	0030182 // neuron differentiation // not recorded//0032012 // regulation of ARF protein signal transduction // inferred from electronic annotation//0043087 // regulation of GTPase activity
1434280_a	0.005254	1.50	-1.12	NM_011874	<i>Psmc4</i>	proteasome (prosome, macropain) 26S subunit, ATPase, 4	0001824 // blastocyst development // inferred from mutant phenotype//0006281 // DNA repair // inferred from electronic annotation//0006310 // DNA recombination // inferred from
1421304_a	0.000755	1.50	1.16	NM_001293650//NM_0012	<i>Prkch</i>	protein kinase C substrate 80K-H	0001701 // in utero embryonic development // inferred from mutant phenotype//0001889 // liver development // inferred from genetic interaction//0006491 // N-glycan processing //
1417178_a	0.						

Table S7

Gene ID	p (Corr)	FC-RSV 1 d	FC-RSV 5 d	RefSeq Transcript ID	Gene Symbol	Gene Title	Gene Ontology Biological Process
1422964_a	0.001088	1.50	1.10	NM_020619//XM_0065064	Mogs	mannosyl-oligosaccharide glucosidase	0008152 // metabolic process // inferred from electronic annotation//0009311 // oligosaccharide metabolic process // inferred from electronic annotation
1428020_a	0.008532	1.50	-1.07	NM_00128201//NM_0089	Psmd4	prosome (prosome, macropain) 26S subunit, non-ATPase, 4	0006511 // ubiquitin-dependent protein catabolic process // inferred from electronic annotation
1450957_a	0.000341	1.50	-1.25	NM_001163512//NM_1734	Rgs12	regulator of G-protein signaling 12	0007165 // signal transduction // inferred from electronic annotation//0035556 // intracellular signal transduction // inferred from electronic annotation//0038032 // termination of G-
1448350_a	0.008598	1.50	-1.18	NM_001004150//NM_0011	A4golt	alpha 1,4-galactosyltransferase	0001576 // glycoside biosynthetic process // inferred from direct assay//0001576 // glycoside biosynthetic process // inferred from mutant phenotype//0006486 // protein glycosylation //
1425582_a	0.001668	1.50	-1.20	NM_028870//XM_0065174	Cltb	clathrin, light polypeptide (Lcb)	0006886 // intracellular protein transport // inferred from electronic annotation//0006192 // vesicle-mediated transport // inferred from electronic annotation
1419569_a	0.000442	1.50	-1.05	NM_027156	Ddx51	DEAD (Asp-Glu-Ala-Asp) box polypeptide 51	0006200 // ATP catabolic process // inferred from electronic annotation//0006364 // rRNA processing // inferred from electronic annotation//0008152 // metabolic process // inferred from
1422140_a	0.000921	1.50	1.13	NM_026938	Tmem160	transmembrane protein 160	
1419506_a	0.004162	1.50	1.31	NM_145594//XM_0065093	Fgl1	fibrinogen-like protein 1	0008203 // cholesterol metabolic process // inferred from mutant phenotype//0010906 // regulation of glucose metabolic process // inferred from mutant phenotype//0035634 // response
1424004_a	0.007267	1.50	1.21	NM_011875	Psmc13//AK165407	prosome (prosome, macropain) 26S subunit, non-ATPase, 13//Mus	0006568 // proteolysis // not recorded//0007127 // meiosis 1 // inferred from mutant phenotype
1436899_a	0.000893	1.49	-1.15	NM_026772	Cdk42ep2	CDK4 effector protein (Rho GTPase binding) 2	0008360 // regulation of cell shape // not recorded//0030306 // actin cytoskeleton organization // not recorded//0030838 // positive regulation of actin filament polymerization // not
1450502_a	0.002174	1.49	-1.24	NM_001048200//NM_0012	Trsf9	TNF receptor-associated factor 3	0001817 // regulation of cytokine production // inferred from mutant phenotype//0002224 // toll-like receptor signaling pathway // inferred from mutant phenotype//0002376 // immune
1423313_a	0.000545	1.49	1.08	NM_011639//XM_0065045	Trifp6	thyroid hormone receptor interactor 6	0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 // regulation of transcription, DNA-templated // inferred from electronic annotation//0007155 //
1434997_a	0.002732	1.49	-1.47	NM_028810	Rnd3	Rho family GTPase 3	0006184 // GTP catabolic process // inferred from electronic annotation//0007165 // signal transduction // inferred from electronic annotation//0007264 // small GTPase mediated signal
1420007_a	0.004957	1.49	1.22	NM_145606	Chmp10	charged multivesicular body protein 1A	0009910 // cytokinesis // not recorded//0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 // regulation of transcription, DNA-templated // inferred
1423896_a	0.002065	1.49	1.06	NM_030238	Dync1h1	dynein cytoplasmic 1 heavy chain 1	0003341 // cilium movement // inferred by curator//0006200 // ATP catabolic process // inferred from electronic annotation//0006810 // transport // inferred from electronic
1437145_s	0.000551	1.49	-1.15	NM_025837//XM_0065107	Mpi	mannose phosphate isomerase	0005975 // carbohydrate metabolic process // inferred from electronic annotation//0006013 // mannose metabolic process // inferred by curator//0009298 // GDP-mannose biosynthetic
1424303_a	0.002070	1.49	1.04	NM_008948	Psmc3	prosome (prosome, macropain) 26S subunit, ATPase 3	0001824 // blastocyst development // inferred from mutant phenotype//0006281 // DNA repair // inferred from electronic annotation//0006310 // DNA recombination // inferred from
1423592_a	0.006144	1.49	1.07	NM_011188	Psmc2	prosome (prosome, macropain) 26S subunit, ATPase 2	0001649 // osteoblast differentiation // not recorded//0006200 // ATP catabolic process // not recorded//0006511 // ubiquitin-dependent protein catabolic process // not
1442761_a	0.006230	1.49	-1.68	NM_001145957//NM_1727	Vwa5a	von Willebrand factor A domain containing 5A	
1419204_a	0.001009	1.49	1.29	NM_001162999//XM_0065	Fnip2	folliculin interacting protein 2	0000122 // negative regulation of transcription from RNA polymerase II promoter // not recorded//0001932 // regulation of protein phosphorylation // not recorded//0006468 // protein
1423855_x	0.000568	1.49	1.06	NM_029353//XM_0065067	Malsu1	mitochondrial assembly of ribosomal large subunit 1	0042273 // ribosomal large subunit biogenesis // not recorded//0007010 // negative regulation of mitochondrial translation // not recorded
1425427_a	0.002796	1.49	1.00	NM_001014996//XM_0065	CenpJ	centromere protein 1	0007099 // centriole replication // not recorded//0030954 // astral microtubule nucleation // not recorded//0046427 // positive regulation of JAK-STAT cascade // not recorded//0046599 //
1427321_s	0.000685	1.49	-1.05	NM_008391//XM_0065092	Irf2	interferon regulatory factor 2	0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 // regulation of transcription, DNA-templated // inferred from electronic
1429809_a	0.008340	1.49	-1.39	NM_008927//XM_0065111	Map2k1	mitogen-activated protein kinase kinase 1	0001665 // MAPK cascade // inferred from mutant phenotype//0001665 // MAPK cascade // not recorded//0000187 // activation of MAPK activity // inferred from mutant
1423274_a	0.008340	1.49	1.09	NM_001166589//NM_0011	Etf5a	eukaryotic translation initiation factor 5A	0006406 // mRNA export from nucleus // not recorded//0006412 // translation // inferred from electronic annotation//0006414 // translational elongation // inferred from electronic
1423992_a	0.001548	1.48	1.05	NM_001276425//NM_0113	Slgcpalnc4	5T6 (alpha N-acetyl-neuraminyl-2,3-beta-galactosyl-1,3)-N-	0004486 // protein glycosylation // inferred from electronic annotation//0008152 // metabolic process // inferred from electronic annotation//0007503 // sialylation // inferred from
1426410_a	0.000212	1.48	-1.02	NM_153167//XM_0065379	Dcof10	DBD1 and CUL4 associated factor 10	0016567 // protein ubiquitination // inferred from electronic annotation
1425214_a	0.003812	1.48	1.01	NM_001111267//NM_1724	Ncoo7	nuclear receptor coactivator 7	0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 // regulation of transcription, DNA-templated // inferred from electronic annotation//0045944 //
1424305_a	0.009295	1.48	1.04	NM_177638//XM_0065241	Crb3	crumbs homolog 3 (Drosophila)	0045198 // establishment of epithelial cell apical/basal polarity // not recorded//0045216 // cell-cell junction organization // not recorded//0007269 // protein localization to plasma
1422617_a	0.006230	1.48	1.11	NM_009729	Atp6v0c	ATPase, H ⁺ transporting, lysosomal V0 subunit C	0006200 // ATP catabolic process // not recorded//0006810 // transport // inferred from electronic annotation//0006811 // ion transport // inferred from electronic annotation//0007035 //
1425025_a	0.002550	1.48	1.01	NM_029391//XM_0065396	Rab4b	RAB4B, member RAS oncogene family	0006184 // GTP catabolic process // inferred from electronic annotation//0006810 // transport // inferred from electronic annotation//0006886 // intracellular protein transport // inferred
1451508_a	0.004366	1.48	-1.27	NM_011504	Sxbp3a	synovial binding protein 3A	0006810 // transport // inferred from electronic annotation//0006887 // exocytosis // inferred from mutant phenotype//0006904 // vesicle docking involved in exocytosis // inferred from
1423855_x	0.000568	1.48	1.06	NM_019803	Ube2g2	ubiquitin-conjugating enzyme E2G 2	0016567 // protein ubiquitination // inferred from electronic annotation//0018279 // protein N-linked glycosylation via asparagine // not recorded//0030433 // ER-associated ubiquitin-
1420710_a	0.002581	1.48	1.19	NM_001037762//NM_0254	Zdhc12	zinc finger, DHHC domain containing 12	0008152 // metabolic process // inferred from electronic annotation//0018345 // protein palmitoylation // not recorded
1434468_a	0.009721	1.48	-1.12	NM_144831	Dhx8	DEAH (Asp-Glu-Ala-His) box polypeptide 8	0006200 // ATP catabolic process // inferred from electronic annotation//0006397 // mRNA processing // inferred from electronic annotation//0008152 // metabolic process // inferred from
1418393_a	0.008230	1.48	1.39	NM_001010836//XM_0065	Ppp1r13l	protein phosphatase 1, regulatory (inhibitor) subunit 13 like	0000122 // negative regulation of transcription from RNA polymerase II promoter // inferred from mutant phenotype//0003215 // cardiac right ventricle morphogenesis // inferred from
1424254_a	0.003040	1.48	1.04	NM_001130479//NM_0167	Nucb2	nucleobindin 2	0006874 // cellular calcium ion homeostasis // traceable author statement
1423765_a	0.002351	1.48	1.06	NM_025433	Rpl7l1	ribosomal protein L7-like 1	
1433442_a	0.002815	1.48	-1.11	NM_001252658//NM_0012	Ldlr	low density lipoprotein receptor	0006629 // lipid metabolic process // inferred from genetic interaction//0006810 // transport // inferred from electronic annotation//0006869 // lipid transport // inferred from electronic
1428795_a	0.002410	1.47	-1.36	NM_181728//XM_0065347	Art3	ADP-ribosyltransferase 3	0006471 // protein ADP-ribosylation // inferred from electronic annotation//0008152 // metabolic process // inferred from electronic annotation
1424975_a	0.003109	1.47	1.02	NM_174338//XM_0065144	Thoc5	THO complex 5	0009902 // cell morphogenesis // inferred from mutant phenotype//0001824 // blastocyst development // inferred from mutant phenotype//0006397 // mRNA processing // inferred from
1435462_a	0.002359	1.47	-1.13	NM_00104805//NM_1304	Dusp16	dipyrrolic phosphatase 16	0000188 // inactivation of MAPK activity // not recorded//0000188 // inactivation of MAPK activity // inferred from direct assay//0006470 // protein dephosphorylation // not
1421216_a	0.006796	1.47	1.16	NM_133803//XM_0065318	Dpp3	dipyrrolic phosphatase 3	0005086 // proteolysis // not recorded
1430845_a	0.003161	1.47	-1.10	NM_010893	Neu1	neuraminidase 1	0005975 // carbohydrate metabolic process // inferred from electronic annotation//0006629 // lipid metabolic process // inferred from electronic annotation//0008152 // metabolic process
1429336_a	0.001179	1.47	-1.37	NM_013885	Clic4	chloride intracellular channel 4 (mitochondrial)	0001525 // angiogenesis // inferred from mutant phenotype//0001886 // endothelial cell morphogenesis // inferred from mutant phenotype//0006810 // transport // inferred from
1449402_a	0.005254	1.47	-1.22	NM_026617	Tmbim4	transmembrane BAX inhibitor motif containing 4	0006915 // apoptotic process // inferred from electronic annotation//0043066 // negative regulation of apoptotic process // not recorded//0005048 // regulation of calcium-mediated
1425215_a	0.001071	1.47	1.01	NM_026538//XM_0065147	Ddx56	DEAD (Asp-Glu-Ala-Asp) box polypeptide 56	0006364 // rRNA processing // inferred from electronic annotation//0008152 // metabolic process // inferred from electronic annotation//0042254 // ribosome biogenesis // inferred from
1431464_a	0.002107	1.47	-1.10	NM_029211//XM_0065082	Rnf121	ring finger protein 121	
1431724_a	0.003280	1.47	-1.10	NM_144866//XM_0065258	Etf1	eukaryotic translation termination factor 1	0000184 // nuclear-transcribed mRNA catabolic process, nonsense-mediated decay // inferred from electronic annotation//0006412 // translation // inferred from electronic
1426315_a	0.003090	1.47	-1.02	NM_080837	D17Wsu104e	DNA segment, Chr 17, Wayne State University 104, expressed	
1416205_a	0.008896	1.47	1.04	NM_009694	Apobec2	apolipoprotein B mRNA editing enzyme, catalytic polypeptide 2	0006397 // mRNA processing // inferred from electronic annotation//0016556 // mRNA modification // inferred from mutant phenotype//0008011 // DNA demethylation // not recorded
1424933_a	0.001883	1.47	1.02	NM_146065	Atf7	activating transcription factor 7	0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 // regulation of transcription, DNA-templated // not recorded
1436528_a	0.001913	1.47	-1.14	NM_011324	Scnn1a	sodium channel, nonvoltage-gated 1 alpha	0006810 // transport // inferred from electronic annotation//0006811 // ion transport // inferred from electronic annotation//0006814 // sodium ion transport // inferred from direct
1434930_a	0.004704	1.47	-1.13	NM_001164406//NM_0252	Sra1	steroid receptor RNA activator 1	0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 // regulation of transcription, DNA-templated // inferred from electronic annotation//0006357 //
1419580_a	0.005494	1.47	1.25	NM_026678//XM_0064985	Bivra	biliverdin reductase A	0042167 // heme catabolic process // not recorded//0055114 // oxidation-reduction process // inferred from direct assay//0055114 // oxidation-reduction process // not recorded
1426628_a	0.001518	1.47	-1.03	NM_172410//XM_0065313	Nup93	nucleoporin 93	0006810 // transport // inferred from electronic annotation//0015031 // protein transport // inferred from electronic annotation//0015028 // mRNA transport // inferred from electronic
1422309_a	0.001552	1.47	1.12	NM_025397	Med11	mediator complex subunit 11	0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 // regulation of transcription, DNA-templated // inferred from electronic annotation//0006357 //
1426433_a	0.005146	1.46	-1.02	NM_001034168//NM_1786	Ank2	ankyrin 2, brain	0002027 // regulation of heart rate // inferred from mutant phenotype//0003283 // atrial septum development // inferred from electronic annotation//0006874 // cellular calcium ion
1429146_a	0.004616	1.46	-1.36	NM_027514	Pvr	poliovirus receptor	0002860 // positive regulation of natural killer cell mediated cytotoxicity directed against tumor cell target // inferred from electronic annotation//0009615 // response to virus // not
1427082_a	0.008031	1.46	-1.05	NM_146216//XM_0065309	Voc14	Vac14 homolog (S. cerevisiae)	0006970 // response to osmotic stress // not recorded//0008219 // cell death // inferred from electronic annotation//0042327 // positive regulation of phosphorylation // not
1449925_a	0.004689	1.46	-1.23	NM_001081394//NM_0278	Tmem248	transmembrane protein 248	
1419669_a	0.002386	1.46	1.24	NM_030131	Cnrl4	cornichon homolog 4 (Drosophila)	0035556 // intracellular signal transduction // inferred from electronic annotation
1434980_a	0.004089	1.46	-1.47	NM_026816	Gtf2f2	general transcription factor IIF, polypeptide 2	0006200 // ATP catabolic process // inferred from electronic annotation//0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 // regulation of
1455184_a	0.002186	1.46	-1.32	NM_025445//XM_0065212	Arfgap3	ADP-ribosylation factor GTPase activating protein 3	0006810 // transport // inferred from electronic annotation//0009306 // protein secretion // inferred from electronic annotation//0009306 // protein secretion // inferred from sequence or
1424226_a	0.007972	1.46	1.05	NM_183257	Hamp2	hepcidin antimicrobial peptide 2	0006879 // cellular iron ion homeostasis // inferred from electronic annotation//0003160 // killing of cells of other organism // inferred from electronic annotation//0042742 // defense
1420964_a	0.003048	1.46	1.18	NM_00114332//NM_0282	Slc16a10	solute carrier family 16 (monocarboxylic acid transporters), member 10	0006810 // transport // inferred from electronic annotation//0055085 // transmembrane transport // inferred from electronic annotation
1424236_a	0.004036	1.46	1.05	NM_024442//XM_0065248	Cyp4f16//Cyp4f37	cytochrome P450, family 4, subfamily 1, polypeptide 16//cytochrome P450,	0055114 // oxidation-reduction process // inferred from electronic annotation
1420768_a	0.00034	1.46	1.19	NM_001081333//NM_1753	Plekha9	pleckstrin homology domain containing, family 16 (with RhoGEF domain)	0032321 // positive regulation of Rho GTPase activity // inferred from electronic annotation//0035023 // regulation of Rho protein signal transduction // inferred from electronic annotation
1433636_a	0.004178	1.46	-1.11	NM_019776//XM_0065051	Snd1	staphyloccocal nuclease and tudor domain containing 1	0001649 // osteoblast differentiation // not recorded//0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 // regulation of transcription, DNA-
1424768_a	0.009416	1.46	1.03	NM_001172136//NM_1724	Exog	endo/exonuclease (5'-3'), endonuclease G-like	0007037 // DNA catabolic process, endonucleolytic // not recorded
1418084_a	0.003096	1.46	1.45	NM_001141930//NM_0234	Ctnnbip1	catenin beta interacting protein 1	0000122 // negative regulation of transcription from RNA polymerase II promoter // inferred from direct assay//0001658 // branching involved in ureteric bud morphogenesis // inferred from
1424938_a	0.009350	1.46	1.02	NM_001163742//NM_0011	Nlr1x	NLR family member X1	0002376 // immune system process // inferred from electronic annotation//0016032 // viral process // inferred from electronic annotation//0019048 // modulation by virus of host
1454759_a	0.005470	1.45	-1.32	NM_008268	Hoxb5	homeobox B5	0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 // regulation of transcription, DNA-templated // inferred from direct assay//0006366 //
1418697_a	0.000306	1.45	1.35	NM_001290299//NM_1449	BC018242	cDNA sequence BC018242	0008152 // metabolic process // inferred from electronic annotation//0016311 // dephosphorylation // inferred from electronic annotation
1421330_a	0.006203	1.45	1.16	NM_144543//XM_0065106	Thyn1	thymocyte nuclear protein 1	
1421692_a	0.004421	1.45	1.11	NM_019511//XM_0065147	Rmp3	receptor (calcitonin) activity modifying protein 3	0001921 // positive regulation of receptor recycling // not recorded//0006810 // transport // inferred from electronic annotation//0006816 // calcium ion transport // not
1423665_a	0.000180	1.45	1.07	NM_027030	Dcps	decapping enzyme, scavenger	0002990 // deadenylation-dependent decapping of nuclear-transcribed mRNA // inferred from electronic annotation//0006397 // mRNA processing // inferred from electronic
1424783_a	0.004054	1.45	1.03	NM_029634//XM_0065118	Ipk6i2	inositol hexaphosphate kinase 2	0006817 // phosphate ion transport // not recorded//0016310 // phosphorylation // inferred from electronic annotation//0030308 // negative regulation of cell growth // not
1423724_a	0.000473	1.45	1.06	NM_201368//XM_0065389	Xkr8	X cell heparan glyco precursor related family member 8 homolog	0006915 // apoptotic process // inferred from electronic annotation//0043652 // engulfment of apoptotic cell // not recorded//0007782 // phosphatidylserine exposure on apoptotic cell
1423215_a	0.003039	1.45	1.09	NM_020517//NM_177041	Flad1//Lenep	RFaD1, flavin adenine dinucleotide synthetase, homologue (yeast)/lens	0006747 // FAD biosynthetic process // inferred from electronic annotation//0006777 // Mo-molybdopter cofactor biosynthetic process // inferred from electronic annotation//0007275 //
1422745_a	0.008022	1.45	1.10	NM_027098//XM_0064956	Gm6238//Mrpl30	predicted pseudogene G238//mitochondrial ribosomal protein L30	
1420499_a	0.000058	1.45	1.20	NM_197993	Tut1	terminal uridylyl transferase 1, U6 snRNA-specific	0006378 // mRNA polyadenylation // not recorded//0006379 // mRNA cleavage // not recorded//0006397 // mRNA processing // inferred from electronic annotation//0016180 // snRNA
1424364_a	0.004357	1.45	1.04	NM_172704	Dnajc11	DnaJ (Hsp40) homolog, subfamily C, member 11	
1427867_a	0.008022	1.45	-1.06	NM_001284332//NM_0258	Shiso5	shisa homolog 5 (Xenopus laevis)	0006915 // apoptotic process // inferred from electronic annotation//0007165 // signal transduction // not recorded//0042771 // intrinsic apoptotic signaling pathway in response to DNA
1425653_a	0.006247	1.45	-1.00	NM_001159375//NM_1449	Etf4a1	eukaryotic translation initiation factor 4A1	0006200 // ATP catabolic process // inferred from electronic annotation//0006412 // translation // inferred from electronic annotation//0006413 // translational initiation // inferred from
1450206_a	0.001995	1.45	-1.24	NM_001171007//NM_1727	Nod1	nucleotide-binding oligomerization domain containing 1	0002376 // immune system process // inferred from electronic annotation//0002606 // positive regulation of dendritic cell antigen processing and presentation // inferred from mutant
1417889_a	0.002420	1.45	1.51	NM_008360//XM_0065100	Il18	interleukin 18	0001665 // MAPK cascade // not recorded//0001525 // angiogenesis // not recorded//0001525 // angiogenesis // inferred from sequence or structural similarity//0001666 // response to
1456398_a	0.000279	1.45	-1.33	NM_001252629//NM_0114	Snm1	survival motor neuron 1	0000387 // spliceosomal snRNP assembly // inferred from sequence or structural similarity//0006397 // mRNA processing // inferred from electronic annotation//0007019 // microtubule

Table S7

Gene ID	p (Corr)	FC-RSV 1 d	FC-RSV 5 d	RefSeq Transcript ID	Gene Symbol	Gene Title	Gene Ontology Biological Process
1421384_a	0.002174	1.44	1.16	NM_029370	<i>Spato25</i>	spermatogenesis associated 25	0007283 // spermatogenesis // inferred from electronic annotation//0030154 // cell differentiation // inferred from electronic annotation
1430433_a	0.001963	1.44	-1.40	NM_008105//NM_023887/	<i>Gcnt2</i>	glucosaminyl (N-acetyl) transferase 2, I-branching enzyme	0006486 // protein glycosylation // not recorded//0007179 // transforming growth factor beta receptor signaling pathway // inferred from mutant phenotype//0007179 // transforming
1437956_a	0.004443	1.44	-1.54	NM_013918//NM_0065230	<i>Usp25</i>	ubiquitin specific peptidase 25	0006508 // proteolysis // not recorded//0006511 // ubiquitin-dependent protein catabolic process // inferred from sequence or structural similarity//0007036 // protein K63-linked
1435573_a	0.004646	1.44	-1.14	NM_133224//NM_0065095	<i>Atp13a1</i>	ATPase type 13A1	0006200 // ATP catabolic process // inferred from electronic annotation//0006810 // transport // inferred from electronic annotation//0006812 // cation transport // inferred from electronic
1427993_a	0.002415	1.44	-1.06	NM_021604//NM_0065384	<i>Agrn</i>	agrin	0001932 // regulation of protein phosphorylation // not recorded//001934 // positive regulation of protein phosphorylation // inferred from direct assay//0007009 // plasma membrane
1423090_x	0.006331	1.44	1.09	NM_013571//NM_0065323	<i>Ksr1</i>	kinase suppressor of ras 1	0006468 // protein phosphorylation // inferred from electronic annotation//001569 // phosphorylation // inferred from electronic annotation//0035556 // actin cytoskeleton signal transduction //
1441268_a	0.004555	1.44	-1.14	NM_027519//NM_0065049	<i>Medag</i>	mesenteric estrogen dependent adipogenesis	0045600 // positive regulation of fat cell differentiation // inferred from mutant phenotype
1421266_x	0.000646	1.44	1.16	NM_029821//NM_0065362	<i>Urah</i>	urate (5-hydroxy) hydrolase	0006144 // purine nucleobase metabolic process // inferred from electronic annotation//0006810 // transport // inferred from electronic annotation//0019628 // urate catabolic process //
1449367_a	0.0012506	1.44	-1.22	NM_133921//NM_0065036	<i>Nfkl</i>	nuclear transcription factor, X-box binding-like 1	0006355 // regulation of transcription, DNA-templated // inferred from electronic annotation
1424090_a	0.001915	1.44	1.05	NM_001290455//NM_2076	<i>Gripap1</i>	GRIP1 associated protein 1	
1451253_a	0.001458	1.44	-1.27	NM_016753//NM_0065319	<i>Sk35b1</i>	solute carrier family 35, member B1	0006810 // transport // inferred from electronic annotation//0008643 // carbohydrate transport // inferred from electronic annotation//0055085 // transmembrane transport // inferred
1421370_a	0.000408	1.44	1.16	NM_145122//NR_028114//	<i>Pex16</i>	peroxisomal biogenesis factor 16	0006625 // protein targeting to peroxisome // not recorded//0007031 // peroxisome organization // not recorded//0016557 // peroxisome membrane biogenesis // not recorded//0016558
1449014_a	0.001733	1.44	-1.20	NM_009045//NM_0065316	<i>Rela</i>	v- <i>rel</i> reticuloendotheliosis viral oncogene homolog A (avian)	0001889 // liver development // inferred from mutant phenotype//0001942 // hair follicle development // inferred from mutant phenotype//0006117 // acetaldehyde metabolic process //
1451475_a	0.004380	1.44	-1.27	NM_001290769//NM_0110	<i>Sqstm1</i>	sequestosome 1	0001934 // positive regulation of protein phosphorylation // not recorded//0002376 // immune system process // inferred from electronic annotation//0006914 // autophagy // not
1452675_a	0.001537	1.44	-1.30	NM_028248//NM_0065002	<i>Tmem87b</i>	transmembrane protein 87B	
1423767_a	0.004810	1.44	1.06	NM_030710//NM_0064968	<i>Slamf6</i>	SLAM family member 6	
1423586_a	0.000154	1.44	1.07	NM_138682	<i>Lrrc4</i>	leucine rich repeat containing 4	0050807 // regulation of synapse organization // inferred from mutant phenotype//0050808 // synapse organization // inferred from direct assay//0007119 // postsynaptic density protein 95
1422847_a	0.000436	1.44	1.10	NM_025624	<i>Pomp</i>	proteasome maturation protein	0043248 // proteasome assembly // not recorded
1418982_a	0.005635	1.44	1.31	NM_008108//NM_0065055	<i>Gdf3</i>	growth differentiation factor 3	0001501 // skeletal system development // not recorded//0001654 // eye development // not recorded//0001701 // in utero embryonic development // inferred from genetic
1450706_a	0.002529	1.44	-1.25	NM_009601//NM_0065320	<i>Chmb1</i>	cholinergic receptor, nicotinic, beta polypeptide 1 (muscle)	0001941 // postsynaptic membrane organization // not recorded//0003009 // skeletal muscle contraction // not recorded//0006810 // transport // inferred from electronic
1426661_a	0.005333	1.43	-1.03	NM_009931//NM_0065086	<i>Col4a1</i>	collagen, type IV, alpha 1	0001525 // angiogenesis // inferred from electronic annotation//0001569 // patterning of blood vessels // not recorded//0007420 // brain development // not recorded//0007528 //
1427981_a	0.002746	1.43	-1.06	NM_172691//NM_0065029	<i>Prpf38a</i>	PRPF38 pre-mRNA processing factor 38 (yeast) domain containing A	0006397 // mRNA processing // inferred from electronic annotation//0008380 // RNA splicing // inferred from electronic annotation
1424438_a	0.007803	1.43	1.04	NM_001149595//NM_0138	<i>Ndrg2</i>	N-myc downstream regulated gene 2	0001818 // negative regulation of cytokine production // inferred from mutant phenotype//0007165 // signal transduction // not recorded//0007275 // multicellular organismal development
1449279_a	0.002587	1.43	-1.21	NM_001025261//NM_0010	<i>Tpds2</i>	Janus protein D52	0008284 // positive regulation of cell proliferation // inferred from direct assay//0003183 // B cell differentiation // inferred from sequence or structural similarity//00030183 // B cell
1426428_a	0.006613	1.43	-1.02	NM_00104817//NM_0084	<i>JoK2</i>	tyrosine kinase 2	0001186 // activation of MAPK activity // not recorded//0002376 // immune system process // inferred from electronic annotation//0006468 // protein phosphorylation // inferred from
1424966_a	0.000293	1.43	1.02	NM_00104414//NM_0065	<i>Grl1</i>	G protein-coupled receptor kinase-interactor 1	0008277 // regulation of G-protein coupled receptor protein signaling pathway // not recorded//0002332 // regulation of ARF GTPase activity // inferred from electronic annotation//0043547
1430886_a	0.002322	1.43	-1.41	NM_146068//NM_0065220	<i>Spidr</i>	scaffolding protein involved in DNA repair	0007724 // double-strand break repair via homologous recombination // not recorded//0006281 // DNA repair // inferred from electronic annotation//0006310 // DNA recombination //
1424886_a	0.000101	1.43	1.02	NM_001195083//NM_0011	<i>Phc2</i>	polyhomocytic-like 2 (Drosophila)	0007275 // multicellular organismal development // inferred from electronic annotation//0007283 // spermatogenesis // inferred from genetic interaction
1423017_a	0.000023	1.43	1.10	NM_028794//NM_0065352	<i>Nudt9</i>	nudix (nucleoside diphosphate linked moiety X)-type motif 9	0046032 // ADP catabolic process // inferred from direct assay//0046709 // IDP catabolic process // inferred from direct assay
1427996_a	0.009613	1.43	-1.06	NM_001293560//NM_1737	<i>Ccbl2</i>	cysteine conjugate beta lyase 2	0006103 // 2-oxoglutarate metabolic process // inferred from direct assay//0006520 // cellular amino acid metabolic process // inferred from direct assay//0009058 // biosynthetic process //
1435725_x	0.005915	1.43	-1.14	NM_028028	<i>Zswim1</i>	zinc finger SWIM-type containing 1	
1421147_a	0.004999	1.43	1.17	NM_009344	<i>Phldo1</i>	pleckstrin homology-like domain, family A, member 1	0006915 // apoptotic process // inferred from electronic annotation//0007010 // cytoskeleton organization // inferred from electronic annotation//0021879 // forebrain neuron
1423771_a	0.000556	1.43	1.06	NM_001164353//NM_0011	<i>Sk25a25</i>	solute carrier family 25 (mitochondrial carrier, phosphate carrier), member 8	0002021 // response to dietary excess // inferred from mutant phenotype//0006810 // transport // inferred from electronic annotation//00014823 // response to activity // inferred from
1423895_a	0.000296	1.43	1.06	NM_025794	<i>Etfdh</i>	electron transferring flavoprotein, dehydrogenase	0006810 // transport // inferred from electronic annotation//0006979 // response to oxidative stress // inferred from direct assay//0022900 // electron transport chain // not
1426411_a	0.000058	1.43	-1.02	NM_028020//NM_0065391	<i>Cpsf3l</i>	cleavage and polyadenylation specific factor 3-like	0008152 // metabolic process // inferred from electronic annotation//0016180 // snRNA processing // inferred from sequence or structural similarity
1422156_a	0.000960	1.43	1.13	NM_001081128//NM_0065	<i>Mtr</i>	5-methyltetrahydrofolate-homocysteine methyltransferase	0006479 // protein methylation // not recorded//0006555 // methionine metabolic process // not recorded//0008652 // cellular amino acid biosynthetic process // inferred from electronic
1421030_a	0.009388	1.43	1.17	NM_001256096//NM_0012	<i>Dtx2</i>	deltex 2 homolog (Drosophila)	0007219 // Notch signaling pathway // inferred from direct assay//0007219 // Notch signaling pathway // traceable author statement//00016567 // protein ubiquitination // inferred from
1425628_a	0.001013	1.43	-1.00	NM_127584	<i>Itpk1</i>	inositol 1,3,4-trisphosphate 5/6 kinase	0016310 // phosphorylation // inferred from electronic annotation//0032957 // inositol trisphosphate metabolic process // inferred from electronic annotation
1448591_a	0.000693	1.43	-1.18	NM_133770//NM_0065404	<i>Adck4</i>	aar domain containing kinase 4	0006468 // protein phosphorylation // inferred from electronic annotation//0008152 // metabolic process // inferred from electronic annotation//0016310 // phosphorylation // inferred
1425587_a	0.003925	1.43	-1.00	NM_018807	<i>Plagl2</i>	pleomorphic adenoma gene-like 2	0006351 // transcription, DNA-templated // inferred from electronic annotation//0006357 // regulation of transcription from RNA polymerase II promoter // not recorded//0006366 //
1427346_a	0.002360	1.43	-1.05	NM_001077363//NM_0012	<i>Ptbp1</i>	polyprotein-ribose tract binding protein 1	0000381 // regulation of alternative mRNA splicing, via spliceosome // not recorded//0006397 // mRNA processing // inferred from electronic annotation//0008380 // RNA splicing // inferred
1421322_a	0.000288	1.43	1.16	NM_001199283//NM_0011	<i>Sk43a2</i>	solute carrier family 43, member 2	0015807 // L-amino acid transport // inferred from direct assay//0005508 // transmembrane transport // inferred from electronic annotation//1902475 // L-alpha-amino acid transmembrane
1448986_x	0.005162	1.43	-1.20	NM_178793//NM_0065360	<i>Cbr1</i>	collagen and calcium binding EGF domains 1	0001525 // angiogenesis // inferred from electronic annotation//0001946 // lymphangiogenesis // inferred from mutant phenotype//0001946 // lymphangiogenesis // not
1449041_a	0.000606	1.42	-1.20	NM_026373//NM_0065317	<i>Cdk2ap2</i>	CDK2-associated protein 2	
1422429_a	0.000279	1.42	1.12	NM_001190443//NM_0138	<i>AkcJ2</i>	ATP-binding cassette, sub-family F (GCN20), member 2	0006200 // ATP catabolic process // inferred from electronic annotation//0008152 // metabolic process // inferred from electronic annotation
1449007_a	0.006070	1.42	-1.20	NM_010303//NM_0065322	<i>Gnao13</i>	guanine nucleotide binding protein, alpha 13	0001525 // angiogenesis // inferred from mutant phenotype//0001569 // patterning of blood vessels // inferred from mutant phenotype//0001701 // in utero embryonic development //
1427305_a	0.001559	1.42	-1.05	NM_023913	<i>Ern1</i>	endoplasmic reticulum (ER) to nucleus signaling 1	0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 // regulation of transcription, DNA-templated // inferred from electronic annotation//0006397 //
1448919_a	0.001534	1.42	-1.20	NM_011715//NM_0065038	<i>Wdr1</i>	WD repeat domain 1	0007605 // sensory perception of sound // not recorded//0048713 // regulation of oligodendrocyte differentiation // --
1423590_a	0.003406	1.42	1.07	NM_008945	<i>Psmb4</i>	proteasome (prosome, macropain) subunit, beta type 4	0002862 // negative regulation of inflammatory response to antigenic stimulus // inferred from mutant phenotype//0006508 // proteolysis // inferred from electronic annotation//0051603 //
1432430_a	0.001699	1.42	-1.11	NM_001256104//NM_1454	<i>Sk10a3</i>	solute carrier family 10 (sodium/bile acid cotransporter family), member 3	0006810 // transport // inferred from electronic annotation//0006814 // sodium ion transport // inferred from electronic annotation//0010033 // response to organic substance // inferred
1427058_a	0.006437	1.42	-1.04	NM_145396	<i>Tb13</i>	transducin (beta)-like 3	0006364 // rRNA processing // inferred from electronic annotation
1426611_a	0.002641	1.42	-1.03	NM_029688	<i>Srxn1</i>	sulfiredoxin 1 homolog (S. cerevisiae)	0006979 // response to oxidative stress // inferred from direct assay//0006979 // response to oxidative stress // not recorded//0005114 // oxidation-reduction process // not recorded
1418577_a	0.005651	1.42	1.37	NM_008258	<i>Hn1</i>	hematological and neurological expressed sequence 1	
1424912_a	0.006070	1.42	1.02	NM_019763//NM_0065390	<i>Spen</i>	SPEN homolog, transcriptional regulator (Drosophila)	0000122 // negative regulation of transcription from RNA polymerase II promoter // not recorded//0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355
1431058_a	0.001170	1.42	-1.10	NM_029572//NM_0065383	<i>Erp44</i>	endoplasmic reticulum protein 44	0006457 // protein folding // not recorded//0006950 // response to stress // inferred from electronic annotation//0006986 // response to unfolded protein // not recorded//0009100 //
1426995_a	0.002420	1.42	-1.15	NM_133765//NM_0065314	<i>Fbxo31</i>	F-box protein 31	0006974 // cellular response to DNA damage stimulus // not recorded//0007049 // cell cycle // inferred from electronic annotation//0008054 // cyclin catabolic process // not
1426823_x	0.000407	1.42	-1.04	NM_026273//NM_0065224	<i>4930453N24Rik</i>	RIKEN cDNA 4930453N24Rik gene	0006915 // apoptotic process // inferred from electronic annotation
1457964_a	0.003425	1.42	-1.33	NM_001159384//NM_0011	<i>Mix</i>	MAX-like protein 3	0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 // regulation of transcription, DNA-templated // inferred from electronic annotation//0006913 //
1421849_a	0.0009491	1.42	1.14	NM_026021//NM_0064982	<i>Zmynd19</i>	zinc finger, MYND domain containing 19	
1415549_a	0.000581	1.42	1.25	NM_021303//XR_390775	<i>Noc2l</i>	nuclear complex associated 2 homolog (S. cerevisiae)	0000122 // negative regulation of transcription from RNA polymerase II promoter // not recorded//0002903 // negative regulation of B cell apoptotic process // not recorded//0006351 //
1430878_a	0.001961	1.42	-1.41	NM_027309//NM_0065114	<i>Lysmd2</i>	LysM, putative peptidoglycan-binding, domain containing 2	0016998 // cell wall macromolecule catabolic process // inferred from electronic annotation
1419872_a	0.008022	1.42	1.23	NM_029546//NM_0065130	<i>Pwp2</i>	PWP2 periodic tryptophan protein homolog (yeast)	
1423855_x	0.000568	1.42	1.06	NM_172624//NM_0065241	<i>Dpp9</i>	dipeptidylpeptidase 9	0006508 // proteolysis // inferred from electronic annotation
1421431_a	0.001198	1.42	1.15	NM_053161//NM_0065345	<i>Mrlp27</i>	mitochondrial ribosomal protein L27	0006412 // translation // not recorded
1426192_a	0.001179	1.42	-1.01	NM_133911//NM_177582	<i>Mlxip</i>	MLX interacting protein	0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 // regulation of transcription, DNA-templated // inferred from electronic annotation//0006913 //
1451063_a	0.004640	1.42	-1.26	NM_027357	<i>Psmid1</i>	proteasome (prosome, macropain) 26S subunit, non-ATPase, 1	0042176 // regulation of protein catabolic process // inferred from electronic annotation//0005790 // regulation of catalytic activity // inferred from electronic annotation
1423455_a	0.001733	1.41	1.08	NM_147201//NM_0065037	<i>Nrbp1</i>	nuclear receptor binding protein 1	0006468 // protein phosphorylation // not recorded//0006888 // ER to Golgi vesicle-mediated transport // not recorded//0007254 // JNK cascade // not recorded
1428075_a	0.005983	1.41	-1.07	NM_133819	<i>Ppp1r15b</i>	protein phosphatase 1, regulatory (inhibitor) subunit 15b	0006417 // regulation of translation // inferred from electronic annotation//0006446 // regulation of translational initiation // inferred from mutant phenotype//0006979 // response to oxidative stress //
1421429_a	0.001914	1.41	1.15	NM_016776	<i>Mybbp1a</i>	MYB binding protein (P160) 1a	0001649 // osteoblast differentiation // not recorded//0006261 // DNA-dependent DNA replication // inferred from electronic annotation//0006351 // transcription, DNA-templated //
1424783_a	0.004054	1.41	1.02	NM_021375//NM_0065018	<i>Rhbq</i>	Rhesus blood group-associated B glycoprotein	0006810 // transport // inferred from electronic annotation//0015695 // organic cation transport // not recorded//0015696 // ammonium transport // inferred from direct assay//0015696
1421105_a	0.002535	1.41	1.17	NM_001110824//NM_0011	<i>Foxp4</i>	forkhead box P4	0000122 // negative regulation of transcription from RNA polymerase II promoter // inferred from direct assay//0006351 // transcription, DNA-templated // inferred from electronic
1424392_a	0.005717	1.41	1.04	NM_175133//NM_0065140	<i>Gucd1</i>	guanylyl cyclase domain containing 1	
1419508_a	0.000509	1.41	1.26	NM_025890//NM_0065113	<i>Khd3c</i>	KH domain containing 3, subcortical maternal complex member	0006468 // protein phosphorylation // inferred from mutant phenotype//0007049 // cell cycle // inferred from electronic annotation//0007094 // mitotic spindle assembly checkpoint //
1421379_a	0.000283	1.41	1.14	NM_001039521	<i>Rnm3</i>	RRN3 RNA polymerase I transcription factor homolog (yeast)	0001701 // in utero embryonic development // inferred from mutant phenotype//0006351 // transcription, DNA-templated // inferred from electronic annotation//0006352 // DNA-
1428096_a	0.003000	1.41	-1.07	NM_024189//NM_0065042	<i>Gm5553//Ormd12</i>	predicted gene 5553//ORF1-like 2 (S. cerevisiae)	0006672 // ceramide metabolic process // not recorded//0006810 // transport // inferred from electronic annotation//0015031 // protein transport // inferred from electronic annotation
1423826_a	0.007469	1.41	1.06	NM_029017	<i>Mrlp47</i>	mitochondrial ribosomal protein L47	0006412 // translation // inferred from electronic annotation
1422063_a	0.004526	1.41	1.13	NM_145140//NM_170680	<i>Abcc10</i>	ATP-binding cassette, sub-family C (CFTR/MRP), member 10	0006200 // ATP catabolic process // inferred from electronic annotation//0006810 // transport // inferred from electronic annotation//0008152 // metabolic process // inferred from
1426386_a	0.001065	1.40	-1.02	NM_001115076//NM_0012	<i>Campsap1</i>	calmodulin regulated spectrin-associated protein 1	0007010 // cytoskeleton organization // not recorded//0022604 // regulation of cell morphogenesis // not recorded//0003175 // neuron projection development // not recorded
1425457_a	0.006058	1.40	1.00	NM_144794//NM_0064967	<i>Tmem63a</i>	transmembrane protein 63a	0006810 // transport // inferred from electronic annotation//0006811 // ion transport // inferred from electronic annotation
1448612_a	0.009119	1.40	-1.18	NM_011965	<i>Psmo1</i>	proteasome (prosome, macropain) subunit, alpha type 1	0002376 // immune system process // inferred from electronic annotation//0002862 // negative regulation of inflammatory response to antigenic stimulus // inferred from mutant
1427465_a	0.000157	1.40	-1.05	NM_001081349//NM_0010	<i>Sk43a1</i>	solute carrier family 43, member 1	0003333 // amino acid transmembrane transport // not recorded//0006810 // transport // inferred from electronic annotation//0006865 // amino acid transport // inferred from electronic
1423106_a	0.003570	1.40	1.09	NM_001177812//NM_0011	<i>Wbp1l</i>	WW domain binding protein 1 like	
1426596_a	0.000400	1.40	-1.03	NM_025542//NM_175297	<i>Rtfcd1</i>	replication termination factor 2 domain containing 1	
1451812_a	0.002065	1.40	-1.28	NM_145931//NR_027502//	<i>Zc3h7a</i>	zinc finger CCCH type containing 7 A	
1423857_a	0.002677	1.40	1.06	NM_001024922//NM_0065	<i>Ddx49</i>	DEAD (Asp-Glu-Ala-Asp) box polypeptide 49	0006200 // ATP catabolic process // inferred from electronic annotation//0008152 // metabolic process // inferred from electronic annotation
1427910_a	0.000677	1.40	-1.06	NM_026490	<i>Mrlp19</i>	mitochondrial ribosomal protein L19	0006412 // translation // inferred from sequence or structural similarity
1426997_a	0.000639	1.40	-1.04	NM_001040683//NM_0012	<i>Med15</i>	mediator complex subunit 15	0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 // regulation of transcription, DNA-templated // inferred from electronic annotation//0006357 //
1424366_a	0						

Table S7

Gene ID	p (Corr)	FC-RSV 1 d	FC-RSV 5 d	RefSeq Transcript ID	Gene Symbol	Gene Title	Gene Ontology Biological Process
1423399_a	0.001632	1.40	1.08	NM_172413//XM_0065415	Rap2c	RAP2C, member of RAS oncogene family	0006184 // GTP catabolic process // inferred from electronic annotation//0007165 // signal transduction // inferred from electronic annotation//0007264 // small GTPase mediated signal
1422603_a	0.004920	1.40	1.11	NM_12876//XM_0065388	Gpatch3	G patch domain containing 3	0001553 // luteinization // inferred from genetic interaction//0001822 // kidney development // inferred from mutant phenotype//0006807 // nitrogen compound metabolic process //
1428874_a	0.002278	1.40	-1.08	NM_017477//NM_201244//	Cogp1	coatamer protein complex, subunit gamma 1	0006810 // transport // inferred from electronic annotation//0006886 // intracellular protein transport // inferred from electronic annotation//0015031 // protein transport // inferred from
1433420_a	0.001333	1.40	-1.43	NM_00111341//NM_0011	Gm21949//Schrip1	predicted gene, 21949//Schwannomin interacting protein 1	0001553 // luteinization // inferred from genetic interaction//0001822 // kidney development // inferred from mutant phenotype//0006807 // nitrogen compound metabolic process //
1454906_a	0.004321	1.40	-1.32	NM_007604	Capo2c	capping protein (actin filament) muscle Z-line, alpha 2	0030036 // actin cytoskeleton organization // inferred from electronic annotation//0051693 // actin filament capping // inferred from electronic annotation
1427691_a	0.000719	1.40	-1.06	NM_026298//XM_0065040	Ifj172	intracellular transporter 172	0001122 // negative regulation of transcription from RNA polymerase II promoter // not recorded//0001841 // neural tube formation // inferred from mutant phenotype//0001843 // neural
1437874_s	0.003503	1.40	-1.16	NM_145705//XM_0065190	Tnfp2	Terf1 (TRF1)-interacting nuclear factor 2	0010833 // telomere maintenance via telomere lengthening // not recorded//0010836 // negative regulation of protein ADP-ribosylation // not recorded//0032202 // telomere assembly //
1419149_a	0.003806	1.40	1.30	NM_011931//NR_028061	Gm8615	glucosamine-6-phosphate deaminase 1//glucosamine-6-phosphate	0005975 // carbohydrate metabolic process // inferred from electronic annotation//0006002 // fructose 6-phosphate metabolic process // not recorded//0006041 // glucosamine metabolic
1423185_a	0.001425	1.40	1.09	NM_025623	Ppp1r11	protein phosphatase 1, regulatory (inhibitor) subunit 11	0043086 // negative regulation of catalytic activity // inferred from direct assay
1451084_a	0.004725	1.40	-1.26	NM_00115393//NM_0011	Il1rnp	interleukin 1 receptor accessory protein	0007165 // signal transduction // inferred from electronic annotation//0019221 // cytokine-mediated signaling pathway // inferred from direct assay//0042094 // interleukin-2 biosynthetic
1415758_a	0.009787	1.40	26.13	NM_006528434//XM_0065	Astx//Astx6//LOC102631953	amplified spermatogenic transcripts X encoded//amplified spermatogenic	0000917 // barrier septum assembly // inferred from electronic annotation//0006184 // GTP catabolic process // inferred from electronic annotation//0054665 // negative regulation of
1428823_a	0.007684	1.39	-1.08	NM_145972//XM_0065219	Bc027231	cDNA sequence BC027231	0006637 // acyl-CoA metabolic process // inferred from direct assay//0008152 // metabolic process // inferred from direct assay//0006637 // acyl-CoA metabolic process // traceable author
1437381_x	0.004337	1.39	-1.15	NM_019736//XM_0065289	Acot9	acyl-CoA thioesterase 9//acyl-CoA thioesterase 10	001525 // angiogenesis // inferred from genetic interaction//0006629 // lipid metabolic process // inferred from electronic annotation//0007165 // signal transduction // inferred from
1419555_a	0.000507	1.39	1.25	NM_001293648//NM_0196	Picd1	phospholipase C, delta 1	0001701 // in utero embryonic development // inferred from mutant phenotype//0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 // regulation of
1427346_a	0.002360	1.39	-1.05	NM_007924	El1	elongation factor RNA polymerase II	0030030 // cell projection organization // inferred from electronic annotation//0042384 // cilium assembly // inferred from mutant phenotype
1437133_x	0.002746	1.39	-1.15	NM_029921	Tmem213	transmembrane protein 213	0042254 // ribosome biogenesis // inferred from electronic annotation
1420382_x	0.001159	1.39	1.21	NM_172148//XM_0065398	B9d2	B9 protein domain 2	0006810 // transport // inferred from electronic annotation//0006897 // endocytosis // inferred from electronic annotation//0015031 // protein transport // inferred from electronic
1422286_a	0.000348	1.39	1.13	NM_02190810//NM_0235	Gm5633//Gm9178//Mrt4	predicted gene 5633//predicted gene 9178//MRT4, mRNA turnover 4,	0008152 // metabolic process // inferred from electronic annotation//0009058 // biosynthetic process // inferred from electronic annotation
1436963_a	0.003533	1.39	-1.15	NM_025383//XM_0065391	Necap2	NECAP endocytosis associated 2	0001574 // ganglioside biosynthetic process // inferred from genetic interaction//0001574 // ganglioside biosynthetic process // inferred from mutant phenotype//0006486 // protein
1422564_a	0.002126	1.39	1.12	NM_001033452	Acscl	1-aminocyclopropane-1-carboxylate synthase (non-functional)-like	
1419591_a	0.002426	1.39	1.25	NM_00124617//NM_0012	B4galnt1	beta-1,4-N-acetyl-galactosaminyl transferase 1	
1423605_a	0.008144	1.39	1.07	NM_025716	Spryd4	SPRY domain containing 4	
1424462_a	0.001411	1.39	1.04	NM_145416	Kri1	KRI1 homolog (S. cerevisiae)	
1433594_a	0.005975	1.39	-1.11	NM_001081079//XM_0064	Ogfr1	opioid growth factor receptor-like 1	
1423781_a	0.002604	1.39	1.06	NM_027198	Zswim7	zinc finger SWIM-type containing 7	0000724 // double-strand break repair via homologous recombination // not recorded//0006281 // DNA repair // inferred from electronic annotation//0006310 // DNA recombination //
1424710_a	0.007938	1.39	1.03	NM_028042//XM_0065177	Ercb8	excision repair-cross-complementing rodent repair deficiency,	0000209 // protein polyubiquitination // not recorded//0006281 // DNA repair // inferred from electronic annotation//0006283 // transcription coupled nucleotide-excision repair // not
1431337_a	0.002563	1.39	-1.10	NM_008131	Glu1	glutamate-ammonia ligase (glutamine synthetase)	0006536 // glutamate metabolic process // not recorded//0006542 // glutamine biosynthetic process // not recorded//0006807 // nitrogen compound metabolic process // inferred from
1418872_x	0.003656	1.39	1.33	NM_011733//NM_139117	Ybx3	Y box protein 3	0001122 // negative regulation of transcription from RNA polymerase II promoter // not recorded//0001701 // in utero embryonic development // inferred from genetic interaction//0006351
1427805_a	0.004673	1.39	-1.06	NM_001159657//NM_1448	Proser2	proline and serine rich 2	
1419532_x	0.000047	1.39	1.25	NM_030678	Gys1	glycogen synthase 1, muscle	0005977 // glycogen metabolic process // not recorded//0005978 // glycogen biosynthetic process // inferred from mutant phenotype//0005978 // glycogen biosynthetic process // not
1424342_a	0.003010	1.39	1.04	NM_013763//XM_0065044	Tbl2	transducin (beta)-like 2	
1418631_a	0.008781	1.39	1.36	NM_025933//XM_0065022	Bcl9	B cell CLL/lymphoma 9	0014908 // myotube differentiation involved in skeletal muscle regeneration // inferred from genetic interaction//0016055 // Wnt signaling pathway // inferred from electronic
1435691_a	0.000877	1.39	-1.49	NM_001081282//NM_1753	Iltk	inhibitor of Bruton agammaglobulinemia tyrosine kinase	0001933 // negative regulation of protein phosphorylation // not recorded//0051209 // release of sequestered calcium ion into cytosol // not recorded//0061099 // negative regulation of
1425491_a	0.003771	1.39	1.00	NM_001042487//NM_0010	Dlgap4	discs, large homolog-associated protein 4 (Drosophila)	0007267 // cell-cell signaling // inferred from electronic annotation
1423535_a	0.000725	1.39	1.08	NM_153419//XM_0065405	Gwd1	glutamate-rich WD repeat containing 1	
1430354_x	0.006685	1.39	-1.09	NM_001290796//NM_0281	Ppp1r14d	protein phosphatase 1, regulatory (inhibitor) subunit 14D	
1421150_a	0.002825	1.39	1.17	NM_001037840//NM_0010	Cklf	chemokine-like factor	
1424111_a	0.006493	1.39	1.05	NM_011185	Psmb1	proteasome (prosome, macropain) subunit, beta type 1	
1437238_x	0.004632	1.39	-1.15	NM_025373//XR_381541	111000816Rik	RIKEN cDNA 111000816L6 gene	
1458424_a	0.000755	1.39	-2.43	NM_007901	S1pr1	sphingosine-1-phosphate receptor 1	
1426534_a	0.002342	1.39	-1.02	NM_028881//XM_0065021	Crtc2	CREB regulated transcription coactivator 2	
1448371_a	0.004421	1.39	-1.18	NM_025583//NM_134105	Tnfrdc11	thymidine diphosphate containing 11	
1417661_a	0.001245	1.38	1.58	NM_011530//XM_0065058	Tbax1	thromboxane A synthase 1, platelet	
1452132_a	0.003072	1.38	-1.29	NM_008384//XM_0064957	Inpp1	inositol polyphosphate-1-phosphatase	
1420725_a	0.007879	1.38	1.19	NM_011716	Wfs1	Wolfram syndrome 1 homolog (human)	
1425272_a	0.007831	1.38	1.01	NM_028863//XM_0065162	Iscs2	iron-sulfur cluster assembly 2 homolog (S. cerevisiae)	
1426877_x	0.001027	1.38	-1.04	NM_001177536	Prdm11	PR domain containing 11	
1423855_x	0.001243	1.38	1.06	NM_138675	Med9	mediator complex subunit 9	
1425869_a	0.001409	1.38	-1.01	NM_025899//XM_0065394	Napa	N-ethylmaleimide sensitive fusion protein attachment protein alpha	
1424681_a	0.003665	1.38	1.03	NM_028404//XM_0065214	Top1mt	DNA topoisomerase 1, mitochondrial	
1424180_a	0.002740	1.38	1.05	NM_007527//XM_0065405	Bax	BCL2-associated X protein	
1449356_a	0.005255	1.38	-1.22	NM_007670	Cdkn2b	cyclin-dependent kinase inhibitor 2B (p15, inhibits CDK4)	
1436699_x	0.000458	1.38	-1.15	NM_017375	Ostf1	osteostatin stimulating factor 1	
1419602_a	0.004551	1.38	1.25	NM_001005475//NM_0011	Iqsec2	IQ motif and Sec7 domain 2	
1424000_a	0.001875	1.38	1.05	NM_145387	Ath1l	ATH1, acid trehalase-like 1 (yeast)	
1424985_a	0.003915	1.38	1.02	NM_025982	Tspan31	tetraspanin 31	
1419688_a	0.006748	1.38	1.24	NM_146152//XM_0065030	Ipo13	importin 13	
1417234_a	0.000920	1.38	1.75	NM_001013024//XM_0065	Usp13	ubiquitin specific peptidase 13 (isopeptidase T-3)	
1439032_x	0.001909	1.38	-1.16	NM_007996//XM_0065100	Fdx1	ferredoxin 1	
1439971_a	0.008930	1.38	-1.60	NM_021451	Pmpo1	phorbol-12-myristate-13-acetate-induced protein 1	
1426626_a	0.004225	1.38	-1.03	NM_026429	Tbpbp	trophoblast specific protein beta	
1417317_x	0.006068	1.38	1.69	NM_008712//XM_0065301	Nosl	nitric oxide synthase 1, neuronal	
1421866_a	0.002725	1.37	1.14	NM_028514	Actr11	actin-related protein T1	
1427169_a	0.009885	1.37	-1.05	NM_009101//XM_0065407	Rras	Harvey rat sarcoma oncogene, subgroup R	
1422528_a	0.000667	1.37	1.12	NM_001205385//NM_0012	Actr3	ARP3 actin-related protein 3	
1436760_a	0.004213	1.37	-1.15	NM_001142950//NM_0273	Nars	asparaginyl-tRNA synthetase	
1422217_a	0.000114	1.37	1.13	NM_009464	Ucp3	uncoupling protein 3 (mitochondrial, proton carrier)	
1427383_a	0.005577	1.37	-1.05	NM_021720//XM_0065230	Donson	downstream neighbor of SON	
1437176_a	0.005174	1.37	-1.53	NM_010817	Psmf7	proteasome (prosome, macropain) 26S subunit, non-ATPase, 7	
1424532_a	0.002487	1.37	1.03	NM_008681//XM_0065205	Ndr1g	N-myc downstream regulated gene 1	
1426947_x	0.000379	1.37	-1.04	NM_007912//NM_207655//	Egfr	epidermal growth factor receptor	
1426133_a	0.000021	1.37	-1.01	NM_133768//XM_0065043	Asl	argininosuccinate lyase	
1423079_a	0.008428	1.37	1.09	NM_020596	Egr4	early growth response 4	
1422046_a	0.000424	1.37	1.13	NM_001109909//NM_0011	Srrt	serrate RNA effector molecule homolog (Arabidopsis)	
1438477_a	0.002771	1.37	-1.16	NM_00104241//NM_0012	Leprc1	leprecan 1	
1427707_a	0.000237	1.36	-1.06	NM_011026//XM_0065301	P2zw4	coactivator-associated arginate-gated ion channel 4	
1423451_a	0.000960	1.36	1.08	NM_021531//NM_153141//	Carm1	coactivator-associated arginate-gated ion channel 1	
1421413_a	0.005362	1.36	1.15	NM_011437//XM_0065206	Sox10	SRF (sex determining region Y)-box 10	
1420527_x	0.001795	1.36	1.20	NM_198613	Ap2s1	adaptor-related protein complex 2, sigma 1 subunit	
1424272_a	0.005993	1.36	1.04	NM_028782	Lomp1	ion lepidase 1, mitochondrial	
1448706_a	0.004689	1.36	-1.19	NM_001217130//NM_0138	Xbp1	X-box binding protein 1	
1431822_a	0.001170	1.36	-1.10	NM_207225//XM_0065293	Hdac4	histone deacetylase 4	
1422596_a	0.002317	1.36	1.11	NM_001164798//NM_0011	Sk38a10	solute carrier family 38, member 10	
1425574_a	0.006580	1.36	-1.00	NM_001290742//NM_1338	Gpn2	GPN-loop GTPase 2	
1450829_a	0.002799	1.36	-1.25	NM_001291448//NM_0012	Foxd1	FAD-dependent oxidoreductase domain containing 1	
1450639_a	0.000087	1.36	-1.24	NM_019736//NM_022816//	Acot10//Acot9	acyl-CoA thioesterase 10//acyl-CoA thioesterase 9	
1448978_a	0.006469	1.36	-1.20	NM_001079847//NM_0010	Gpr64	G protein-coupled receptor 64	
1423461_a	0.009173	1.36	1.08	NM_023680//XM_0065086	Tnfrsf22//Tnfrsf23	tumor necrosis factor receptor superfamily, member 22//tumor necrosis	

Table S7

Gene ID	p (Corr)	FC-RSV 1 d	FC-RSV 5 d	RefSeq Transcript ID	Gene Symbol	Gene Title	Gene Ontology Biological Process
1425668_a	0.005396	1.36	-1.00	NM_027898//NM_0065401	<i>Gramd1a</i>	GRAM domain containing 1A	
1427386_a	0.004503	1.36	-1.05	NM_001159908//NM_1333	<i>Zfand2a</i>	zinc finger, AN1-type domain 2A	0032436 // positive regulation of proteasomal ubiquitin-dependent protein catabolic process // inferred from mutant phenotype//0071243 // cellular response to arsenic-containing substance
1424755_a	0.009083	1.36	1.03	NM_009975//NM_0065235	<i>Csnk2b</i>	casein kinase 2, beta polypeptide	0101862 // positive regulation of pathway-restricted SMAD protein phosphorylation // not recorded//0016055 // Wnt signaling pathway // inferred from electronic annotation//0016310 //
1441540_a	0.001767	1.36	-1.65	NM_026825//NM_177807/	<i>Lrrc16a</i>	leucine rich repeat containing 16A	0016477 // cell migration // not recorded//0030032 // lamellipodium assembly // not recorded//0030335 // positive regulation of cell migration // inferred from mutant
1449009_a	0.008997	1.35	-1.20	NM_172133//NM_0065329	<i>Adap2</i>	ARFGap with dual PH domains 2	007507 // heart development // non-traceable author statement//0032312 // regulation of ARF GTPase activity // inferred from electronic annotation//0043547 // positive regulation of
1434059_a	0.005146	1.35	-1.12	NM_175226//NM_0065215	<i>Rnf139</i>	ring finger protein 139	0008285 // negative regulation of cell proliferation // not recorded//0016567 // protein ubiquitination // not recorded//0017148 // negative regulation of translation // not recorded
1434015_a	0.003385	1.35	-1.44	NM_028925//NM_0065021	<i>Polr3c</i>	polymrase (RNA III) (DNA directed) polypeptide C	0002376 // immune system process // inferred from electronic annotation//0006351 // transcription, DNA-templated // inferred from electronic annotation//0006383 // transcription from
1422841_a	0.003133	1.35	1.10	NM_17343//NM_0065215	<i>Pus7l</i>	guangioside-induced differentiation-associated-protein 2	001522 // pseudouridine synthesis // inferred from electronic annotation//0008033 // tRNA processing // inferred from electronic annotation//0009451 // RNA modification // inferred from
1435290_x	0.003920	1.35	-1.13	NM_010266//NR_104341/	<i>Gdap2</i>	oligosaccharyltransferase complex subunit	0032526 // response to retinoic acid // inferred from direct assay
1433488_x	0.001715	1.35	-1.11	NM_025509	<i>Ostc</i>	ZW10 interactor	
1455338_x	0.002720	1.35	-1.22	NM_001293683//NM_0012	<i>Zwint</i>	solute carrier protein 52, member 2	000070 // mitotic sister chromatid segregation // not recorded//0007049 // cell cycle // inferred from electronic annotation//0007067 // mitotic nuclear division // inferred from electronic
1424078_x	0.005255	1.35	1.05	NM_029643//NM_0065211	<i>Skc2a2</i>	solute carrier protein 52, member 2	0006810 // transport // inferred from electronic annotation//0032218 // riboflavin transport // not recorded
1439771_x	0.000473	1.35	-1.17	NM_008349//NM_0065229	<i>Il10rb</i>	interleukin 10 receptor, beta	019221 // cytokine-mediated signaling pathway // inferred from mutant phenotype
1420849_a	0.001800	1.35	1.18	NM_001131020//NM_0102	<i>Gfap</i>	glial fibrillary acidic protein	0009611 // response to wounding // not recorded//0010625 // positive regulation of Schwann cell proliferation // inferred from mutant phenotype//0010977 // negative regulation of neuron
1425119_a	0.000087	1.35	1.01	NM_011192//NM_0065325	<i>Psme3</i>	proteasome (prosome, macropain) activator subunit 3 (PA28 gamma, Ki)	0006508 // proteolysis // inferred from electronic annotation//0006915 // apoptotic process // inferred from electronic annotation//0007049 // cell cycle // inferred from electronic
1444258_a	0.000852	1.35	-1.72	NM_017370	<i>Hp</i>	haptoglobin	001666 // response to hypoxia // inferred from electronic annotation//0001889 // liver development // not recorded//0002376 // immune system process // inferred from electronic
1428394_a	0.000490	1.35	-1.08	NM_026472	<i>Nifk</i>	nucleolar protein interacting with the FHA domain of MKI67	010923 // negative regulation of phosphatase activity // not recorded
1426348_a	0.000655	1.35	-1.02	NM_001164071//NM_0011	<i>Tank</i>	TRAF family member-associated NF-kappa B activator	007249 // t-kappaB kinase/NF-kappaB signaling // inferred from direct assay
1424412_a	0.004570	1.35	1.04	NM_001252662//NM_0012	<i>Dmtn</i>	desmin actin binding protein	0006461 // protein complex assembly // inferred from direct assay//0006461 // protein complex assembly // not recorded//0007010 // cytoskeleton organization // inferred from electronic
1421900_a	0.001722	1.35	1.14	NM_144887	<i>Zdhxc5</i>	zinc finger, DHHC domain containing 5	0007275 // multicellular organismal development // inferred from electronic annotation//0018345 // protein palmitoylation // inferred from direct assay//0018345 // protein palmitoylation
1426843_a	0.005961	1.35	-1.04	NM_010192	<i>Fem1a</i>	feminization 1 homolog (a C. elegans)	016567 // protein ubiquitination // inferred from electronic annotation//0043407 // negative regulation of MAP kinase activity // inferred from direct assay//0005728 // protein regulation
1422932_a	0.001364	1.35	1.10	NM_019735//NM_0064999	<i>Apip</i>	APAF1 interacting protein	0006915 // apoptotic process // inferred from electronic annotation//0008652 // cellular amino acid biosynthetic process // inferred from electronic annotation//0009086 // methionine
1421902_a	0.003131	1.35	1.14	NM_001039392//NM_0011	<i>Tmsb10</i>	thymosin, beta 10	0007010 // cytoskeleton organization // inferred from electronic annotation//0030036 // actin cytoskeleton organization // traceable author statement//0042989 // sequestering of actin
1419743_x	0.001007	1.35	1.23	NM_009526//NM_0064958	<i>Wnt6</i>	wingless-type MMTV integration site family, member 6	0001658 // branching involved in ureteric bud morphogenesis // inferred from genetic interaction//0007165 // signal transduction // traceable author statement//0007267 // cell-cell
1419328_x	0.000415	1.35	1.28	NM_001015889//NM_0271	<i>A6g/Taf9</i>	adenylate kinase isoenzyme 6//TAF9 RNA polymerase II, TATA box binding	0006200 // ATP catabolic process // inferred from electronic annotation//0006351 // transcription, DNA-templated // inferred from electronic annotation//0006352 // DNA-templated
1418437_x	0.009656	1.35	1.39	NM_001290574//NM_1386	<i>Ccdc22/Ppp1r3f</i>	coiled-coil domain containing 22//protein phosphatase 1, regulatory	003979 // regulation of glycogen biosynthetic process // not recorded//0004665 // regulation of glycogen (starch) synthase activity // not recorded
1417597_x	0.003048	1.34	1.60	NM_010311//NM_0065165	<i>Gng4</i>	guanine nucleotide binding protein (G protein), gamma 4	0006184 // GTP catabolic process // not recorded//0007165 // signal transduction // inferred from electronic annotation//0007186 // G-protein coupled receptor signaling pathway // not
1449166_a	0.000192	1.34	-1.20	NM_025456//NM_0065161	<i>Eppp</i>	E2F-associated phosphoprotein	0008284 // positive regulation of cell proliferation // not recorded//0032968 // positive regulation of transcription elongation from RNA polymerase II promoter // not recorded//0034244 //
1426648_x	0.000940	1.34	-1.03	NM_027221//NM_0065040	<i>Krtcap3</i>	keratinocyte associated protein 3	
1422563_a	0.002641	1.34	1.12	NM_001033187//NR_02407	<i>Btdb19</i>	BTB (POZ) domain containing 19	
1427859_x	0.004279	1.34	-1.16	NM_013557	<i>Elf2ak1</i>	eukaryotic translation initiation factor 2 alpha kinase 1	0006417 // regulation of translation // inferred from mutant phenotype//0006468 // protein phosphorylation // inferred from mutant phenotype//0006950 // response to stress // inferred
1426300_a	0.002154	1.34	-1.02	NM_018736//NM_0065100	<i>Mre11a</i>	meiotic recombination 11 homolog A (S. cerevisiae)	0007723 // telomere maintenance // not recorded//0006259 // DNA metabolic process // inferred from electronic annotation//0006281 // DNA repair // inferred from electronic
1426022_a	0.003048	1.34	-1.50	NM_130451	<i>Skc2a10</i>	solute carrier family 2 (facilitated glucose transporter), member 10	0006810 // transport // inferred from electronic annotation//0006842 // carbohydrate transport // inferred from electronic annotation//0015758 // glucose transport // not
1436026_a	0.008819	1.34	-1.14	NM_019807//NM_207668	<i>Acpp</i>	acid phosphatase, prostate	0006144 // purine nucleobase metabolic process // inferred from mutant phenotype//0006772 // thiamine metabolic process // inferred from mutant phenotype//0009117 // nucleotide
1434291_a	0.005516	1.34	-1.12	NM_001164171//NM_0168	<i>Psmid10</i>	proteasome (prosome, macropain) 26S subunit, non-ATPase, 10	0001122 // negative regulation of transcription from RNA polymerase II promoter // not recorded//0006915 // apoptotic process // inferred from electronic annotation//0007253 //
1421253_a	0.005070	1.34	-1.16	NM_001081407//NM_0300	<i>Pib1</i>	phospholipase B1	0006629 // lipid metabolic process // inferred from electronic annotation//0006644 // phospholipid metabolic process // not recorded//0016042 // lipid catabolic process // inferred from
1424354_a	0.000150	1.34	1.04	NM_010155//NM_0065395	<i>Erf</i>	Ets2 repressor factor	0001122 // negative regulation of transcription from RNA polymerase II promoter // not recorded//0001701 // in utero embryonic development // inferred from mutant phenotype//0006351
1426414_a	0.000491	1.34	-1.02	NM_024206	<i>Sec13</i>	SEC13 homolog (S. cerevisiae)	0006810 // transport // inferred from electronic annotation//0006888 // ER to Golgi vesicle-mediated transport // not recorded//0015031 // protein transport // inferred from electronic
1428018_x	0.001190	1.34	-1.07	NM_008850	<i>Pitpna</i>	phosphatidylinositol transfer protein, alpha	0006810 // transport // inferred from electronic annotation//0015914 // phospholipid transport // not recorded
1434772_a	0.002168	1.34	-1.13	NM_178648//NM_0065089	<i>Ubxn8</i>	UBX domain domain 8	0030433 // ER-associated ubiquitin-dependent protein catabolic process // not recorded
1434602_a	0.003207	1.34	-1.46	NM_178791//NM_0065191	<i>Vstm4</i>	V-set and transmembrane domain containing 4	
1422813_a	0.002941	1.34	-1.10	NM_001138063//NM_0012	<i>Gfmr1</i>	glial cell line derived neurotrophic factor family receptor alpha 4	0007169 // transmembrane receptor protein tyrosine kinase signaling pathway // traceable author statement//0019321 // cytokine-mediated signaling pathway // not recorded//0030279 //
1410359_a	0.001372	1.34	1.06	NM_027422//NM_0065140	<i>Mier2</i>	mesoderm induction early response 1, family member 2	0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 // regulation of transcription, DNA-templated // inferred from electronic annotation
1419874_x	0.005618	1.34	1.23	NM_024465//NM_0065093	<i>Ahhid12</i>	ahydrolyase domain containing 12	0006660 // phosphatidylserine catabolic process // inferred from mutant phenotype//0007628 // adult walking behavior // inferred from mutant phenotype//0008152 // metabolic process //
1431055_a	0.000408	1.33	-1.10	NM_001285800//NM_0228	<i>Polr1e</i>	polymrase (RNA I) polypeptide E	0001189 // RNA polymerase I transcriptional preinitiation complex assembly at the promoter for the nuclear large rRNA transcript // inferred from direct assay//0006351 // transcription, DNA-
1434744_a	0.002644	1.33	-1.13	NM_013736	<i>Tceb3</i>	transcription elongation factor B (SII), polypeptide 3	0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 // regulation of transcription, DNA-templated // inferred from electronic annotation//0006357 //
1426635_x	0.004279	1.33	-1.03	NM_133998//NM_0065130	<i>Fam207a</i>	family with sequence similarity 207, member A	
1427178_x	0.004912	1.33	-1.05	NM_001040399//NM_0276	<i>Larp1b/LOC102632135</i>	La ribonucleoprotein domain family, member 1B//la-related protein 1B-	
1426278_x	0.001900	1.33	-1.02	NM_025579//NM_0065391	<i>Taf12</i>	TAF12 RNA polymerase II, TATA box binding protein (TBP)-associated factor	0006351 // transcription, DNA-templated // inferred from electronic annotation//0006352 // DNA-templated transcription, initiation // not recorded//0006355 // regulation of transcription,
1424343_a	0.003485	1.33	1.04	NM_010558	<i>Il5</i>	interleukin 5	0006954 // inflammatory response // inferred from electronic annotation//0006955 // immune response // inferred from electronic annotation//0008284 // positive regulation of cell
1434690_a	0.002581	1.33	-1.13	NM_009294//NM_0065075	<i>Sxk4</i>	proteasome (prosome, macropain) 26S subunit, non-ATPase, 9	0032024 // positive regulation of insulin secretion // not recorded//0032024 // positive regulation of insulin secretion // inferred from sequence or structural similarity//0045893 // positive
1425772_a	0.002505	1.33	-1.01	NM_009294//NM_0065075	<i>Sxk4</i>	syntaxin 4A (placental)	0006461 // protein complex assembly // not recorded//0006810 // transport // inferred from electronic annotation//0006836 // neurotransmitter transport // inferred from electronic
1423196_a	0.007970	1.33	1.09	NM_011900//NM_0065333	<i>Mpdv1</i>	mannose-6-phosphate utilization defect 1	0006810 // transport // inferred from electronic annotation//0009312 // oligosaccharide biosynthetic process // not recorded
1419368_x	0.002796	1.33	1.27	NM_001190376//NM_0011	<i>Camt2</i>	calmodulin binding transcription activator 2	0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 // regulation of transcription, DNA-templated // inferred from electronic annotation//0006357 //
1418230_a	0.001772	1.33	1.42	NM_025958//NM_0065064	<i>Cond2</i>	cullin-associated and neddylation-dissociated 2 (putative)	
1427689_a	0.000639	1.33	-1.06	NM_001163684//NM_0255	<i>Nosip</i>	nitric oxide synthase interacting protein	0043086 // negative regulation of catalytic activity // not recorded//0051001 // negative regulation of nitric-oxide synthase activity // not recorded
1434348_a	0.000186	1.33	-1.12	NM_001029838//NM_1489	<i>Pknox2</i>	Pbx/knotted 1 homeobox 2	0006355 // regulation of transcription, DNA-templated // inferred from electronic annotation//0006357 // regulation of transcription from RNA polymerase II promoter // inferred from
1437273_a	0.006775	1.33	-1.53	NM_010581//NM_0065218	<i>Cd47</i>	CD47 antigen (Rb-related antigen, integrin-associated signal transducer)	0007155 // cell adhesion // inferred from electronic annotation//0007165 // signal transduction // not recorded//0007229 // integrin-mediated signaling pathway // inferred from electronic
1433516_a	0.000404	1.33	-1.11	NM_028221//NM_0065305	<i>Fam192a</i>	family with sequence similarity 192, member A	
1423811_x	0.008393	1.33	1.06	NM_146226//NM_0065117	<i>Apeh</i>	acylpeptide hydrolase	0006508 // proteolysis // not recorded//0005043 // beta-amyloid metabolic process // not recorded
1426915_x	0.004421	1.33	-1.04	NM_027420	<i>26100304818rik</i>	RIKEN cDNA 26100304818 gene	0030336 // negative regulation of cell migration // inferred from sequence or structural similarity//0033058 // directional locomotion // inferred from sequence or structural
1416823_x	0.002544	1.33	1.07	NM_001272097//NM_0012	<i>Fobp5</i>	fatty acid binding protein 5, epidermal	0006006 // glucose metabolic process // inferred from mutant phenotype//0006629 // lipid metabolic process // inferred from mutant phenotype//0006656 // phosphatidylcholine
1449025_x	0.000164	1.33	-1.20	NM_011672//NR_028403//	<i>Ufd1l</i>	ubiquitin fusion degradation 1 like	0006511 // ubiquitin-dependent protein catabolic process // inferred from electronic annotation//0043161 // proteasome-mediated ubiquitin-dependent protein catabolic process // inferred
1422510_a	0.003315	1.32	1.12	NM_018783	<i>Tjp11</i>	tufelin interacting protein 11	0000390 // spliceosomal complex disassembly // inferred from mutant phenotype//0000390 // spliceosomal complex disassembly // not recorded//0006355 // regulation of transcription,
1421072_a	0.002476	1.32	1.17	NM_026909//NM_0065225	<i>Thap7</i>	THAP domain containing 7	0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 // regulation of transcription, DNA-templated // inferred from electronic annotation//0045892 //
1429115_x	0.009810	1.32	-1.09	NM_024231//NM_0065318	<i>Zfp11</i>	zinc finger like protein 1	0006810 // transport // inferred from electronic annotation//0016192 // vesicle-mediated transport // inferred from electronic annotation
1429719_x	0.006087	1.32	-1.38	NM_018869//NM_0065266	<i>Grk5</i>	G protein-coupled receptor kinase 5	0002029 // desensitization of G-protein coupled receptor protein signaling pathway // not recorded//0006468 // protein phosphorylation // inferred from electronic annotation//0006915 //
1450897_x	0.008664	1.32	-1.25	NM_001253681//NM_0012	<i>Immt</i>	inner membrane protein, mitochondrial	0009409 // response to cold // inferred from electronic annotation//0005160 // mitochondrial calcium ion homeostasis // inferred from mutant phenotype
1428365_x	0.009643	1.32	-1.08	NM_024177	<i>Mrlp38</i>	mitochondrial ribosomal protein L38	
1417119_a	0.009725	1.32	1.82	NM_009983	<i>Ctsd</i>	cathepsin D	0000045 // autophagic vacuole assembly // inferred from mutant phenotype//0006508 // proteolysis // inferred by curator//0006508 // proteolysis // inferred from direct assay//0006508 //
1421924_a	0.001124	1.32	1.14	NM_133916	<i>Elf3b</i>	eukaryotic translation initiation factor 3, subunit B	001731 // formation of translation preinitiation complex // inferred from electronic annotation//0006412 // translation // inferred from electronic annotation//0006413 // translational
1451019_x	0.003078	1.32	-1.26	NM_001122685//NM_0297	<i>Rhbd1</i>	rhomboid domain containing 1	0006508 // proteolysis // inferred from electronic annotation//0006915 // apoptotic process // inferred from electronic annotation//0007283 // spermatogenesis // inferred from electronic
1422818_x	0.004255	1.32	1.10	NM_001025617//NM_0010	<i>Cont1</i>	calcium activated nucleotidease 1	0007165 // signal transduction // not recorded//0009191 // ribonucleoside diphosphate catabolic process // inferred by curator//0030166 // proteoglycan biosynthetic process // not
1427157_a	0.007587	1.32	-1.05	NM_009740	<i>Bcl10</i>	B cell leukemia/lymphoma 10	0001783 // B cell apoptotic process // inferred from direct assay//0001783 // B cell apoptotic process // inferred from mutant phenotype//0001843 // neural tube closure // inferred from
1449465_x	0.006872	1.32	-1.22	NM_031865//NM_0065302	<i>Prkab1</i>	protein kinase, AMP-activated, beta 1 non-catalytic subunit	0006468 // protein phosphorylation // not recorded//0006468 // protein phosphorylation // traceable author statement//0006629 // lipid metabolic process // inferred from electronic
1433467_x	0.002171	1.32	-1.11	NM_025865//NM_0065165	<i>Sr1</i>	signal sequence receptor, alpha	
1422797_x	0.004940	1.32	1.10	NM_001113355//NM_1336	<i>Vps26a</i>	vacuolar protein sorting 26 homolog A (yeast)	
1425866_x	0.003708	1.32	-1.01	NM_022427//NM_0065018	<i>Gpr88</i>	G-protein coupled receptor 88	0006810 // transport // inferred from electronic annotation//0007034 // vacuolar transport // inferred from electronic annotation//0015031 // protein transport // inferred from electronic
1423006_x	0.006748	1.32	1.10	NM_010731//NM_0065132	<i>Zbtb7a</i>	zinc finger and BTB domain containing 7a	0007165 // signal transduction // inferred from electronic annotation//0007186 // G-protein coupled receptor signaling pathway // inferred from sequence or structural similarity//0007626
1422554_a	0.004640	1.32	1.12	NM_153195//NM_0065140	<i>Fbxo7</i>	F-box protein 7	0001122 // negative regulation of transcription from RNA polymerase II promoter // inferred from direct assay//0006351 // transcription, DNA-templated // inferred from electronic
1416884_a	0.000623	1.32	2.00	NM_025582	<i>Fam213b</i>	family with sequence similarity 213, member B	0004422 // mitochondrial degradation // not recorded//0006626 // protein targeting to mitochondrion // not recorded//0016567 // protein ubiquitination // not recorded//0031647 //
1418077_x	0.000527	1.32	1.46	NM_001177646//NM_0011	<i>Srpa</i>	signal-regulatory protein alpha	0001516 // prostaglandin biosynthetic process // inferred from direct assay//0006629 // lipid metabolic process // inferred from electronic annotation//0006631 // fatty acid metabolic
1449345_a	0.005333	1.32	-1.22	NM_008381	<i>Inhb</i>	inhibin beta-B	0002244 // hematopoietic progenitor cell differentiation // inferred from mutant phenotype//0006910 // phagocytosis, recognition // inferred from direct assay//0006911 // phagocytosis,
1419062_a	0.001525	1.32	1.31	NM_009720	<i>Atax1</i>	ATX1 (antioxidant protein 1) homolog 1 (yeast)	001654 // eye development // traceable author statement//0009267 // cellular response to starvation // inferred from expression pattern//0009605 // response to external stimulus //
1448729_x	0.000997	1.32	-1.19	NM_019929//NM_0065134	<i>Sumo3</i>	SMT3 suppressor of mif 2 homolog 3 (yeast)	0006810 // transport // inferred from electronic annotation//0006811 // ion transport // inferred from electronic annotation//0006825 // copper ion transport // inferred from mutant
1448385_x	0.008579	1.32	-1.18	NM_028816//NM_0065082	<i>Xpo6</i>	exportin 6	016925 // protein sumoylation // inferred from direct assay//0016925 // protein sumoylation // not recorded//0034504 // protein localization to nucleus // inferred from direct
1421640_a	0.005320	1.32					

Table S7

Gene ID	p (Corr)	FC-RSV 1 d	FC-RSV 5 d	RefSeq Transcript ID	Gene Symbol	Gene Title	Gene Ontology Biological Process
1427875_a	0.000680	1.32	-1.06	NM_016736//XM_006357	Nub1	negative regulator of ubiquitin-like proteins 1	0006511 // ubiquitin-dependent protein catabolic process // not recorded//0016567 // protein ubiquitination // not recorded//0032436 // positive regulation of proteasomal ubiquitin-
1450826_a	0.000576	1.32	-1.25	NM_172877//XM_0065388	Pramef8	PRAME family member 8	
1423949_a	0.006828	1.32	1.05	NM_023409	Npc2	Niemann-Pick type C2	0006629 // lipid metabolic process // inferred from electronic annotation//0008202 // steroid metabolic process // inferred from electronic annotation//0008203 // cholesterol metabolic
1435840_x	0.000982	1.31	-1.14	NM_018743//XM_0065089	Agpat6	1-acylglycerol-3-phosphate O-acyltransferase 6 (lysophosphatidic acid	0002071 // glandular epithelial cell maturation // inferred from mutant phenotype//0006629 // lipid metabolic process // inferred from electronic annotation//0006631 // fatty acid metabolic
1424189_a	0.004362	1.31	1.05	NM_173180//XM_0064982	Pmpca	peptidase (mitochondrial processing) alpha	0006508 // proteolysis // not recorded//0008152 // metabolic process // inferred from electronic annotation
1424001_a	0.006284	1.31	1.05	NM_026549//XM_0065403	Pdcd2l	programmed cell death 2-like	0007049 // cell cycle // inferred from electronic annotation
1427489_a	0.000165	1.31	-1.06	NM_009011	RAD23b	RAD23b homolog (S. cerevisiae)	0000715 // nucleotide-excision repair, DNA damage recognition // not recorded//0006281 // DNA repair // inferred from electronic annotation//0006289 // nucleotide-excision repair // not
1419835_x	0.006752	1.31	1.23	NM_026720	Ankrd13d	ankyrin repeat domain 13 family, member D	
1437923_a	0.009411	1.31	-1.54	NM_013470//XM_0065347	Anxa3	annexin A3	
1418601_a	0.008095	1.31	1.36	NM_001161338//NM_0244	Sh3bp5l	SH3 binding domain protein 5 like	0006909 // phagocytosis // not recorded//0010595 // positive regulation of endothelial cell migration // not recorded//0042742 // defense response to bacterium // not recorded//0043086
1448697_a	0.006446	1.31	-1.20	NM_172424//XM_0065304	Med13l	mediator complex subunit 13-like	
1420852_a	0.004893	1.31	1.18	NM_009682	Ap3s2	adaptor-related protein complex 3, sigma 2 subunit	0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 // regulation of transcription, DNA-templated // inferred from electronic annotation//0006357 //
1421408_a	0.000805	1.31	1.15	NM_016906	Sec61a1	Sec61 alpha 1 subunit (S. cerevisiae)	0006810 // transport // inferred from electronic annotation//0006885 // intracellular protein transport // traceable audio statement//0008089 // anterograde axon cargo transport //
1417230_a	0.004875	1.31	1.75	NM_009308	Syt4	synaptotagmin IV	0006614 // SRP-dependent cotranslational protein targeting to membrane // not recorded//0006620 // posttranslational protein targeting to membrane // not recorded//0006810 //
1435660_a	0.004689	1.31	-1.14	NM_00110101//NM_0012	Lsm2	LSM2 homolog, U6 small nuclear RNA associated (S. cerevisiae)	0006810 // transport // inferred from electronic annotation//0006887 // exocytosis // inferred from electronic annotation//0007269 // neurotransmitter secretion // inferred from direct
1426834_x	0.006187	1.31	-1.04	NM_001113345//NM_0011	Gatad2a	GATA zinc finger domain containing 2A	0000244 // spliceosomal tri-snRNP complex assembly // not recorded//0006397 // mRNA processing // inferred from electronic annotation//0006402 // mRNA catabolic process // not
1449027_a	0.002432	1.31	-1.20	NM_001039718//NM_0530	Cntf//Zfp91//Zfp91Cntf	ciliary neurotrophic factor//zinc finger protein 91//Zfp91-Cntf	0001568 // blood vessel development // inferred from mutant phenotype//0001701 // in utero embryonic development // inferred from mutant phenotype//0001842 // neural fold
1425412_a	0.000368	1.31	1.00	NM_146032	Srp68	signal recognition particle 68	0007250 // activation of NF-kappaB-inducing kinase activity // not recorded//0007259 // IAK-STAT cascade // not recorded//0007275 // multicellular organismal development // inferred from
1432474_a	0.003859	1.31	-1.11	NM_029512//NM_181734//	Ttpal	tocopherol (alpha) transfer protein-like	0006614 // SRP-dependent cotranslational protein targeting to membrane // inferred from electronic annotation//0042493 // response to drug // not recorded
1435431_a	0.005541	1.30	-1.13	NM_026130	Spr	signal recognition particle receptor ('docking protein')	0006810 // transport // inferred from electronic annotation
1423386_a	0.002189	1.30	1.08	NM_030035//XM_0065220	Golgb1	golgi autoantigen, golgin subfamily b, macrogolin 1	0006184 // GTP catabolic process // inferred from electronic annotation//0006614 // SRP-dependent cotranslational protein targeting to membrane // inferred from electronic
1419717_a	0.003143	1.30	1.24	NM_026658	Mto1	mitochondrial translation optimization 1 homolog (S. cerevisiae)	
1426544_a	0.007375	1.30	-1.03	NM_153538//XM_0065172	Zcchc6	zinc finger, CCHC domain containing 6	0002098 // tRNA wobble uridine modification // inferred from genetic interaction//0008033 // tRNA processing // inferred from electronic annotation//0055114 // oxidation-reduction
1421812_a	0.000196	1.30	1.18	NM_146093//XM_0065269	Ubxn1	UBX domain protein 1	0031123 // RNA 3'-end processing // not recorded//0071044 // histone mRNA catabolic process // inferred from sequence or structural similarity
1424444_a	0.004581	1.30	1.04	NM_145922//XM_0065024	Kcnk4	potassium voltage gated channel, Shaw-related subfamily, member 4	0031397 // negative regulation of protein ubiquitination // not recorded//0032435 // negative regulation of proteasomal ubiquitin-dependent protein catabolic process // not recorded
1428447_a	0.008443	1.30	-1.35	NM_00113565//NM_0089	LOC102641972//Ptptr	receptor-type tyrosine-protein phosphatase eta-like//protein tyrosine	0006810 // transport // inferred from electronic annotation//0006813 // ion transport // inferred from electronic annotation//0006813 // potassium ion transport // inferred from electronic
1429474_a	0.004401	1.30	-1.09	NM_001289535//NM_0012	Sxv18	synixin 18	0001570 // vasculogenesis // inferred from mutant phenotype//0001954 // positive regulation of cell-matrix adhesion // inferred from direct assay//0006470 // protein dephosphorylation //
1426476_a	0.000826	1.30	-1.02	NM_001252520//NM_0012	Pcalm	phosphatidylinositol binding clathrin assembly protein	0006810 // transport // inferred from electronic annotation//0006886 // intracellular protein transport // inferred from electronic annotation//0015031 // protein transport // inferred from
1424880_a	0.001063	1.30	1.02	NM_033217	Ngfr	nerve growth factor receptor (TNFR superfamily, member 16)	000897 // endocytosis // inferred from electronic annotation//0006898 // receptor-mediated endocytosis // inferred from direct assay//0006898 // receptor-mediated endocytosis // inferred from
1422188_x	0.004511	1.30	1.13	NM_001290381//NM_0235	Tjpt	TCF3 (E2A) fusion partner	000886 // intracellular protein transport // inferred from mutant phenotype//0006915 // apoptotic process // inferred from electronic annotation//0007165 // signal transduction //
1427471_a	0.000970	1.30	-1.05	NM_013497	Creb3	cAMP responsive element binding protein 3	0006281 // DNA repair // inferred from electronic annotation//0006310 // DNA recombination // inferred from electronic annotation//0006351 // transcription, DNA-templated // inferred
1448016_a	0.001662	1.30	-1.17	NM_001285412//NM_0075	Calu	calumenin	0001558 // regulation of cell growth // not recorded//0002230 // positive regulation of defense response to virus by host // not recorded//0006351 // transcription, DNA-templated // not
1448194_a	0.007268	1.30	-1.17	NM_00100606//NM_0195	Adat3//Scamp4	adenosine deaminase, tRNA-specific 3//secretory carrier membrane	0043086 // negative regulation of catalytic activity // not recorded
1426496_a	0.004653	1.30	-1.02	NM_016866//XM_0064998	Stk39	serine/threonine kinase 39	0006810 // transport // inferred from electronic annotation//0008033 // tRNA processing // inferred from electronic annotation//0015031 // protein transport // inferred from electronic
1431107_a	0.005086	1.30	-1.10	NM_026885//XM_0065403	Chmp2a	charged multivesicular body protein 2A	0006468 // protein phosphorylation // not recorded//0008152 // metabolic process // inferred from electronic annotation//0016310 // phosphorylation // inferred from electronic
1424522_a	0.006794	1.30	1.03	NM_127590//XM_0065175	Wdr41	WD repeat domain 41	0006810 // transport // inferred from electronic annotation//0015031 // protein transport // inferred from electronic annotation//0045184 // establishment of protein localization // not
1434129_x	0.008990	1.30	-1.45	NM_011970//XM_0065031	Psmb2	proteasome (prosome, macropain) subunit, beta type 2	
1423096_a	0.002598	1.30	1.09	NM_001077265//NM_0010	Hnmpd	heterogeneous nuclear ribonucleoprotein D	0006508 // proteolysis // inferred from electronic annotation//0010243 // response to organonitrogen compound // inferred from electronic annotation//0014070 // response to organic
1424917_a	0.004422	1.30	1.02	NM_001166669//NM_0011	Gemin5	gem (nuclear organelle) associated protein 5	0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 // regulation of transcription, DNA-templated // inferred from electronic annotation//0042752 //
1437216_a	0.004213	1.29	-1.15	NM_029780//XM_0065053	Raf1	v-rf-leukemia viral oncogene 1	0000387 // spliceosomal snRNP assembly // not recorded//0006397 // mRNA processing // inferred from electronic annotation//0008380 // RNA splicing // inferred from electronic
1427610_a	0.003360	1.29	-1.06	NM_00125389//NM_0089	Pkar1b	protein kinase, cAMP dependent regulatory, type 1 beta	0001665 // MAPK cascade // not recorded//0000186 // activation of MAPK activity // not recorded//0001666 // response to hypoxia // not recorded//0006468 // protein phosphorylation //
1424065_a	0.000923	1.29	1.05	NM_007879	Drg1	developmentally regulated GTP binding protein 1	0001932 // regulation of protein phosphorylation // inferred from electronic annotation//0006468 // protein phosphorylation // traceable audio statement//0007165 // signal transduction
1420952_a	0.001587	1.29	1.18	NM_00114604//NM_0011	Httap2	Httv-1 tat interactive protein 2, homolog (human)	001586 // ferritin iron transport // inferred from electronic annotation
1436249_a	0.001685	1.29	-1.14	NM_001290684//NM_0012	Shroom2	shroom family member 2	0001525 // angiogenesis // inferred from electronic annotation//0006915 // apoptotic process // inferred from electronic annotation//0007275 // multicellular organismal development //
1417937_a	0.008938	1.29	1.50	NM_175103	Bola2	bola-like 2 (E. coli)	0000902 // cell morphogenesis // inferred from direct assay//0002089 // lens morphogenesis in camera-type eye // inferred from sequence or structural similarity//0007275 // multicellular
1448435_x	0.006085	1.29	-1.18	NM_172735//XM_0065050	Zc3hc1	zinc finger, C3HC type 1	0007049 // cell cycle // inferred from electronic annotation//0007067 // mitotic nuclear division // inferred from electronic annotation//0016567 // protein ubiquitination // inferred from
1435413_x	0.009682	1.29	-1.13	NM_025927	Mrlp45	mitochondrial ribosomal protein L45	
1424162_a	0.005563	1.29	1.05	NM_026042	Med29	mediator complex subunit 29	0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 // regulation of transcription, DNA-templated // inferred from electronic annotation
1433620_a	0.009001	1.29	-1.43	NM_175236//NR_027664//	Adhfe1	alcohol dehydrogenase, iron containing, 1	0015993 // molecular hydrogen transport // not recorded//0055114 // oxidation-reduction process // not recorded
1448297_a	0.002171	1.29	-1.17	NM_024454//XM_0065135	Rab21	RAB21, member RAS oncogene family	0006184 // GTP catabolic process // not recorded//0006810 // transport // inferred from electronic annotation//0006886 // intracellular protein transport // inferred from electronic
1421404_a	0.000272	1.29	1.16	NM_026467//XM_0065113	Rps27l	ribosomal protein S27-like	0006281 // DNA repair // not recorded//0006412 // translation // not recorded//0006919 // activation of cysteine-type endopeptidase activity involved in apoptotic process //
1450327_a	0.008650	1.29	-1.04	NM_027352//NR_027343//	Gorasp2	golgi reassembly stacking protein 2	0006996 // organelle organization // not recorded//0007030 // Golgi organization // not recorded
1423855_x	0.000568	1.29	1.26	NM_001080999//NM_0010	Trmt2a	TRMT2 RNA methyltransferase 2A	0001510 // RNA methylation // inferred from electronic annotation//0006396 // RNA processing // inferred from electronic annotation//0006400 // tRNA modification // inferred from
1422739_a	0.001647	1.29	1.11	NM_001252413//NM_0012	Rpain	RPA interacting protein	0006261 // DNA-dependent DNA replication // not recorded//0006281 // DNA repair // not recorded//0006310 // DNA recombination // not recorded//0006606 // protein import //
1428113_x	0.002452	1.29	-1.07	NM_023153//XM_0065105	Cwc15	CWC15 homolog (S. cerevisiae)	0000398 // mRNA splicing, via spliceosome // inferred from electronic annotation//0006397 // mRNA processing // inferred from electronic annotation//0008380 // RNA splicing // inferred
1423045_a	0.007715	1.29	1.10	NM_001271873//NM_1339	Ano10	anoxamin 10	0006812 // cation transport // not recorded//0006821 // chloride transport // not recorded//1902476 // chloride transmembrane transport // not recorded
1421223_a	0.007469	1.28	1.16	NM_026238//XM_0065248	Narf1	nuclear prelamin A recognition factor-like	0001666 // response to hypoxia // not recorded//0002244 // hematopoietic progenitor cell differentiation // inferred from mutant phenotype//0006355 // regulation of transcription, DNA-
1427275_a	0.001170	1.28	-1.05	NM_001007581//NM_0238	2810408M09Rik//Trp53rk	RIKEN cDNA 2810408M09 gene//transformation related protein 53	0006468 // protein phosphorylation // not recorded//0008033 // tRNA processing // inferred from electronic annotation//0009103 // lipopolysaccharide biosynthetic process // inferred from
1427463_a	0.000849	1.28	-1.05	NM_028152//XM_0065273	Mms19	MMS19 (MET18 S. cerevisiae)	0006259 // DNA metabolic process // not recorded//0006281 // DNA repair // not recorded//0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 //
1421846_a	0.005980	1.28	1.14	NM_026422//XM_005982	Mrfj	mitochondrial ribosome recycling factor	0006412 // translation // inferred from electronic annotation//0032790 // ribosome disassembly // not recorded
1416503_a	0.008527	1.28	2.50	NM_001160112//NM_0082	Foxp1	forkhead box G1	000122 // negative regulation of transcription from RNA polymerase II promoter // —//0002052 // positive regulation of neuroblast proliferation // inferred from mutant
1432466_a	0.000303	1.28	-1.11	NM_177461//XM_0065210	Mical1	microtubule associated monoxygenase, calponin and LIM domain	0006612 // protein targeting to membrane // not recorded//0006810 // transport // inferred from electronic annotation//0006897 // endocytosis // not recorded//0006898 // receptor-
1429505_a	0.004776	1.28	-1.38	NM_001199122//NM_0784	Ghltm	growth hormone inducible transmembrane protein	0006915 // apoptotic process // inferred from electronic annotation
1426654_a	0.008039	1.28	-1.03	NM_001256059//XM_0065	Ccdc149	coiled-coil domain containing 149	
1425202_a	0.003048	1.28	1.01	NM_194348//XM_0065317	Atg2a	autophagy related 2A	0000045 // autophagic vacuole assembly // —//0000422 // mitochondrial degradation // —//0006914 // autophagy // inferred from electronic annotation//0006995 // cellular response to
1426106_a	0.008491	1.28	-1.01	NM_175016//XM_0065302	Alkbh2	alkB, alkylation repair homolog 2 (E. coli)	0006281 // DNA repair // inferred from electronic annotation//0006307 // DNA dealkylation involved in DNA repair // not recorded//0006974 // cellular response to DNA damage stimulus //
1419201_a	0.004980	1.28	1.29	NM_011706//XM_0065331	Trpv2	transient receptor potential cation channel, subfamily V, member 2	0006810 // transport // inferred from electronic annotation//0006811 // ion transport // inferred from electronic annotation//0006812 // cation transport // not recorded//0006816 //
1424968_a	0.002126	1.28	1.02	NM_001112729//NM_0011	Tu12	TELO2 interacting protein 2	
1435275_a	0.004727	1.28	-1.13	NM_133895//XM_0065042	Sk15a4	solute carrier family 15, member 4	0006810 // transport // inferred from electronic annotation//0006855 // drug transmembrane transport // not recorded//0006857 // oligopeptide transport // inferred from electronic
1427158_a	0.007825	1.28	-1.05	NM_001191001//NM_1528	Lins	lins homolog (Drosophila)	
1416610_a	0.001624	1.28	2.41	NM_028910//XM_0065081	Olfrr701	olfactory receptor 701	0007165 // signal transduction // inferred from electronic annotation//0007186 // G-protein coupled receptor signaling pathway // not recorded//0007608 // sensory perception of smell //
1422403_a	0.001541	1.28	1.12	NM_026391//XM_0065080	Ppp2r2d	protein phosphatase 2, regulatory subunit B, delta	0007049 // cell cycle // inferred from electronic annotation//0007067 // mitotic nuclear division // inferred from electronic annotation//0007165 // signal transduction // inferred from
1455958_x	0.005878	1.28	-1.32	NM_024185//XM_0064975	Fam188a	family with sequence similarity 188, member A	0006915 // apoptotic process // inferred from electronic annotation
1425091_a	0.004221	1.28	1.01	NM_197985//XM_0065065	Adipor2	adiponectin receptor 2	0006629 // lipid metabolic process // inferred from electronic annotation//0006631 // fatty acid metabolic process // inferred from electronic annotation//0007507 // heart development //
1423800_a	0.001355	1.28	1.06	NM_001109752//NM_0078	Diga	discs, large homolog 4 (Drosophila)	0001973 // adenosine receptor signaling pathway // inferred from sequence or structural similarity//0002091 // negative regulation of receptor internalization // not recorded//0006461 //
1417317_x	0.000587	1.28	1.69	NM_028748//XM_0065115	Papf5	progestin and adipocytokine receptor family member V	0007275 // multicellular organismal development // inferred from electronic annotation//0030154 // cell differentiation // inferred from electronic annotation//0048477 // eogenesis //
1444090_a	0.002422	1.27	-1.72	NM_001113368//NM_0011	Ceacam3//Ceacam1	carcinoembryonic antigen-related cell adhesion molecule	0007156 // homophilic cell adhesion // inferred from direct assay//0016032 // viral process // inferred from electronic annotation//0019048 // modulation by virus of host morphology or
1424786_x	0.009414	1.27	1.02	NM_001160149//NM_0267	Cgref1	cell growth regulator with EF hand domain 1	0007049 // cell cycle // inferred from electronic annotation//0007050 // cell cycle arrest // inferred from electronic annotation//0007155 // cell adhesion // inferred from electronic
1450093_x	0.001963	1.27	-1.23	NM_134013//XM_0065144	Psmc4	proteasome (prosome, macropain) activator subunit 4	0006281 // DNA repair // inferred from mutant phenotype//0006974 // cellular response to DNA damage stimulus // inferred from direct assay//0007275 // multicellular organismal
1428061_a	0.002373	1.27	-1.07	NM_019650//XM_0065338	Gosr2	golgi SNAP receptor complex member 2	0006810 // transport // inferred from electronic annotation//0015031 // protein transport // inferred from electronic annotation//0016192 // vesicle-mediated transport // inferred from
1419159_a	0.005934	1.27	1.30	NM_029364	Gns	glucosaminase (N-acetyl)-6-sulfatase	0008152 // metabolic process // inferred from electronic annotation//0030203 // glycosaminoglycan metabolic process // inferred from electronic annotation
1434604_a	0.001699	1.27	-1.13	NM_133210	Sertad3	SERTA domain containing 3	0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 // regulation of transcription, DNA-templated // not recorded//0030308 // negative regulation of
1448674_a	0.006287	1.27	-1.19	NM_011400//XM_0065058	Slc2a3	solute carrier family 2 (facilitated glucose transporter), member 3	0006810 // transport // inferred from electronic annotation//0008643 // carbohydrate transport // inferred from electronic annotation//0015758 // glucose transport // inferred from direct
1426030_a	0.009491	1.27	-1.01	NM_144824//XM_0065328	Wrap53	WD repeat containing, antisense to Trp53	0032203 // telomere formation via telomerase // not recorded//0051973 // positive regulation of telomerase activity // not recorded
1434632_a	0.002192	1.27	-1.46	NM_007952	Pdia3	protein disulfide isomerase associated 3	0006457 // protein folding // not recorded//0006662 // glycerol ether metabolic process // inferred from electronic annotation//0034976 // response to endoplasmic reticulum stress // not
1422794_a	0.008593	1.27	1.10	NM_001080815//XM_0065	Gipr	gastric inhibitory polypeptide receptor	0002029 // desensitization of G-protein coupled receptor protein signaling pathway // not recorded//0007165 // signal transduction // inferred from electronic annotation//0007166 // cell
1426999_a	0.009414	1.27	-1.04	NM_138583//XM_0065222	Tango2	transport and golgi organization 2	
1452648_a	0.000786	1.27	-1.30	NM_025623//XM_0065381	Nipsnap3b	nipsnap homolog 3B (C. elegans)	

Table S7

Gene ID	p (Corr)	FC-RSV 1 d	FC-RSV 5 d	RefSeq Transcript ID	Gene Symbol	Gene Title	Gene Ontology Biological Process
1445962_a	0.001733	1.27	-1.23	NM_010749	<i>M6pr</i>	mannose-6-phosphate receptor, cation dependent	0006810 // transport // inferred from electronic annotation//0006886 // intracellular protein transport // traceable author statement//0015761 // mannose transport // inferred from
1434244_x	0.009849	1.27	-1.12	NM_001291146//NM_0012	<i>Der12</i>	Der1-like domain family, member 2	0001967 // sucking behavior // inferred from mutant phenotype//0006986 // response to unfolded protein // inferred from electronic annotation//0008284 // positive regulation of cell
1419312_a	0.009103	1.27	1.28	NM_025636//XM_0065312	<i>Ntpcr</i>	nucleotide-triphosphatase, cancer-related	0008152 // metabolic process // inferred from electronic annotation//0016311 // dephosphorylation // inferred from electronic annotation
1434709_a	0.005323	1.27	-1.13	NM_028198	<i>Xpo5</i>	exportin 5	0006611 // protein export from nucleus // inferred from direct assay//0006810 // transport // inferred from electronic annotation//0006886 // intracellular protein transport // inferred from
1434386_a	0.000852	1.27	-1.12	NM_016846//XM_0065292	<i>Rgl1</i>	ral guanine nucleotide dissociation stimulator, 2-like 1	0007165 // signal transduction // inferred from electronic annotation//0007264 // small GTPase mediated signal transduction // inferred from electronic annotation//0043547 // positive
1449288_a	0.000429	1.27	-1.21	NM_026700//NM_027293//	<i>Dopey2</i>	dopey family member 2	0006810 // transport // inferred from electronic annotation//0015031 // protein transport // inferred from electronic annotation
1435697_a	0.008593	1.27	-1.14	NM_009010//XM_0065307	<i>Rd23a</i>	RAO23a homologue (S. cerevisiae)	0006281 // DNA repair // inferred from electronic annotation//0006289 // nucleotide-excision repair // not recorded//0006974 // cellular response to DNA damage stimulus // inferred from
1421600_a	0.002351	1.26	1.15	NM_021511	<i>Rn1</i>	RRS1 ribosome biogenesis regulator homolog (S. cerevisiae)	0002244 // hematopoietic progenitor cell differentiation // inferred from mutant phenotype//0007080 // mitotic metaphase plate congression // not recorded//0042254 // ribosome
1433773_a	0.009012	1.26	-1.12	NM_144893//XM_0065101	<i>Med17</i>	mediator complex subunit 17	0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 // regulation of transcription, DNA-templated // inferred from electronic annotation//0006357 //
1421450_a	0.003021	1.26	1.15	NM_026953//XM_0065088	<i>Pev11g</i>	peroxisomal biogenesis factor 11 gamma	0016559 // peroxisome fission // not recorded//0004375 // regulation of peroxisome size // not recorded
1426146_a	0.004279	1.26	-1.01	NM_024453//XM_0065389	<i>Lusp1</i>	leucine zipper protein 1	0003281 // ventricular septum development // inferred from mutant phenotype//0021503 // neural fold bending // inferred from mutant phenotype//0006840 // artery development //
1448638_a	0.000859	1.26	-1.18	NM_001113374//NM_0011	<i>Mocs2</i>	molybdenum cofactor synthesis 2	0006777 // Mo-molybdopterin cofactor biosynthetic process // not recorded
1428326_a	0.000859	1.26	-1.08	NM_025418//XM_0065128	<i>Vta1</i>	Vps20-associated 1 homolog (S. cerevisiae)	0006810 // transport // inferred from electronic annotation//0015031 // protein transport // inferred from electronic annotation
1452063_a	0.003385	1.26	-1.29	NM_001039351//NM_0010	<i>Nolc1</i>	nucleolar and coiled-body phosphoprotein 1	0007000 // nucleolus organization // inferred from direct assay
1422959_s	0.001030	1.26	1.10	NM_001162412//NM_1337	<i>Cyslrt2</i>	cysteiny leukotriene receptor 2	0007165 // signal transduction // inferred from electronic annotation//0007186 // G-protein coupled receptor signaling pathway // inferred from direct assay//0007186 // G-protein coupled
1434879_a	0.004478	1.26	-1.13	NM_001172062//NM_0274	<i>Lman1</i>	lectin, mannose-binding, 1	0006810 // transport // inferred from electronic annotation//0006888 // ER to Golgi vesicle-mediated transport // traceable author statement//0007029 // endoplasmic reticulum
1448821_a	0.000997	1.26	-1.19	NM_198620//XM_0065035	<i>Rundc3b</i>	RUN domain containing 3B	
1427932_s	0.007373	1.26	-1.06	NM_019456//XM_0064981	<i>Apbb1ip</i>	amyloid beta (A4) precursor protein-binding, family B, member 1	0007165 // signal transduction // inferred from electronic annotation
1424958_a	0.000364	1.26	1.02	NM_146000	<i>Bud13</i>	BUD13 homolog (yeast)	
1448595_a	0.003399	1.26	-1.18	NM_144884	<i>Tor1a</i>	torsin family 1, member A (torsin A)	0000338 // protein deneddylation // not recorded//0006200 // ATP catalytic process // not recorded//0006979 // response to oxidative stress // not recorded//0006996 // organelle
1429613_a	0.008068	1.26	-1.38	NM_025668//XM_0065081	<i>Spes2</i>	signal peptidase complex subunit 2 homolog (S. cerevisiae)	0006465 // signal peptide processing // inferred from electronic annotation//0006508 // proteolysis // inferred from electronic annotation
1427183_a	0.000529	1.26	-1.05	NM_023894//XM_0065414	<i>Rhox9</i>	reproductive homeobox 9	0006355 // regulation of transcription, DNA-templated // inferred from electronic annotation
1428053_a	0.006027	1.26	-1.07	NM_175179	<i>Amer1</i>	APC membrane recruitment 1	0001822 // kidney development // inferred from mutant phenotype//0016055 // Wnt signaling pathway // inferred from electronic annotation//00060348 // bone development // inferred
1426856_a	0.006155	1.26	-1.04	NM_001008550//XM_0065	<i>Zfyve26</i>	zinc finger, FYVE domain containing 26	0000724 // double-strand break repair via homologous recombination // not recorded//0000910 // cytokinesis // not recorded//0006281 // DNA repair // inferred from electronic
1427447_a	0.002796	1.25	-1.05	NM_011590	<i>Tmm17a</i>	translocase of inner mitochondrial membrane 17a	0006810 // transport // inferred from electronic annotation//0006886 // intracellular protein transport // inferred from electronic annotation//0015031 // protein transport // inferred from
1448388_a	0.000657	1.25	-1.18	NM_181470//XM_0065127	<i>Lw1</i>	LTV1 homolog (S. cerevisiae)	
1420515_s	0.002373	1.25	1.20	NM_001163431//NM_0269	<i>Tmem258</i>	transmembrane protein 258	
1433661_a	0.001865	1.25	-1.11	NM_0011932//XM_0065015	<i>Dapp1</i>	dual adaptor for phosphotyrosine and 3-phosphoinositides 1	0043551 // regulation of phosphatidylinositol 3-kinase activity // inferred from electronic annotation
1448521_a	0.006007	1.25	-1.18	NM_001177464//NM_1830	<i>Zfp516</i>	zinc finger protein 516	0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 // regulation of transcription, DNA-templated // inferred from electronic annotation
1424222_s	0.002796	1.25	1.05	NM_172687//XM_0065378	<i>Cog3</i>	coenzyme Q3 homolog, methyltransferase (yeast)	0006071 // glycerol metabolic process // not recorded//0006479 // protein methylation // inferred from electronic annotation//0006744 // ubiquinone biosynthetic process // not
1430005_a	0.003547	1.25	-1.09	NM_0023764//XM_0065086	<i>Tollip</i>	toll interacting protein	0002376 // immune system process // inferred from electronic annotation//0006954 // inflammatory response // inferred from electronic annotation//0007165 // signal transduction // not
1433482_a	0.007972	1.25	-1.11	NM_001290536//NM_0012	<i>Otu45</i>	OTU domain containing 5	0006508 // proteolysis // not recorded//0032496 // response to lipopolysaccharide // inferred from sequence or structural similarity//0032496 // response to lipopolysaccharide // inferred
1437253_a	0.005154	1.25	-1.15	NM_027462//XM_0065020	<i>Wars2</i>	tryptophanyl tRNA synthetase 2 (mitochondrial)	0001570 // vasculogenesis // inferred from direct assay//0006412 // translation // inferred from electronic annotation//0006418 // tRNA aminoacylation for protein translation // inferred
1426994_a	0.004171	1.24	-1.04	NR_015348	<i>Hoxa11os</i>	homeobox A11, opposite strand	
1416319_a	0.000258	1.24	3.19	NM_152839	<i>Igj</i>	immunoglobulin joining chain	0002250 // adaptive immune response // not recorded//0003094 // glomerular filtration // not recorded//0006959 // humoral immune response // inferred from sequence or structural
1418034_a	0.003048	1.24	1.47	NM_020582	<i>Atp5a3</i>	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit	0006200 // ATP catalytic process // not recorded//0006754 // ATP biosynthetic process // inferred from electronic annotation//0006810 // transport // inferred from electronic
1419172_a	0.003582	1.24	1.29	NM_172692//XM_0065378	<i>Gba2</i>	glucosidase beta 2	0006629 // lipid metabolic process // inferred from electronic annotation//0006665 // sphingolipid metabolic process // inferred from electronic annotation//0006680 // glucosylceramide
1428370_a	0.009271	1.24	-1.34	NM_008179	<i>Gsp12</i>	G1 to S phase transition 2	0000184 // nuclear-transcribed mRNA catabolic process, nonsense-mediated decay // inferred from electronic annotation//0006184 // GTP catalytic process // inferred from electronic
1419625_a	0.007322	1.24	1.25	NM_183019	<i>Arhgef4</i>	Rho guanine nucleotide exchange factor (GEF) 4	0030032 // lamellipodium assembly // not recorded//0032314 // regulation of Rac GTPase activity // not recorded//0032321 // positive regulation of Rho GTPase activity // inferred from
1434279_a	0.001297	1.24	-1.12	NM_001285940//NM_0012	<i>Fez2</i>	fasciculation and elongation protein beta 2 (zyglin II)	
1438758_a	0.003912	1.24	-1.16	NM_008689//XM_0065011	<i>Nfk1</i>	nuclear factor of kappa light polypeptide gene enhancer in B cells 1, p105	0000122 // negative regulation of transcription from RNA polymerase II promoter // not recorded//0001818 // negative regulation of cytokine production // inferred from mutant
1424220_a	0.001435	1.24	1.05	NM_148929//NM_178371	<i>SK9a8</i>	solute carrier family 9 (sodium/hydrogen exchanger), member 8	0006810 // transport // inferred from electronic annotation//0006811 // ion transport // inferred from electronic annotation//0006812 // cation transport // inferred from electronic
1430678_a	0.000790	1.24	1.00	NM_020651//XM_0065351	<i>Srsf5a3</i>	steroid 5 alpha-reductase 3	0006486 // protein glycosylation // inferred from electronic annotation//0006488 // dolichol-linked oligosaccharide biosynthetic process // inferred from mutant phenotype//0006488 //
1421116_a	0.008677	1.24	1.17	NM_080708//XM_0065347	<i>Bmp2k</i>	BMP2 inducible kinase	0006468 // protein phosphorylation // inferred from direct assay//0016310 // phosphorylation // inferred from electronic annotation//0030500 // regulation of bone mineralization //
1425222_x	0.000863	1.24	1.01	NM_011479	<i>Sptlc2</i>	serine palmitoyltransferase, long chain base subunit 2	0006629 // lipid metabolic process // inferred from electronic annotation//0006665 // sphingolipid metabolic process // inferred from electronic annotation//0006686 // sphingomyelin
1455462_a	0.004421	1.24	-1.32	NM_028922	<i>Pppad2c</i>	phosphatidic acid phosphatase type 2 domain containing 2	0008152 // metabolic process // inferred from electronic annotation
1418826_a	0.001541	1.24	1.33	NM_030083	<i>Naa38</i>	N(alpha)-acetyltransferase B3, NatC auxiliary subunit	0043066 // negative regulation of apoptotic process // not recorded
1419478_a	0.000098	1.24	1.26	NM_001166350//NM_1993	<i>Serpina11</i>	serine (or cysteine) peptidase inhibitor, clade A (alpha-1) antiprotease, DnaI (Hsp40) homolog, subfamily B, member 9	0010466 // negative regulation of peptidase activity // inferred from electronic annotation//0010951 // negative regulation of endopeptidase activity // not recorded//0030162 // regulation
1432184_a	0.003238	1.24	-1.42	NM_013760	<i>Dnajb9</i>	UDF-Gal:betaGalNac beta 1,4- galactosyltransferase, polypeptide 1	0030433 // ER-associated ubiquitin-dependent protein catabolic process // inferred from direct assay//0030433 // ER-associated ubiquitin-dependent protein catabolic process // not recorded
1418322_a	0.003566	1.24	1.40	NM_022305//XM_0065376	<i>B4galt1</i>	DPH1 homolog (S. cerevisiae) // candidate tumor suppressor in ovarian	0020664 // epithelial cell development // inferred from mutant phenotype//0002526 // acute inflammatory response // inferred from mutant phenotype//0005975 // carbohydrate metabolic
1450499_a	0.001982	1.24	-1.24	NM_0027136//NM_144491	<i>Dph1</i>	oligonucleotide/oligosaccharide-binding fold containing 1	0008283 // cell proliferation // inferred from mutant phenotype//0017183 // peptidyl-diphthamide biosynthetic process from peptidyl-histidine // inferred from electronic
1426208_x	0.002564	1.24	-1.01	NM_175360//XM_0065265	<i>Obfc1</i>	exocyst complex component 1	0000723 // telomere maintenance // not recorded//0010833 // telomere maintenance via telomere lengthening // not recorded//0045740 // positive regulation of DNA replication // inferred
1427297_a	0.001305	1.24	-1.05	NM_001289770//NM_0012	<i>Exoc1</i>	RUN and SH3 domain containing 1	0006810 // transport // inferred from electronic annotation//0006887 // exocytosis // inferred from electronic annotation//0015031 // protein transport // inferred from electronic
1424407_s	0.006027	1.24	1.04	NM_001083807//NM_0010	<i>Rusc1</i>	serine/arginine-rich protein specific kinase 1	0002029 // protein polyubiquitination // not recorded
1417333_a	0.000755	1.23	1.67	NM_016795//XM_0065239	<i>Srp1</i>	ras homolog gene family, member A	0006397 // mRNA processing // inferred from electronic annotation//0006468 // protein phosphorylation // inferred from direct assay//0006468 // protein phosphorylation // not
1425014_a	0.007616	1.23	1.01	NM_016802//XM_0065116	<i>Rhoa</i>	UDF-GlcNAc:betaGal beta 1,3-N-acetylglucosaminyltransferase 2	0009002 // cell morphogenesis // inferred from genetic interaction//0001666 // response to hypoxia // inferred from electronic annotation//0006184 // GTP catalytic process // inferred
1440405_a	0.008224	1.23	-1.72	NM_001169114//NM_0168	<i>B3gnt2</i>	alkB, alkylation repair homolog 1 (E. coli)	0006486 // protein glycosylation // inferred from mutant phenotype//0006878 // cellular copper ion homeostasis // --//0007411 // axon guidance // inferred from mutant
1428515_a	0.004929	1.23	-1.08	NM_001102565	<i>Alkh1</i>	potassium channel modulatory factor 1	0000737 // DNA catalytic process, endonucleolytic // not recorded//0001701 // in utero embryonic development // inferred from mutant phenotype//0001764 // neuron migration //
1431920_a	0.002674	1.23	-1.10	NM_019715	<i>Kcnf1</i>	polymerase (RNA) III (DNA directed) polypeptide B	0008152 // metabolic process // inferred from electronic annotation//0016567 // protein ubiquitination // not recorded
1437667_a	0.005362	1.23	-1.16	NM_027423//XR_380439	<i>Poli3b</i>	Crm, crooked neck-like 1 (Drosophila)	0002376 // immune system process // inferred from electronic annotation//0006351 // transcription, DNA-templated // inferred from electronic annotation//0006383 // transcription from
1430704_a	0.000178	1.23	-1.40	NM_025820	<i>Crnk1</i>	ferredoxin 1-like//Raver1-Fdx1 readthrough	000245 // spliceosomal complex assembly // not recorded//0000398 // mRNA splicing, via spliceosome // not recorded//0006396 // RNA processing // inferred from electronic
1423702_a	0.009722	1.23	1.07	NM_001039824//NR_03808	<i>Fdx1l</i>	receptor-type tyrosine-protein phosphatase eta-like//protein tyrosine	0006810 // transport // inferred from electronic annotation//0005114 // oxidation-reduction process // inferred from electronic annotation
1429420_a	0.009725	1.23	-1.37	NM_001135657//NM_0089	<i>LOC102641972//Ptptrj</i>	methionine sulfoxide reductase (cobalamin deficiency) cblD type, with	0001570 // vasculogenesis // inferred from mutant phenotype//0001954 // positive regulation of cell-matrix adhesion // inferred from direct assay//0006470 // protein dephosphorylation //
1449880_s	0.005753	1.23	-1.22	NM_133839//XM_0064975	<i>Mmadhc</i>	glutaredione 2 (thioltransferase)	0009235 // cobalamin metabolic process // inferred from electronic annotation
1424518_a	0.000096	1.23	1.04	NM_001038592//NM_0010	<i>Glxr2</i>	3-hydroxyisobutyrate dehydrogenase	0006810 // transport // inferred from electronic annotation//0008152 // metabolic process // inferred from electronic annotation//0010033 // response to organic substance // not
1427803_a	0.009022	1.23	-1.06	NM_145567	<i>Hibad8</i>	RIKEN cDNA 1810043G02 gene	0006098 // pentose-phosphate shunt // inferred from electronic annotation//0006573 // valine metabolic process // inferred from electronic annotation//0006574 // valine catabolic process
1423433_a	0.001699	1.23	1.08	NM_026431//XM_0065140	<i>1810043G02Rik</i>	prolactin family 6, subfamily A, member 1	0007010 // cytoskeleton organization // not recorded//0007224 // smoothened signaling pathway // inferred from mutant phenotype//0008360 // regulation of cell shape // not
1416985_a	0.008410	1.22	1.89	NM_011166	<i>Pr16a</i>	WD repeat and SOCS box-containing 2	0016567 // protein ubiquitination // inferred from electronic annotation//0035556 // intracellular signal transduction // inferred from electronic annotation
1430293_a	0.003025	1.22	-1.09	NM_021539//XM_0065304	<i>Wsb2</i>	Lim2-containing protein kinase 2	0006468 // protein phosphorylation // inferred from mutant phenotype//0006468 // protein phosphorylation // not recorded//0007283 // spermatogenesis // inferred from mutant
1448287_a	0.000573	1.22	-1.17	NM_001034030//NM_0107	<i>Limk2</i>	---	0019058 // viral life cycle // inferred from electronic annotation
1416824_a	0.001292	1.22	2.07	NM_142226	<i>Gm14226</i>	PAK1 interacting protein 1	0008283 // cell proliferation // inferred from physical interaction//0009968 // negative regulation of signal transduction // inferred from electronic annotation//00060021 // palate
1450892_a	0.008607	1.22	-1.25	NM_026550	<i>Pak1ip1</i>	DnaI (Hsp40) homolog, subfamily C, member 13	0001649 // osteoblast differentiation // not recorded
1425548_a	0.002056	1.22	-1.00	NM_001163026//XM_0065	<i>Dnajc13</i>	proteasome (prosome, macropain) inhibitor subunit 1	0006511 // ubiquitin-dependent protein catabolic process // not recorded//1901799 // negative regulation of proteasomal protein catabolic process // not recorded
1448931_a	0.000852	1.22	-1.20	NM_144889//NM_212446	<i>Psmf1</i>	solute carrier family 35, member F5	0006511 // transport // inferred from electronic annotation
1448047_a	0.006071	1.21	-1.20	NM_028781//XM_0065299	<i>SK35f5</i>	noncompact myelin associated protein	0031643 // positive regulation of myelination // not recorded//0032290 // peripheral nervous system myelin formation // not recorded
1433966_a	0.000136	1.21	-1.12	NM_001168498//NM_0011	<i>Wip1</i>	WD repeat domain, phosphoinositide interacting 1	0000405 // autophagic vacuole assembly // not recorded//0006914 // autophagy // inferred from electronic annotation//0040203 // vesicle targeting, trans-Golgi to endosome // not
1424029_a	0.002359	1.22	1.05	NM_145490	<i>Wip1</i>	TNFRSF1A-associated via death domain	0006915 // apoptotic process // inferred from reviewed computational analysis//0007165 // signal transduction // inferred from electronic annotation//0042981 // regulation of apoptotic
1423289_a	0.004007	1.22	1.08	NM_001033161	<i>Tradd</i>	fibrosar	0048146 // positive regulation of fibroblast proliferation // inferred from direct assay
1432462_a	0.001483	1.22	-1.11	NM_010183//XM_0065073	<i>Fhrs</i>	amyloid beta (A4) precursor protein binding, family A, member 1	0001701 // in utero embryonic development // inferred from genetic interaction//0006810 // transport // inferred from electronic annotation//0006886 // intracellular protein transport //
1422617_a	0.006230	1.22	1.11	NM_177034//XM_0065271	<i>Apb1</i>	potassium voltage-gated channel, Isk-related subfamily, member 1	0002070 // epithelial cell maturation // inferred from mutant phenotype//0006487 // protein N-linked glycosylation // inferred from electronic annotation//0006487 // protein N-linked
1423823_a	0.002862	1.22	1.06	NM_008424//XM_0065229	<i>Kcne1</i>	RAB interacting factor	0006810 // transport // inferred from electronic annotation//0007264 // small GTPase mediated signal transduction // inferred from electronic annotation//0015031 // protein transport //
1449164_a	0.004669	1.22	-1.20	NM_145510	<i>Rab1f</i>	IMP4, U3 small nuclear ribonucleoprotein, homolog (yeast) // DNA	0006364 // RNA processing // traceable author statement//0002254 // ribosome biogenesis // inferred from electronic annotation
1436760_a	0.004213	1.21	-1.15	NM_178601//XR_104542//	<i>Imp4</i>	PDx1 C-terminal inhibiting factor 1	0010923 // negative regulation of phosphatase activity // not recorded
1424961_a	0.001500	1.21	1.02	NM_146129	<i>Pcf1</i>	ER membrane protein complex subunit 7	0006810 // transport // inferred from electronic annotation//0007340 // acrosome reaction // inferred from direct assay//0006478 // acrosomal vesicle exocytosis // not recorded
1435981_a	0.002928	1.21	-1.14	NM_133749//XM_0065002	<i>Emc7</i>	synaptotagmin VI	0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 // regulation of transcription, DNA-templated // not recorded//0006366 // transcription from RNA
1424784_a	0.004814	1.21	1.02	NM_001276676//NM_0012	<i>Syt6</i>	POU domain, class 3, transcription factor 4	0007275 // multicellular organismal development // inferred from electronic annotation//0007283 // spermatogenesis // inferred from electronic annotation//0030154 // cell differentiation

Table S7

Gene ID	p (Corr)	FC-RSV 1 d	FC-RSV 5 d	RefSeq Transcript ID	Gene Symbol	Gene Title	Gene Ontology Biological Process
1452178_a	0.000862	1.21	-1.29	NM_009419//NM_0065348	<i>Tpst2</i>	protein-tyrosine sulfotransferase 2	0006478 // peptidyl-tyrosine sulfation // inferred from mutant phenotype//0007342 // fusion of sperm to egg plasma membrane // inferred from mutant phenotype//00060468 // prevention
1426072_a	0.000410	1.21	-1.01	NM_144835	<i>Heatr1</i>	HEAT repeat containing 1	
1434329_s	0.009836	1.21	-1.12	NM_026235	<i>Larpe6</i>	La ribonucleoprotein domain family, member 6	0006396 // RNA processing // inferred from electronic annotation//0006417 // regulation of translation // inferred from electronic annotation
1425516_a	0.001914	1.21	1.00	NM_013581//NM_0065323	<i>Cog1</i> ///LOC102641618	component of oligomeric golgi complex 1//conserved oligomeric Golgi	0006810 // transport // inferred from electronic annotation//0015031 // protein transport // inferred from electronic annotation
1450639_a	0.000087	1.21	-1.24	NM_019651//NM_0065112	<i>Ptpn9</i>	protein tyrosine phosphatase, non-receptor type 9	0006470 // protein dephosphorylation // inferred from electronic annotation//0016311 // dephosphorylation // inferred from electronic annotation//0035335 // peptidyl-tyrosine
1425078_x	0.000024	1.21	1.01	NM_030046	<i>Dnajc21</i>	DnaI (Hsp40) homolog, subfamily C, member 21	
1425163_a	0.003099	1.21	1.01	NM_008718//NM_0065396	<i>Npas1</i>	neuronal PAS domain protein 1	0000122 // negative regulation of transcription from RNA polymerase II promoter // inferred from direct assay//0001964 // startle response // inferred from genetic interaction//0006351 //
1429394_a	0.009027	1.21	-1.37	NM_026267	<i>Necap1</i>	NECAP endocytosis associated 1	0006810 // transport // inferred from electronic annotation//0006897 // endocytosis // inferred from mutant phenotype//0015031 // protein transport // inferred from electronic annotation
1449265_a	0.0013685	1.21	-1.21	NM_0011648250//NM_1340	<i>Mtbp</i>	Mdm2, transformed 3T3 cell double minute p53 binding protein	0007049 // cell cycle // inferred from electronic annotation//0007050 // cell cycle arrest // inferred from electronic annotation//0007089 // traversing start control point of mitotic cell cycle//
1426670_a	0.0009086	1.21	-1.03	NM_172300	<i>Ubc2</i>	ubiquitin-conjugating enzyme E22 (putative)	0006913 // apoptotic process // inferred from electronic annotation//0016567 // protein ubiquitination // inferred from electronic annotation
1425364_a	0.002574	1.20	1.00	NM_021500//NM_0065040	<i>Naes1</i>	macrophage erythroid blast attachment	0007010 // cytoskeleton organization // inferred from mutant phenotype//0007049 // cell cycle // inferred from electronic annotation//0007155 // cell adhesion // not recorded//0033033 //
1420590_a	0.001055	1.20	1.20	NM_001190444//NM_1461	<i>Aamp</i>	angio-associated migratory protein	0014909 // smooth muscle cell migration // inferred from electronic annotation
1451761_a	0.007843	1.20	-1.28	NM_015806//NM_027418	<i>Mapk6</i>	mitogen-activated protein kinase 6	0000165 // MAPK cascade // inferred from direct assay//0006468 // protein phosphorylation // inferred from direct assay//0007049 // cell cycle // inferred from electronic
1451416_a	0.000173	1.20	-1.27	NM_033572//NM_0065045	<i>Wbscr16</i>	Williams-Beuren syndrome chromosome region 16 homolog (human)	0032316 // regulation of Ran GTPase activity // non-traceable author statement//0032853 // positive regulation of Ran GTPase activity // non-traceable author statement
1429390_a	0.002843	1.20	-1.37	NM_001112705//NM_0012	<i>Ttk2</i>	tousled-like kinase 2 (Arabidopsis)	0001672 // regulation of chromatin assembly or disassembly // not recorded//0006468 // protein phosphorylation // not recorded//0006974 // cellular response to DNA damage stimulus //
1423025_a	0.004058	1.20	1.10	NM_008503//NM_0010036	<i>Gm10420</i> ///Gm6139//Gm884	predicted gene 10420//predicted gene 6139//predicted gene	0000028 // ribosomal small subunit assembly // not recorded//0001731 // formation of translation preinitiation complex // not recorded//0006412 // translation // inferred from electronic
1422455_s	0.004673	1.20	1.12	NM_146150//NM_0065029	<i>Nrd1</i>	nardilysin, N-arginine diabolic convertase, NRD convertase 1	0006508 // proteolysis // not recorded//0008152 // metabolic process // inferred from electronic annotation//0051044 // positive regulation of membrane protein ectodomain proteolysis //
1433702_a	0.008617	1.20	-1.11	NM_009680//NM_0065175	<i>Ap3b1</i>	adaptor-related protein complex 3, beta 1 subunit	0006622 // protein targeting to lysosome // inferred from mutant phenotype//0006810 // transport // inferred from electronic annotation//0006829 // zinc ion transport // traceable author
1422617_a	0.006230	1.20	1.11	NM_007433//NM_0065290	<i>Alppl2</i>	alkaline phosphatase, placental-like 2	0008152 // metabolic process // inferred from electronic annotation//0016311 // dephosphorylation // inferred from direct assay
1423007_a	0.007621	1.20	1.10	NM_172518//NM_0065387	<i>Fbxo42</i>	F-box protein 42	
1423986_a	0.001055	1.20	1.05	NM_013581//NM_0065323	<i>Cog1</i> ///LOC102641618	component of oligomeric golgi complex 1//conserved oligomeric Golgi	0006810 // transport // inferred from electronic annotation//0015031 // protein transport // inferred from electronic annotation
1419513_a	0.003973	1.20	1.26	NM_175546//NM_0065190	<i>Wdfy2</i>	WD repeat and FYVE domain containing 2	
1426258_x	0.001085	1.19	-1.02	NM_145521//NM_0064979	<i>Rabepk</i>	Rab9 effector protein with kelch motifs	0000226 // microtubule cytoskeleton organization // inferred from electronic annotation
1449203_a	0.001173	1.19	-1.21	NM_00128600//NM_0012	<i>Tgpcp2</i>	tubulin, gamma complex associated protein 2	
1436989_s	0.007878	1.19	-1.15	NM_00114264//NM_001285	<i>Fbrs1</i>	fibrosin-like 1	
1446702_a	0.002029	1.19	-1.79	NM_001039185//NM_0010	<i>Ceacam2</i> ///Ceacam2	carcinoembryonic antigen-related cell adhesion molecule	
1437301_a	0.009197	1.19	-1.15	NM_016856//NM_0065160	<i>Cpsf2</i>	cleavage and polyadenylation specific factor 2	
1417785_a	0.000294	1.19	1.54	NM_009351//NM_0065187	<i>Tep1</i>	telomerase associated protein 1	
1451573_a	0.007494	1.19	-1.27	NM_001081304//NM_0064	<i>Atf6</i>	activating transcription factor 6	
1451858_x	0.000187	1.19	-1.28	NM_008740	<i>Nsf</i> ///AK160502	N-ethylmaleimide sensitive fusion protein//Mus musculus adult male	
1425182_x	0.006369	1.19	1.01	NM_011678//NM_0065116	<i>Usp4</i>	ubiquitin specific peptidase 4 (proto-oncogene)	
1417365_a	0.002506	1.19	1.67	NM_029355	<i>Pr17b1</i>	prolactin family 7, subfamily b, member 1	
1427071_a	0.007460	1.19	-1.05	NM_031404//NM_0065046	<i>Actl6b</i>	actin-like 6B	0006333 // chromatin assembly or disassembly // inferred by curator//0006338 // chromatin remodeling // not recorded//0006351 // transcription, DNA-templated // inferred from
1448655_a	0.001168	1.19	-1.19	NM_0011246	<i>Rasgrp1</i>	RAS guanyl releasing protein 1	0001816 // cytokine production // inferred from mutant phenotype//0002437 // inflammatory response to antigenic stimulus // inferred from mutant phenotype//0007269 // small GTPase
1438068_a	0.009245	1.19	-1.54	NM_026268	<i>Dusp6</i>	dual specificity phosphatase 6	0001188 // inactivation of MAPK activity // not recorded//0001933 // negative regulation of protein phosphorylation // inferred from mutant phenotype//0006470 // protein
1448621_a	0.001602	1.19	-1.18	NM_030564//NM_0065305	<i>Rnf34</i>	ring finger protein 34	0006915 // apoptotic process // inferred from electronic annotation//0016567 // protein ubiquitination // not recorded//0043161 // proteasome-mediated ubiquitin-dependent protein
1416164_a	0.000058	1.19	4.68	NM_053110	<i>Gpnm6</i>	glycoprotein (transmembrane) nm6	0001649 // osteoblast differentiation // inferred from electronic annotation//0007155 // cell adhesion // inferred from direct assay//0030282 // bone mineralization // inferred from
1416700_a	0.006868	1.19	2.18	NM_001166497//NM_0065	3110052M02Rik	RIKEN cDNA 3110052M02 gene	0006355 // regulation of transcription, DNA-templated // not recorded
1428011_a	0.009682	1.19	-1.07	NM_026435	<i>Ufm1</i>	ubiquitin-fold modifier 1	0034976 // response to endoplasmic reticulum stress // not recorded//0071569 // protein ufmylation // inferred from direct assay//0071569 // protein ufmylation // not recorded
1449586_a	0.000126	1.19	-1.22	NM_025782//NM_027238	<i>Ttc39b</i>	tetratricopeptide repeat domain 39B	
1428500_a	0.001295	1.19	-1.08	NM_001109993//NM_0012	<i>Ptpn11</i>	protein tyrosine phosphatase, non-receptor type 11	0000077 // DNA damage checkpoint // inferred from mutant phenotype//0000187 // activation of MAPK activity // inferred from mutant phenotype//0006470 // protein dephosphorylation
1430421_a	0.002018	1.19	-1.09	NM_007926	<i>Amp1</i>	aminocyclitol synthetase complex-interacting multifunctional protein 1	0001525 // angiogenesis // inferred from electronic annotation//0001937 // negative regulation of endothelial cell proliferation // not recorded//0005975 // carbohydrate metabolic process
1416897_a	0.000741	1.18	1.06	NM_028362//NR_015504	2410018L13Rik	RIKEN cDNA 2410018L13 gene	0006355 // regulation of transcription, DNA-templated // inferred from electronic annotation
1436025_s	0.004056	1.18	-1.50	NM_00128989//NM_0012	<i>Csnk1e</i>	casein kinase 1, epsilon	0006468 // protein phosphorylation // inferred from direct assay//0006468 // protein phosphorylation // inferred from mutant phenotype//0006468 // protein phosphorylation // not
1419999_a	0.001385	1.18	1.22	NM_001128605//NM_0011	<i>Psen2</i>	presenilin 2	0000122 // negative regulation of transcription from RNA polymerase II promoter // inferred from mutant phenotype//0001666 // response to hypoxia // inferred from electronic
1451613_a	0.000410	1.18	-1.28	NM_013531//NM_0065354	<i>Gnb4</i>	guanine nucleotide binding protein (G protein), beta 4	0006184 // GTP catalytic process // not recorded//0007165 // signal transduction // inferred from electronic annotation//0007186 // G-protein coupled receptor signaling pathway //
1449158_a	0.005352	1.18	-1.20	NM_009000//NM_0065171	<i>Rab24</i>	RAB24, member RAS oncogene family	0006184 // GTP catalytic process // inferred from electronic annotation//0006810 // transport // inferred from electronic annotation//0006886 // intracellular protein transport // inferred
1431551_a	0.004558	1.18	-1.42	NM_008444//XR_374419	<i>Klf3b</i>	kinase family member 3B	0007018 // microtubule-based movement // inferred from electronic annotation//0008152 // metabolic process // inferred from electronic annotation//0032467 // positive regulation of
1424459_a	0.000687	1.18	1.04	NM_025340//NM_0065202	<i>Sharpin</i>	SHANK-associated RH domain interacting protein	0007005 // mitochondrion organization // inferred from mutant phenotype//0007420 // brain development // inferred from electronic annotation//0008544 // epidermis development //
1450010_a	0.001409	1.18	-1.23	NM_175090//NM_0065377	<i>Scl3a1</i>	solute carrier family 31, member 1	0006810 // transport // inferred from electronic annotation//0006811 // ion transport // inferred from electronic annotation//0006825 // copper ion transport // inferred from electronic
1430448_x	0.009787	1.18	-1.40	NM_011631	<i>Hsp90b1</i>	heat shock protein 90, beta (Grp94), member 1	0001666 // response to hypoxia // not recorded//0006457 // protein folding // inferred from electronic annotation//0006950 // response to stress // inferred from electronic
1426645_a	0.001963	1.18	-1.03	NM_080854//NM_0064976	<i>Scl3a3</i>	solute carrier family 34 (sodium phosphate), member 3	0006810 // transport // inferred from electronic annotation//0006811 // ion transport // inferred from electronic annotation//0006814 // sodium ion transport // not recorded//0006817 //
1434330_a	0.008046	1.18	-1.12	NM_133945//NM_0065405	<i>Vrk3</i>	vacuolin related kinase 3	0006468 // protein phosphorylation // inferred from electronic annotation//0032516 // positive regulation of phosphoprotein phosphatase activity // inferred from physical
1451317_a	0.006754	1.18	1.27	NM_00116654//NM_0011	<i>E4efn1f</i>	eryukary translation initiation factor 4E nuclear import factor 1	0006810 // transport // inferred from electronic annotation//0015031 // protein transport // inferred from electronic annotation
1424488_a	0.000388	1.18	1.04	NM_130892//XR_380055	<i>Rtn4p1</i>	reticulon 4 interacting protein 1	0055114 // oxidation-reduction process // inferred from electronic annotation
1428828_x	0.002862	1.18	-1.36	NM_007479	<i>Arf4</i>	ADP-ribosylation factor 4	0006471 // protein ADP-ribosylation // not recorded//0006810 // transport // inferred from electronic annotation//0006886 // intracellular protein transport // inferred from electronic
1417916_a	0.002476	1.18	1.50	NM_175638//NM_0065341	<i>Wnk4</i>	WNK lysine deficient protein kinase 4	0006468 // protein phosphorylation // not recorded//0006811 // ion transport // inferred from direct assay//0006821 // chloride transport // inferred from direct assay//0008104 // protein
1435530_a	0.002064	1.18	-1.14	NM_001286538//NM_0012	<i>Sigmar1</i>	sigma non-opioid intracellular receptor 1	0006696 // ergosterol biosynthetic process // inferred from electronic annotation//0006810 // transport // inferred from electronic annotation//0006869 // lipid transport // inferred from
1417371_a	0.005672	1.18	1.67	NM_00111100//NM_00124	<i>Lipa</i>	lysosomal acid lipase A	0000902 // cell morphogenesis // inferred from mutant phenotype//0001816 // cytokine production // inferred from mutant phenotype//0006629 // lipid metabolic process // inferred from
1450183_a	0.007621	1.18	-1.23	NM_019439//NM_0065246	<i>Gobt1</i>	gamma-aminobutyric acid (GABA) B receptor, 1	0005975 // carbohydrate metabolic process // inferred from electronic annotation//0008152 // metabolic process // inferred from electronic annotation//0016052 // carbohydrate catabolic
1428760_a	0.008193	1.18	-1.08	NM_00129370//NM_0088	<i>Pip5k1a</i>	phosphatidylinositol-4-phosphate 5-kinase, type 1 alpha	0006854 // phospholipid biosynthetic process // not recorded//00101761 // fibroblast migration // inferred from mutant phenotype//0016310 // phosphorylation // inferred from electronic
1428648_a	0.002564	1.18	-1.08	NM_025665//NM_0065064	<i>Srrnp27</i>	small nuclear ribonucleoprotein 27 (U4/U6.U5)	0006397 // mRNA processing // inferred from electronic annotation//0008380 // RNA splicing // inferred from electronic annotation
1452619_a	0.006878	1.18	-1.30	NM_024255//NM_0065382	<i>Hsd12</i>	hydroxysteroid dehydrogenase like 2	0008152 // metabolic process // inferred from electronic annotation//0055114 // oxidation-reduction process // inferred from electronic annotation
1424923_a	0.007339	1.17	1.02	NM_146201//NM_0065077	<i>Zfp553</i>	zinc finger protein 553	0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 // regulation of transcription, DNA-templated // inferred from electronic annotation
1434322_a	0.004776	1.17	-1.45	NM_001290628//NM_1390	<i>Vps54</i>	vacuolar protein sorting 54 (yeast)	0006810 // transport // inferred from electronic annotation//0015031 // protein transport // inferred from electronic annotation//0040007 // growth // inferred from mutant
1417546_a	0.009552	1.17	1.61	NM_001256521//NM_0012	C330006A16Rik	RIKEN cDNA C330006A16 gene	0008284 // positive regulation of cell proliferation // not recorded//0048524 // positive regulation of viral process // not recorded
1423870_a	0.000283	1.17	1.06	NM_007658//NM_0065119	<i>Cdc25a</i>	cell division cycle 25A	0000082 // G1/S transition of mitotic cell cycle // not recorded//0000087 // mitotic M phase // inferred from electronic annotation//0006470 // protein dephosphorylation // inferred from
1428608_a	0.008144	1.17	-1.08	NM_001113384//NM_0103	<i>Gnao1</i>	guanine nucleotide binding protein, alpha O	0006184 // GTP catalytic process // not recorded//0007165 // signal transduction // inferred from electronic annotation//0007186 // G-protein coupled receptor signaling pathway //
1434688_x	0.002717	1.17	-1.13	NM_019694//NM_0065040	<i>Letm1</i>	leucine zipper-EF-hand containing transmembrane protein 1	0042407 // cristae formation // not recorded
1451025_a	0.007911	1.17	-1.26	NM_001277330//NM_0012	<i>Pex5</i>	peroxisomal biogenesis factor 5	0000038 // very long-chain fatty acid metabolic process // inferred from mutant phenotype//0001764 // neuron migration // inferred from mutant phenotype//0006625 // protein targeting
1417320_a	0.005965	1.17	1.68	NM_176920	<i>Lrtm1</i>	leucine-rich repeats and transmembrane domains 1	
1420376_a	0.007550	1.17	1.21	NM_001294302//NM_0167	<i>Preb</i>	proline regulatory element binding	0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 // regulation of transcription, DNA-templated // not recorded//0006355 // regulation of
1449911_a	0.007232	1.17	-1.23	NM_001271584//NM_0012	<i>Dnajc5</i>	DnaI (Hsp40) homolog, subfamily C, member 5	0043524 // negative regulation of neuron apoptotic process // inferred from genetic interaction
1449277_a	0.000545	1.17	-1.21	NM_009564//NM_0030845	LOC100502777//Zfp64	zinc finger protein 64-like//zinc finger protein 64	0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 // regulation of transcription, DNA-templated // inferred from electronic annotation//0007275 //
1430571_s	0.008628	1.17	-1.10	NM_026992//NR_033993	<i>Dnajc24</i>	DnaI (Hsp40) homolog, subfamily C, member 24	0006810 // transport // inferred from electronic annotation//0017183 // peptidyl-diphosphatase biosynthetic process from peptidyl-histidine // inferred from electronic annotation//0032781
1416280_a	0.003868	1.16	3.28	NM_001042711//NM_0011	<i>Amy2a2</i> ///Amy2a3	amylase 2a1//amylase 2a2//amylase 2a3//amylase 2a4//amylase 2a5	0006355 // regulation of transcription, DNA-templated // inferred from electronic annotation//0006355 // regulation of transcription, DNA-templated // inferred from electronic annotation//0006915 //
1429533_a	0.000163	1.16	-1.09	NM_020483//NM_0065338	<i>Sap30bp</i>	SAP30 binding protein	
1426218_a	0.002506	1.16	-1.01	NM_022428//NM_0065312	<i>Ir6b</i>	iraoquols related homeobox 6 (Drosophila)	0006355 // regulation of transcription, DNA-templated // inferred from electronic annotation
1435796_a	0.008611	1.16	-1.49	NM_0011764//NM_0065308	<i>Zfp90</i>	zinc finger protein 90	0000122 // negative regulation of transcription from RNA polymerase II promoter // inferred from direct assay//0006351 // transcription, DNA-templated // inferred from electronic
1439549_a	0.009031	1.16	-1.58	NM_001177955//NM_0011	<i>Gpm6b</i>	glycoprotein m6b	0001503 // ossification // inferred from electronic annotation//0006810 // transport // inferred from electronic annotation//0015031 // protein transport // inferred from electronic
1429084_a	0.004764	1.16	-1.36	NM_001290489//NM_0268	<i>Med27</i>	mediator complex subunit 27	0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 // regulation of transcription, DNA-templated // inferred from electronic annotation//0006357 //
1435572_a	0.006333	1.16	-1.31	NM_001110850//NM_0011	<i>Crem</i>	cAMP responsive element modulator	0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 // regulation of transcription, DNA-templated // not recorded//0006687 // glycosphingolipid
1437423_a	0.002140	1.16	-1.16	NM_198303//NM_0064959	<i>Eif5b</i>	eukaryotic translation initiation factor 5B	0006184 // GTP catalytic process // inferred from electronic annotation//0006413 // translation // not recorded//0006413 // translational initiation // not recorded//0006446 // regulation
1449347_a	0.002485	1.16	-1.22	NM_021525//NM_0065272	<i>Rcl1</i>	RNA terminal phosphate cyclase-like 1	0006364 // rRNA processing // not recorded//0006396 // RNA processing // inferred from electronic annotation//0042254 // ribosome biogenesis // inferred from electronic annotation
1436576_a	0.005557	1.16	-1.52	NM_018828//NM_0064999	<i>Frbp4</i>	formin binding protein 4	
1434063_a	0.002451	1.15	-1.44	NM_172338	<i>Dnajc16</i>	DnaI (Hsp40) homolog, subfamily C, member 16	0045454 // cell redox homeostasis // inferred from electronic annotation
1417477_a	0.008117	1.15	1.63	NM_001025305//NM_0012	<i>Tfpab2</i>	transcription factor AP-2 beta	0000122 // negative regulation of transcription from RNA polymerase II promoter // inferred from direct assay//0000122 // negative regulation of transcription from RNA polymerase II
1435887_a	0.007279	1.15	-1.49	NM_021305//NM_0064975	<i>Sec61a2</i>	Sec61, alpha subunit 2 (S.	

Gene ID	p (Kort)	FC-RSV 1 d	FC-RSV 5 d	RefSeq Transcript ID	Gene Symbol	Gene Title	Gene Ontology Biological Process
14212998.x	0.00369	1.15	1.14	NM_023912//XM_0065318	Scyl1	SCY1-like 1 (S. cerevisiae)	0006468 // protein phosphorylation // inferred from electronic annotation//0006810 // transport // inferred from electronic annotation//0006890 // retrograde vesicle-mediated transport, chromobox 4
1429273.x	0.02048	1.15	-1.37	NM_007625	Cbx4	chromobox 4	0001022 // negative regulation of transcription from RNA polymerase II promoter // inferred from direct assay//0001022 // negative regulation of transcription from RNA polymerase II
1425506.x	0.005915	1.15	-1.30	NM_025885	Med19	mediator complex subunit 19	0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 // regulation of transcription, DNA-templated // inferred from electronic annotation//0006357 //
1418216.x	0.000576	1.15	1.42	NM_007531	Phb2	prohibitin 2	0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 // regulation of transcription, DNA-templated // inferred from electronic annotation//0003147 //
1427086.x	0.001982	1.15	-1.05	NM_016714	Nup50	nucleoporin 50	0001841 // neural tube formation // inferred from mutant phenotype//0006810 // transport // inferred from electronic annotation//0006913 // nucleocytoplasmic transport // traceable
1451821.x	0.000095	1.15	-1.28	NM_011081//XM_0065287	Pigo	phosphatidylinositol glycan anchor biosynthesis, class A	0005066 // GPI anchor biosynthetic process // inferred from mutant phenotype//0005058 // biosynthetic process // inferred from electronic annotation
1449049.x	0.003434	1.15	-1.20	NM_177648	Dolk	dolichol kinase	016310 // phosphorylation // not recorded//0043048 // dolichyl monophosphate biosynthetic process // not recorded
1417440.x	0.007091	1.15	1.64	NM_001081391//XM_0065	CsmD3	CUB and Sushi multiple domains 3	0003009 // skeletal muscle contraction // not recorded//0006810 // transport // inferred from electronic annotation//0006811 // ion transport // inferred from electronic
1427168.x	0.000743	1.15	-1.05	NM_009603//XM_0065320	Chmd	cholinergic receptor, nicotinic, epsilon polypeptide	0006810 // transport // inferred from electronic annotation//0006811 // ion transport // inferred from electronic annotation//0006820 // mRNA transport // inferred from electronic
1435454.x	0.001068	1.15	-1.13	NM_011695	Vdac2	voltage-dependent anion channel 2	
1435454.x	0.001068	1.15	-1.13	NM_0013352//XM_0281	Twin7	twin 7-like 1	
1431038.x	0.001662	1.15	-1.41	NM_009453//NM_178794	Znr2	zinc finger (CCHC type), RNA binding motif and serine/arginine rich-2	0002045 // spliceosome complex assembly // not recorded//0003098 // mRNA splicing, via spliceosome // not recorded//0006397 // mRNA processing // inferred from electronic
1438673.x	0.000909	1.15	-1.16	NM_025442	Alg5	asparagine-linked glycosylation 5 [dolichyl-phosphate beta-asparagine with sequence similarity 175, member 8]	0001496 // protein glycosylation // inferred from electronic annotation//0007368 // determination of left/right symmetry // inferred from mutant phenotype//0008152 // metabolic process
1424269.x	0.001622	1.14	1.04	NM_198017	Fam175b	fam175b family glycosylase similarity 175, member 8	0074497 // cellular response to freezing // inferred from genetic interaction
1450562.x	0.000473	1.14	-1.24	NM_008507//XM_0065301	Shn2b	SH2B adaptor protein 3	003097 // hemopoiesis // inferred from mutant phenotype//0030154 // cell differentiation // inferred from mutant phenotype//0035162 // embryonic hemopoiesis // inferred from direct
1450118.x	0.006690	1.14	-1.23	NM_025525	Rnf132a2	ring finger protein 132a2	
1417851.x	0.001998	1.14	1.52	NM_172453//XM_0065109	Pf1	PIF1-5'-to-3' DNA helicase homolog (S. cerevisiae)	0000002 // mitochondrial genome maintenance // inferred from electronic annotation//0000723 // telomere maintenance // inferred from electronic annotation//0006200 // ATP catabolic
1416731.x	0.001865	1.14	1.12	NM_001012305//XM_0064	Sc39a12	scarp carrier family 39 (zinc transporter), member 12	0007165 // signal transduction // inferred from direct assay//0010975 // regulation of neuron projection development // inferred from mutant phenotype//0030001 // metal ion transport //
1450672.x	0.000454	1.14	-1.25	NM_139149//XM_0065077	Fus	fused in sarcoma	
1460351.x	0.000982	1.14	-1.33	NM_033570	Cnnm4	cyclin M4	0006810 // transport // inferred from electronic annotation//0006811 // ion transport // inferred from electronic annotation//0007601 // visual perception // inferred from electronic
1460424.x	0.002246	1.14	-1.34	NM_001122754//NM_0012	Tsk	TXK tyrosine kinase	0001816 // cytokine production // inferred from mutant phenotype//0001865 // NK T cell differentiation // inferred from genetic interaction//0002250 // adaptive immune response //
1422965.x	0.000958	1.14	1.10	NM_001005225//NM_0104	Hira	histone cell cycle regulation defective homolog A (S. cerevisiae)	0001649 // osteoblast differentiation // inferred from genetic interaction//0006336 // DNA replication-independent nucleosome assembly // not recorded//0006351 // transcription, DNA-
1451855.x	0.002796	1.14	-1.28	NM_001293694//NM_1338	Cept1	choline/ethanolaminephosphotransferase 1	0006629 // lipid metabolic process // inferred from electronic annotation//0006646 // phosphatidylethanolamine biosynthetic process // inferred from electronic annotation//0006656 //
1416740.x	0.001525	1.14	2.11	NM_022987//XM_0065193	Zic5	zinc finger protein of the cerebellum 5	0001843 // neural tube closure // inferred from mutant phenotype//0006355 // regulation of transcription, DNA-templated // inferred from direct assay//0007275 // multicellular organismal
1432628.x	0.007875	1.14	-1.11	NM_009424//XM_0064991	Traf6	TNF receptor-associated factor 6	0001022 // negative regulation of transcription from RNA polymerase II promoter // not recorded//0000209 // protein polyubiquitination // not recorded//0001503 // ossification // inferred
1427016.x	0.006473	1.13	-1.04	NM_030189//XM_0065392	Stpg1	spem tail PG rich repeat containing 1	0006915 // apoptotic process // inferred from electronic annotation
1429881.x	0.001391	1.13	-1.39	NM_00108450//NM_0011	Med1	mediator complex subunit 1	0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 // regulation of transcription, DNA-templated // inferred from electronic annotation//0006357 //
1430370.x	0.001673	1.13	-1.24	NM_019584//XM_0065331	Aten1	actin 1, autoinhibitory, N-terminus region related	0000045 // autophagic vacuole assembly // not recorded//0000910 // cytokinesis // not recorded//0001666 // response to hypoxia // inferred from electronic annotation//0006914 //
1451163.x	0.00137	1.12	1.26	NM_011568//XR_388401//	Allyref1	Aly/REF export factor // Aly/REF export factor 2	0006397 // mRNA processing // inferred from electronic annotation//0006810 // transport // inferred from electronic annotation//0008380 // RNA splicing // inferred from electronic
1424400.x	0.001245	1.13	1.04	NM_025362	DnaI30	DnaI (Hsp40) homolog, subfamily C, member 30	
1448490.x	0.001978						

Table S7

Gene ID	p (Corr)	FC-RSV 1 d	FC-RSV 5 d	RefSeq Transcript ID	Gene Symbol	Gene Title	Gene Ontology Biological Process
1415834_a	0.000404	1.09	18.21	NM_001040669//NM_0010	Gm10058//Gm10096//Gm10	predicted gene 10058//predicted gene 10096//predicted gene	
1418576_a	0.006155	1.09	1.37	NM_001290654//NM_0012	Ahsa2	AH1, activator of heat shock protein ATPase 2	0006950 // response to stress // inferred from electronic annotation//0032781 // positive regulation of ATPase activity // inferred from electronic annotation
1418101_a	0.000974	1.09	1.45	NM_001164557//NM_0011	Pdk1ip1	PDK21 interacting protein 1	
1415340_a	0.001696	1.09	-1.27	NM_001164768//NM_0011	Fbxw2	F-box and WD-40 domain protein 2	
1415382_a	0.001546	1.09	-1.27	NM_008396	Itoa2	integrin alpha 2	0001666 // response to hypoxia // inferred from electronic annotation//0001894 // tissue homeostasis // inferred from electronic annotation//0002687 // positive regulation of leukocyte
1416143_a	0.000915	1.09	4.76	NM_001103158//XR_00617	Gm13242//Rex2//Zfp600//	predicted gene 13242//reduced expression 2//zinc finger protein	0002244 // hematopoietic progenitor cell differentiation // inferred from mutant phenotype//0006355 // regulation of transcription, DNA-templated // not recorded
1449009_a	0.008897	1.09	-1.20	NM_009442//NM_0064978	Tt1	transcription termination factor, RNA polymerase I	0006338 // chromatin remodeling // inferred from direct assay//0006351 // transcription, DNA-templated // inferred from electronic annotation//0006353 // DNA-templated transcription,
1449007_a	0.006070	1.09	-1.20	NM_144861//NM_0065258	Rpr1a	regulation of nuclear pre-mRNA domain containing 1A	0070940 // dephosphorylation of RNA polymerase II C-terminal domain // not recorded
1451264_a	0.001961	1.09	-1.27	NM_051393//NM_0065345	Trim16	tripartite motif-containing 16	0043966 // histone H3 acetylation // not recorded//0003957 // histone H4 acetylation // not recorded//0045618 // positive regulation of keratinocyte differentiation // not
1439536_a	0.008049	1.09	-1.58	NM_001271797//NM_0265	Rchy1	ring finger and CCHC zinc finger domain containing 1	0016567 // protein ubiquitination // not recorded//0031388 // positive regulation of protein ubiquitination // not recorded//0032436 // positive regulation of proteasomal ubiquitin-
1435760_a	0.000175	1.09	-1.49	NM_001163671//NM_0011	Mapk9	mitogen-activated protein kinase 9	0000165 // MAPK cascade // inferred from electronic annotation//0001836 // release of cytochrome c from mitochondria // not recorded//0001934 // positive regulation of protein
1450334_a	0.004802	1.08	-1.24	NM_001290988//NM_0531	Trim11	tripartite motif-containing 11	0016567 // protein ubiquitination // inferred from direct assay//0032897 // negative regulation of viral transcription // inferred from direct assay//0032897 // negative regulation of viral
1430185_a	0.001110	1.08	-1.39	NM_003886//NM_198010/	Ankrd17	ankyrin repeat domain 17	0001955 // blood vessel maturation // inferred from mutant phenotype//0007492 // endoderm development // traceable autor statement//0051151 // negative regulation of smooth
1428214_a	0.000703	1.08	-1.07	NM_009431	Ctr9	Ctr9, Paf1/RNA polymerase II complex component, homolog (S. cerevisiae)	0000122 // negative regulation of transcription from RNA polymerase II promoter // inferred from mutant phenotype//0001711 // endodermal cell fate commitment // inferred from mutant
1451142_a	0.007878	1.08	-1.26	NM_001290497//NM_0012	Tmem91	transmembrane protein 91	0002244 // hematopoietic progenitor cell differentiation // inferred from mutant phenotype//0009607 // response to biotic stimulus // inferred from electronic annotation
1420551_a	0.007493	1.08	1.20	NM_025611	Cul7	cullin 7	0000226 // microtubule cytoskeleton organization // inferred from sequence or structural similarity//0000281 // mitotic cytokinesis // inferred from sequence or structural
1420159_a	0.006393	1.08	1.22	NM_001142807//NM_0011	Skc6a8	solute carrier family 6 (neurotransmitter transporter, creatine), member 8	0006810 // transport // inferred from electronic annotation//0006811 // ion transport // inferred from electronic annotation//0006814 // sodium ion transport // inferred from electronic
1451164_a	0.004241	1.08	-1.26	NM_023844//NM_0065230	Jam2	junction adhesion molecule 2	0007162 // negative regulation of cell adhesion // inferred from genetic interaction
1457231_a	0.002216	1.08	-2.19	NM_009178//NM_0065101	Sl3ga14	ST3 beta-galactoside alpha 2,3-sialyltransferase 4	0006486 // protein glycosylation // inferred from direct assay//0097503 // sialylation // inferred from direct assay//0097503 // sialylation // not recorded
1448475_a	0.000445	1.08	-1.18	NM_027134//NM_0065114	Mtfmt1	mitochondrial methionyl-tRNA formyltransferase	0006412 // translation // inferred from electronic annotation//0006413 // translational initiation // inferred from electronic annotation//0009058 // biosynthetic process // inferred from
1433738_a	0.003646	1.08	-1.44	NM_026609	Leptot1	leptin receptor overlapping transcript-like 1	
1455106_a	0.004570	1.08	-1.30	NM_019490//NM_0065351	Uso1	USO1 vesicle docking factor	0006810 // transport // inferred from electronic annotation//0006886 // intracellular protein transport // inferred from direct assay//0006888 // ER to Golgi vesicle-mediated transport // not
1427477_a	0.002903	1.08	-1.05	NM_001083937//NM_0784	Sk35a2	solute carrier family 35 (UDP-galactose transporter), member A2	0006810 // transport // inferred from mutant phenotype//0008643 // carbohydrate transport // inferred from direct assay//0015780 // nucleotide-sugar transport // inferred from electronic
1422041_a	0.000187	1.08	1.13	NM_001242407//NM_1753	Fam73b	family with sequence similarity 73, member B	000348 // bone development // inferred from mutant phenotype
1419514_a	0.000875	1.08	1.26	NM_001025608//NM_0012	Sard1	SUZ RNA binding domain containing 1	
1451846_a	0.007394	1.07	-1.28	NM_025691	Srp72	signal recognition particle 72	
1434684_a	0.005337	1.07	-1.46	NM_011278//NM_0065038	Rnf4	ring finger protein 4	0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 // regulation of transcription, DNA-templated // inferred from electronic annotation//0016567 //
1454921_a	0.005529	1.07	-1.32	NM_026654//NM_0065033	Toc1	target of EGR1, member 1 (nuclear)	
1428403_a	0.002732	1.07	-1.34	NM_010305	Gnai1	guanine nucleotide binding protein (G protein), alpha inhibiting 1	0006184 // GTP catalytic process // not recorded//0007049 // cell cycle // inferred from electronic annotation//0007165 // signal transduction // inferred from electronic
1450150_a	0.001215	1.07	-1.23	NM_001005767//NM_0065	Parl	presenilin associated, rhomboid-like	0005058 // proteolysis // inferred from electronic annotation//0009201 // negative regulation of release of cytochrome c from mitochondria // inferred from mutant phenotype//2001243 //
1437694_a	0.005322	1.07	-1.54	NM_001293703//NM_0280	Papad1b	phosphatidic acid phosphatase type 2 domain containing 1B	0046839 // phospholipid dephosphorylation // not recorded
1454606_a	0.000473	1.07	-1.31	NM_011882//NM_0065295	Rnasel	ribonuclease L (2', 5'-oligoadenylate synthetase-dependent)	0006364 // rRNA processing // not recorded//0006397 // mRNA processing // inferred from electronic annotation//0006468 // protein phosphorylation // inferred from electronic
1449277_a	0.000545	1.07	-1.21	NM_001291144//NM_1457	Dhx35	DEAH (Asp-Glu-Ala-His) box polypeptide 35	0006200 // ATP catalytic process // inferred from electronic annotation//0008152 // metabolic process // inferred from electronic annotation
1417452_a	0.005533	1.07	1.63	NM_153054//NM_0065095	Sk18a1	solute carrier family 18 (vesicular monoamine), member 1	0006810 // transport // inferred from electronic annotation//0006836 // neurotransmitter transport // inferred from electronic annotation//0006855 // drug transmembrane transport //
1451227_a	0.001373	1.06	-1.27	NM_026698//NM_0065040	Tmem129	transmembrane protein 129	
1429323_a	0.006765	1.06	-1.37	NM_025697//NM_0065193	Spryd7	SPRY domain containing 7	
1418835_a	0.007009	1.06	1.33	NM_011206//NM_0064958	Ptpn18	protein tyrosine phosphatase, non-receptor type 18	0006470 // protein dephosphorylation // inferred from electronic annotation//0016311 // dephosphorylation // inferred from electronic annotation//0035335 // peptidyl-tyrosine
1426942_a	0.000465	1.06	-1.04	NM_001030014//NM_0065	Mcat	malonyl CoA:ACP acyltransferase (mitochondrial)	0006629 // lipid metabolic process // inferred from electronic annotation//0006631 // fatty acid metabolic process // inferred from electronic annotation//0006633 // fatty acid biosynthetic
1416279_a	0.000369	1.06	3.33	NM_172829//NM_0065242	Sl6gal2	beta galactoside alpha 2,6 sialyltransferase 2	0005975 // carbohydrate metabolic process // inferred from electronic annotation//0006054 // N-acetylneuraminic acid metabolic process // inferred by curator//0006486 // protein
1418266_a	0.000130	1.06	1.41	NM_001081040//NM_0065	Coq10a	coenzyme Q10 homolog A (yeast)	
1435239_a	0.000487	1.06	-1.13	NM_001081240//NM_1789	Prrt10	protein arginine methyltransferase 10 (putative)	0006479 // protein methylation // inferred from electronic annotation//0032259 // methylation // inferred from electronic annotation
1435111_a	0.000947	1.06	-1.47	NM_001286948//NM_0231	Plg2g12a	phospholipase A2, group XIA	0006629 // lipid metabolic process // inferred from electronic annotation//0006644 // phospholipid metabolic process // inferred from electronic annotation//0016042 // lipid catabolic
1418051_a	0.005890	1.06	1.46	NM_001037857//NM_0077	Csf1r	colony stimulating factor 1 receptor	0001934 // positive regulation of protein phosphorylation // not recorded//0002376 // immune system process // inferred from electronic annotation//0006468 // protein phosphorylation //
1429472_a	0.000814	1.06	-1.38	NM_016676	Rab10	RAB10, member RAS oncogene family	0006184 // GTP catalytic process // not recorded//0006810 // transport // inferred from electronic annotation//0006886 // intracellular protein transport // traceable autor
1421571_a	0.000023	1.06	1.15	NM_009479//NM_0065075	Uras	uroporphyrinogen III synthase	0006779 // porphyrin-containing compound biosynthetic process // inferred from direct assay//0006779 // porphyrin-containing compound biosynthetic process // inferred from mutant
1420260_a	0.007736	1.06	1.21	NM_022995//NM_0064999	Pmpa1	prostate transmembrane protein, androgen induced 1	
1430479_a	0.009085	1.06	-1.40	NM_018804	Mtx2	metaxin 2	0006626 // protein targeting to mitochondrion // inferred from electronic annotation//0006810 // transport // inferred from electronic annotation//0015031 // protein transport // inferred
1430641_a	0.003224	1.06	-1.40	NM_133225	Acd3d	acyl-Coenzyme A binding domain containing 3	0006629 // lipid metabolic process // inferred from electronic annotation//0006694 // steroid biosynthetic process // inferred from electronic annotation//0006810 // transport // inferred
1434337_a	0.002157	1.06	-1.45	NM_172402//NM_0065213	Sk25a32	solute carrier family 25, member 32	0006810 // transport // inferred from electronic annotation
1419370_a	0.007616	1.06	1.27	NM_009081//NM_0014739	Gm10051//Rpl28	predicted pseudogene 10051//ribosomal protein L28	0006412 // translation // inferred from electronic annotation
1419474_a	0.001802	1.06	1.26	NM_021428//NM_0065234	Dexi	dexamethasone-induced transcript	
1436618_a	0.001298	1.06	-1.52	NM_011030//NM_0065133	P4ha1	procollagen-proline, 2-oxoglutarate 4-dioxygenase (proline 4-hydroxylase),	0018401 // peptidyl-proline hydroxylation to 4-hydroxy-L-proline // inferred from direct assay//0030199 // collagen fibril organization // inferred from mutant phenotype//0055114 //
1417856_a	0.001997	1.05	-1.52	NM_001168356//NM_1342	Bnpl1	BCL2/adenovirus E18 19kD interacting protein like	0006915 // apoptotic process // not recorded//0008285 // negative regulation of cell proliferation // not recorded//0040009 // regulation of growth rate // not recorded//0070782 //
1453892_a	0.005944	1.05	-1.93	NM_011595	Timp3	tissue inhibitor of metalloproteinase 3	0007269 // neutrophil maturation // inferred from electronic annotation//0008152 // metabolic process // inferred from electronic annotation//0001046 // negative regulation of
1431173_a	0.005399	1.05	-1.41	1700028N14Rik		RIKEN cDNA 1700028N14 gene	0000165 // MAPK cascade // --//0000165 // MAPK cascade // inferred from electronic annotation//0000186 // activation of MAPKK activity // --//0000186 // activation of MAPKK activity //
1420527_a	0.001795	1.05	-1.20	NM_011588	Trim28	tripartite motif-containing 28	0000122 // negative regulation of transcription from RNA polymerase II promoter // inferred from direct assay//0000122 // negative regulation of transcription from RNA polymerase II
1429554_a	0.005128	1.05	-1.09	NM_00121473//NM_0065032	Akr1a1	aldo-keto reductase family 1, member A1 (aldehyde reductase)	0019853 // L-ascorbic acid biosynthetic process // inferred from direct assay//0042840 // D-glucuronate catabolic process // inferred from direct assay//0046185 // aldehyde catabolic process
1431808_a	0.009499	1.05	-1.10	NM_001164593//NM_0011	Pdzn4	PZD domain containing RING finger 4	0006952 // defense response // inferred from electronic annotation
1453467_a	0.007064	1.05	-1.31	NM_0010861//NM_0065301	Ctla4	Mus musculus class II transactivator (Ctla), transcript variant 3, mRNA	0034341 // response to interferon-gamma // inferred from direct assay//0045892 // negative regulation of transcription, DNA-templated // inferred from mutant phenotype//0046677 //
1418677_a	0.004303	1.05	1.35	NM_172814//NM_0065209	Lrp12	low density lipoprotein-related protein 12	0006897 // endocytosis // inferred from electronic annotation
1416465_a	0.005187	1.04	2.30	9020417H13Rik		RIKEN cDNA 9020417H13 gene	
1434482_a	0.005470	1.04	-1.46	NM_009551//NM_0065270	Zfand5	zinc finger, AN1-type domain 5	0001701 // in utero embryonic development // inferred from mutant phenotype//0001944 // vasculature development // inferred from mutant phenotype//0003016 // respiratory system
1421457_a	0.000130	1.04	1.15	NM_001164187//NM_0195	Nagk	N-acetylglucosamine kinase	0006044 // N-acetylglucosamine metabolic process // inferred from direct assay//0016310 // phosphorylation // inferred from electronic annotation//0019262 // N-acetylneuraminic
1460238_a	0.008277	1.04	-1.33	NM_153591//NM_0065078	Nars2	asparaginyl-tRNA synthetase 2 (mitochondrial)(putative)	0006412 // translation // inferred from electronic annotation//0006418 // tRNA aminoacylation for protein translation // inferred from electronic annotation//0006421 // asparaginyl-tRNA
1441996_a	0.002737	1.04	-1.66	NM_001085407//NM_0010	Scdca93	serologically defined colon cancer antigen 3	
1418021_a	0.001525	1.04	1.47	NM_010299	Gm2a	Gm2 ganglioside activator protein	0001573 // ganglioside metabolic process // inferred from electronic annotation//0006629 // lipid metabolic process // inferred from electronic annotation//0006665 // sphingolipid
1422939_a	0.005380	1.04	1.10	NM_001034097//NM_0010	Tnfsf12//Tnfsf12Tnfsf13//Tn	tumor necrosis factor (ligand) superfamily, member 12//Tnfsf12-Tnfsf13	0001525 // angiogenesis // inferred from electronic annotation//0002376 // immune system process // inferred from electronic annotation//0002426 // immunoglobulin production //
1416176_a	0.002070	1.04	4.36	NM_001033793//NM_0065	Ubf1f1	ubiquitin binding transcription factor, RNA polymerase I-like 1	0001832 // angiostatic growth // inferred from mutant phenotype//0007275 // multicellular organismal development // inferred from electronic annotation//0007566 // embryo implantation
1418354_a	0.009950	1.04	1.40	NM_020519	Slurp1	secreted lyg/Plaur domain containing 1	0001775 // cell activation // not recorded
1417561_a	0.001826	1.04	1.61	NM_023842//NM_0065165	Dsp	desmosoplakin	002934 // desmosome organization // inferred from mutant phenotype//0003223 // ventricular compact myocardium morphogenesis // inferred from mutant phenotype//0001637 // single
1419050_a	0.004401	1.04	1.31	NM_010091//NM_0065385	Dvl1	dishevelled, dsh homolog 1 (Drosophila)	0001505 // regulation of neurotransmitter levels // inferred from mutant phenotype//0001932 // regulation of protein phosphorylation // inferred from genetic interaction//0001933 //
1416720_a	0.000811	1.04	2.15	NM_001286750//NM_1531	Olfm3	olfactomedin 3	0042462 // eye photoreceptor cell development // not recorded
1455622_a	0.004787	1.04	-2.01	NM_001166661//NM_0011	Ccdc85a	coiled-coil domain containing 85A	
1436340_a	0.009301	1.04	-1.51	NM_023324//NM_0065147	Pell1	pellino 1	0000209 // protein polyubiquitination // inferred from mutant phenotype//0001819 // positive regulation of cytokine production // inferred from mutant phenotype//0008063 // Toll
1448962_a	0.001733	1.04	-1.23	NM_001024954//NM_0305	Pv4	pre B cell leukemia homeobox 4	0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 // regulation of transcription, DNA-templated // inferred from electronic annotation//0006357 //
1415794_a	0.004425	1.04	2.88	NM_010861//NM_0065301	Myl2	myosin, light polypeptide 2, regulatory, cardiac, slow	0003097 // heart morphogenesis // inferred from genetic interaction//0007507 // heart development // inferred from mutant phenotype//0008793 // post-embryonic development //
1416226_a	0.002537	1.04	3.77	NM_007501//NM_0065131	Neurod4	neurogenic differentiation 4	0001764 // neuron migration // inferred from genetic interaction//0001764 // neuron migration // inferred from mutant phenotype//0006351 // transcription, DNA-templated // inferred
1442130_a	0.000157	1.04	-1.66	NM_008640	Laptn4a	lysosomal-associated protein transmembrane 4A	0006810 // transport // inferred from electronic annotation
1417291_a	0.003459	1.04	1.74	NM_025968	Ptgr1	prostaglandin reductase 1	0006693 // prostaglandin metabolic process // inferred from electronic annotation//0009636 // response to toxic substance // inferred from electronic annotation//0055114 // oxidation-
1451658_a	0.000441	1.04	-1.28	NM_033370	Copb1	coatamer protein complex, subunit beta 1	0006810 // transport // inferred from electronic annotation//0006886 // intracellular protein transport // inferred from electronic annotation//0006891 // intra-Golgi vesicle-mediated
1420107_a	0.002037	1.03	-1.34	NM_024258//NM_0065231	Usp16	ubiquitin specific peptidase 16	0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 // regulation of transcription, DNA-templated // inferred from electronic annotation//0006357 //
1448670_a	0.007601	1.03	-1.19	NM_008224//NM_0065278	Hcfc1	host cell factor C1	0000122 // negative regulation of transcription from RNA polymerase II promoter // not recorded//0006355 // regulation of transcription, DNA-templated // not recorded//0006366 //
1428491_a	0.001941	1.03	-1.35	NM_026369//NM_0065298	Arcp5	actin related protein 2/3 complex, subunit 5	0030833 // regulation of actin filament polymerization // inferred from electronic annotation
1460323_a	0.000285	1.03	-1.33	NM_146047	Clptm1l	CLPTM1-like	0006915 // apoptotic process // inferred from electronic annotation
1424684_a	0.001640	1.03	1.03	NM_018768//NM_0065337	Sox8	syntaxin 8	0006810 // transport // inferred from electronic annotation//0006886 // intracellular protein transport // not recorded//0006906 // vesicle fusion // not recorded//0008333 // endosome to
1419676_a	0.000023	1.03	1.24	NM_026027	Pfdn1	prefoldin 1	0006457 // protein folding // inferred from electronic annotation//00021537 // telencephalon development // inferred from mutant phenotype//00021549 // cerebellum development //
1418500_a	0.002013	1.03	1.38	NM_001033476//NM_0065	Ahnak2	AHNAK nucleoprotein 2	0001778 // plasma membrane repair // inferred from mutant phenotype
1420330_a	0.000324	1.02	2.18	NM_001033305	Ndufb6	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 6	0006810 // transport // inferred from electronic annotation//0055114 // oxidation-reduction process // inferred from electronic annotation

Table S7

Gene ID	p (Corr)	FC-RSV 1 d	FC-RSV 5 d	RefSeq Transcript ID	Gene Symbol	Gene Title	Gene Ontology Biological Process
1434401_a	0.005535	1.02	-1.45	NM_009270	Sqle	squalene epoxidase	0006725 // cellular aromatic compound metabolic process // not recorded // 0008152 // metabolic process // inferred from electronic annotation // 0008203 // cholesterol metabolic process //
1416026_a	0.002706	1.02	8.31	NM_001031518 // NM_0011	Gm132442 // Rex2 // Zfp600	predicted gene 132442 // reduced expression 2 // zinc finger protein 600	0002244 // hematopoietic progenitor cell differentiation // inferred from mutant phenotype // 0006355 // regulation of transcription, DNA-templated // not recorded
1422781_a	0.000739	1.02	1.10	NM_021556	Mrps30	mitochondrial ribosomal protein S30	0006412 // translation // inferred from electronic annotation
1452948_a	0.007786	1.02	-1.88	NM_024239 // XM_0065065	Stambp	STAM binding protein	0000281 // mitotic cytokinesis // not recorded // 0006508 // proteolysis // not recorded // 0014067 // negative regulation of phosphatidylinositol 3-kinase signaling // not recorded // 0016579
1443466_s	0.004518	1.02	-1.70	NM_023239	Ndn12	neccin-like 2	0006281 // DNA repair // inferred from electronic annotation // 0006310 // DNA recombination // inferred from electronic annotation // 0006355 // regulation of transcription, DNA-templated
1433859_s	0.000126	1.02	-1.12	NM_01163102	Eme2	essential meiotic endonuclease 1 homolog 2 (S. pombe)	0001701 // in utero embryonic development // inferred from mutant phenotype // 0006281 // DNA repair // inferred from electronic annotation // 0006310 // DNA recombination // inferred
1438311_a	0.000372	1.02	-1.55	NM_01288586 // NM_0107	Mdm2	transformed mouse 3T3 cell double minute 2	0000122 // negative regulation of transcription from RNA polymerase II promoter // not recorded // 0006461 // protein complex assembly // not recorded // 0006977 // DNA damage response,
1421291_a	0.009725	1.02	1.16	NM_011296 // NM_138946	Rps18	ribosomal protein S18	0006412 // translation // not recorded // 0042254 // ribosome biogenesis // not recorded
1421299_a	0.004044	1.01	1.16	NM_00128594 // NM_0012	Ef3k	eukaryotic translation initiation factor 3, subunit K	0001731 // formation of translation preinitiation complex // inferred from electronic annotation // 0006412 // translation // inferred from electronic annotation // 0006413 // translational
1449473_s	0.006469	1.01	-1.22	NM_018855 // NM_207678	Ccn2	cyclin L2	000079 // regulation of cyclin-dependent protein serine/threonine kinase activity // inferred from electronic annotation // 0006351 // transcription, DNA-templated // inferred from electronic
1418650_a	0.004592	1.01	1.35	NM_010288 // NM_0065125	Gja1	gap junction protein, alpha 1	0001649 // osteoblast differentiation // inferred from mutant phenotype // 0001701 // in utero embryonic development // inferred from mutant phenotype // 0001764 // neuron migration //
1456437_x	0.002426	1.01	-1.33	NM_001035509 // NM_0010	Zcchc18	zinc finger, CCHC domain containing 18	0030509 // BMP signaling pathway // not recorded
1418688_s	0.000619	1.01	1.35	NM_178645	Blmh	bleomycin hydrolase	0005508 // proteolysis // inferred from mutant phenotype // 0009636 // response to toxic substance // inferred from mutant phenotype // 0042493 // response to drug // inferred from mutant
1437557_a	0.005146	1.01	-1.54	NM_178908	Fom26e	family with sequence similarity 26, member E	0006810 // transport // inferred from electronic annotation // 0006811 // ion transport // inferred from electronic annotation
1449277_a	0.000545	1.01	-1.21	NM_026031	Utp11	UTP11-like, U3 small nuclear ribonucleoprotein, (yeast)	0006364 // rRNA processing // not recorded // 0007399 // nervous system development // not recorded // 0042274 // ribosomal small subunit biogenesis // not recorded // 0043065 // positive
1422671_s	0.000761	1.01	1.11	NM_01122666 // NM_1786	Suds3	suppressor of defective silencing 3 homolog (S. cerevisiae)	0000122 // negative regulation of transcription from RNA polymerase II promoter // not recorded // 0006351 // transcription, DNA-templated // inferred from electronic annotation // 0006355
1422617_a	0.006230	1.01	1.11	NM_018799	Ef3i	eukaryotic translation initiation factor 3, subunit I	0001731 // formation of translation preinitiation complex // inferred from electronic annotation // 0006412 // translation // inferred from electronic annotation // 0006413 // translational
1452424_a	0.005868	1.01	-1.29	NM_030685	Serp1	stress-associated endoplasmic reticulum protein 1	0001501 // skeletal system development // inferred from mutant phenotype // 0006006 // glucose metabolic process // inferred from mutant phenotype // 0006486 // protein glycosylation //
1429325_a	0.000118	1.01	-1.37	NM_001293776 // NM_0012	Chtop	chromatin target of PRMT1	0006351 // transcription, DNA-templated // inferred from electronic annotation // 0006355 // regulation of transcription, DNA-templated // inferred from electronic annotation // 0006406 //
1429909_a	0.000610	1.01	-1.39	NM_008929	Dnajc3	DnaJ (Hsp40) homolog, subfamily C, member 3	0006469 // negative regulation of protein kinase activity // inferred from sequence or structural similarity // 0006986 // response to unfolded protein // inferred from electronic
1442067_a	0.007232	1.01	-1.66	NM_01285839 // NM_0280	Osgsep1	O-sialoglycoprotein endopeptidase-like 1	0006529 // asparagine biosynthetic process // inferred from electronic annotation // 0006541 // glutamine metabolic process // inferred from electronic annotation // 0008033 // tRNA
1422141_s	0.000083	1.01	1.13	NM_026610 // XM_0014765	Gm3244 // Gm3873 // Ndufb4	predicted pseudogene 3244 // predicted gene 3873 // NADH	0006979 // response to oxidative stress // not recorded // 0055114 // oxidation-reduction process // inferred from electronic annotation
1440406_a	0.000186	1.00	-1.44	NM_01242358 // NM_0012	Trn1	RNA nucleotidyl transferase, CCA-adding, 1	0001680 // tRNA 3'-terminal CCA addition // inferred from electronic annotation // 0006396 // RNA processing // inferred from electronic annotation // 0008033 // tRNA processing // not
1419426_s	0.002505	1.00	1.26	NM_001081108	Lamtor4	late endosome/lysosomal adaptor, MAPK and MTOR activator 4	0008361 // regulation of cell size // not recorded // 0032008 // positive regulation of TOR signaling // not recorded // 0043087 // regulation of GTPase activity // not recorded // 0043547 //
1424339_a	0.000038	1.00	1.04	NM_025924 // NM_006508	Upf3a	UPF3 regulator of nonsense transcripts homolog A (yeast)	0008986 // response to unfolded protein // not recorded // 0045727 // positive regulation of translation // not recorded
1420470_a	0.005385	1.00	1.20	NM_011289	Rp127	ribosomal protein L27	0006412 // translation // inferred from electronic annotation
1450519_a	0.001662	1.00	-1.24	NM_013753 // NM_0065379	Nbn	nibrin	0000077 // DNA damage checkpoint // not recorded // 0000723 // telomere maintenance // not recorded // 0001701 // in utero embryonic development // inferred from mutant
1450949_a	0.001063	1.00	-1.25	NM_001081265	Heatr2	HEAT repeat containing 2	
1428269_a	0.001179	1.00	-1.34	NM_008410	Iitm2b	integral membrane protein 2b	
1421101_a	0.000716	1.00	1.17	NM_012052	Rps3	ribosomal protein S3	0042985 // negative regulation of amyloid precursor protein biosynthetic process // not recorded // 0009719 // extrinsic apoptotic signaling pathway in absence of ligand // inferred from direct
1433877_a	0.000810	-1.00	-1.44	NM_010432 // XM_0065010	Hipk1	homeodomain interacting protein kinase 1	000737 // DNA catalytic process, endonucleolytic // not recorded // 0000218 // cytoplasmic translation // not recorded // 0006281 // DNA repair // not recorded // 0006412 // translation //
1453152_a	0.000220	-1.00	-1.90	NM_001168525 // NM_0011	Sgms1	sphingomyelin synthase 1	0000122 // negative regulation of transcription from RNA polymerase II promoter // inferred from sequence or structural similarity // 0006351 // transcription, DNA-templated // inferred from
1438096_a	0.004957	-1.00	-1.16	NM_001037940 // NM_0010	Dnajb6	DnaJ (Hsp40) homolog, subfamily B, member 6	0006629 // lipid metabolic process // inferred from electronic annotation // 0006665 // sphingolipid metabolic process // inferred from electronic annotation // 0006686 // sphingomyelin
1433501_a	0.009725	-1.00	-1.43	NM_174852 // NM_0065334	Phf12	PHD finger protein 12	0006457 // protein folding // not recorded // 0030036 // actin cytoskeleton organization // inferred from mutant phenotype // 0030198 // extracellular matrix organization // inferred from
1451189_a	0.001909	-1.00	-1.26	NM_001130408 // NM_0074	Arf1	ADP-ribosylation factor 1	0000122 // negative regulation of transcription from RNA polymerase II promoter // not recorded // 0006351 // transcription, DNA-templated // inferred from electronic annotation // 0006355
1451329_a	0.000101	-1.00	-1.27	NM_001159866 // NM_0195	Uchl5	ubiquitin carboxyl-terminal esterase L5	002090 // regulation of receptor internalization // not recorded // 0006810 // transport // inferred from electronic annotation // 0006878 // cellular copper ion homeostasis // not
1423398_a	0.000812	-1.00	1.08	NM_001198859 // NM_0011	Ctbp1	C-terminal binding protein 1	0006281 // DNA repair // inferred from electronic annotation // 0006310 // DNA recombination // inferred from electronic annotation // 0006351 // transcription, DNA-templated // inferred
1421196_a	0.002764	-1.00	1.16	NM_026364 // NM_0065340	Prpsap1	phosphoribosyl pyrophosphate synthetase-associated protein 1	0000122 // negative regulation of transcription from RNA polymerase II promoter // inferred from mutant phenotype // 0000122 // negative regulation of transcription from RNA polymerase II
1433623_a	0.009050	-1.01	-1.43	NM_028521 // NM_0065002	Phospho2	phosphatase, orphan 2	0009165 // nucleotide biosynthetic process // inferred from electronic annotation // 0033673 // negative regulation of kinase activity // not recorded
1433412_a	0.007451	-1.01	-1.43	NM_009201 // NM_0065396	Sklas	solute carrier family 1 (neutral amino acid transporter), member 5	0008152 // metabolic process // inferred from electronic annotation // 0016311 // dephosphorylation // inferred from electronic annotation
1416689_a	0.002754	-1.01	1.22	NM_00129039 // NM_0086	Mylb1	myelin basic protein 1	0003333 // amino acid transmembrane transport // inferred from direct assay // 0003333 // amino acid transmembrane transport // not recorded // 0006810 // transport // inferred from
1419537_a	0.001721	-1.01	2.25	NM_007708 // NM_0065301	Cr	cytochrome c	0006351 // transcription, DNA-templated // inferred from electronic annotation // 0006355 // regulation of transcription, DNA-templated // inferred from electronic annotation // 0006355
1425641_x	0.000158	-1.01	-1.38	NM_177301 // NM_0065395	Hmnp1	heterogeneous nuclear ribonucleoprotein L	0000070 // mitotic sister chromatid segregation // inferred from mutant phenotype // 0000086 // G2/M transition of mitotic cell cycle // not recorded // 0009010 // cytokinesis // inferred from
1419234_a	0.006920	-1.01	1.29	NM_025394	Tomm7	translocase of outer mitochondrial membrane 7 homolog (yeast)	0006397 // mRNA processing // inferred from electronic annotation
1431091_a	0.009902	-1.01	-1.41	NM_001035259 // NM_1722	Sfswap	splice factor, suppressor of white-apricot locus (Drosophila)	0006810 // transport // inferred from electronic annotation // 0015031 // protein transport // inferred from electronic annotation // 0003010 // protein import into mitochondrial matrix //
1423405_a	0.007877	-1.02	1.08	NM_133701	Prrf6	PRP6 pre-mRNA splicing factor 6 homolog (yeast)	0006351 // transcription, DNA-templated // inferred from electronic annotation // 0006355 // regulation of transcription, DNA-templated // inferred from electronic annotation // 0006396 //
1421047_a	0.001703	-1.02	1.17	NM_009087 // NM_181730	Por1d	polymerase (RNA) I polypeptide D	0000244 // spliceosomal tri-snRNP complex assembly // not recorded // 0000398 // mRNA splicing, via spliceosome // inferred from electronic annotation // 0006396 // RNA processing //
1456001_a	0.000008	-1.02	-1.32	NM_026197 // NM_0065339	Mettl16	methyltransferase like 16	0006351 // transcription, DNA-templated // inferred from electronic annotation // 0006360 // transcription from RNA polymerase I promoter // not recorded // 0006383 // transcription from RNA
1423676_a	0.001715	-1.02	1.07	NM_001290984 // NM_1337	Asnsd1	asparagine synthetase domain containing 1	0032259 // methylation // inferred from electronic annotation // 0006479 // protein methylation // inferred from electronic annotation
1428721_a	0.000473	-1.02	-1.35	NM_001039045 // NM_0260	Pigc	phosphatidylinositol glycan anchor biosynthesis, class C	0006529 // asparagine biosynthetic process // inferred from electronic annotation // 0006541 // glutamine metabolic process // inferred from electronic annotation // 0008033 // tRNA
1417206_a	0.001818	-1.03	1.76	NM_001110009 // NM_0074	Apoc1	apolipoprotein C-I	0006506 // GPI anchor biosynthetic process // inferred from electronic annotation
1417693_a	0.009183	-1.03	1.56	NM_010382	H2-Eb1	histocompatibility 2, class II antigen E beta	0006641 // triglyceride metabolic process // inferred from mutant phenotype // 0006810 // transport // inferred from electronic annotation // 0006869 // lipid transport // inferred from
1439158_a	0.005262	-1.03	-1.57	NM_029457 // NR_027488 //	Senp2	SUMO1/sentrin specific peptidase 2	0002376 // immune system process // inferred from electronic annotation // 0002504 // antigen processing and presentation of peptide or polysaccharide antigen via MHC class II // inferred
1428461_a	0.008072	-1.03	-1.35	NM_025816 // NM_0065063	Tax1bp1	Tax (human T cell leukemia virus type I) binding protein 1	0001934 // positive regulation of protein phosphorylation // not recorded // 0006351 // transcription, DNA-templated // inferred from electronic annotation // 0006355 // regulation of
1418323_a	0.002906	-1.03	1.40	NM_010422	Hexb	hexosaminidase B	0006915 // apoptotic process // inferred from electronic annotation // 0032088 // negative regulation of NF-kappaB transcription factor activity // inferred from mutant phenotype // 0043066
1448891_a	0.000647	-1.03	-1.19	NM_146006 // NM_0065132	Lss	lanosterol synthase	0001501 // skeletal system development // inferred from genetic interaction // 0005975 // carbohydrate metabolic process // inferred from electronic annotation // 0006044 // N-
1421345_a	0.007565	-1.03	1.16	NM_009143 // NM_0065326	Sdf2	stromal cell derived factor 2	0006629 // lipid metabolic process // inferred from electronic annotation // 0006694 // steroid biosynthetic process // inferred from electronic annotation // 0006695 // cholesterol biosynthetic
1434260_a	0.001365	-1.03	-1.45	NM_023343 // NM_0065298	Ilkap	integrin-linked kinase-associated serine/threonine phosphatase 2C	
1419314_a	0.000272	-1.03	1.28	NM_053071	Cox6c	cytochrome c oxidase subunit VIc	0006470 // protein dephosphorylation // not recorded // 0008152 // metabolic process // inferred from electronic annotation // 0033262 // regulation of nuclear cell cycle DNA replication //
1430974_a	0.002896	-1.03	-1.41	NM_001167829 // NM_0264	Fam55p	family with sequence similarity 45, member A	1902600 // hydrogen ion transmembrane transport // inferred from electronic annotation
1433767_a	0.003034	-1.03	-1.44	NM_024457	Rap1b	RAS related protein 1b	
1444740_a	0.003691	-1.03	-1.75	NM_026194 // NM_0065382	Upl1	UFM1 specific ligase 1	0006194 // GTP catalytic process // not recorded // 0006886 // intracellular protein transport // inferred from electronic annotation // 0006913 // nucleocytoplasmic transport // inferred from
1451013_a	0.002544	-1.03	-1.25	NM_010748 // NM_0065165	Lyst	lysosomal trafficking regulator	0006200 // ATP catalytic process // not recorded // 0006754 // ATP biosynthetic process // inferred from electronic annotation // 0006810 // transport // inferred from electronic
1419086_a	0.001965	-1.03	1.30	NM_013795	Atps1	ATP synthase, H ⁺ transporting, mitochondrial F0 complex, subunit G	0007165 // signal transduction // not recorded // 0043123 // positive regulation of I-kappaB kinase/NF-kappaB signaling // not recorded
1431695_a	0.003788	-1.03	-1.42	NM_020050	Tmem9b	TMEM9 domain family, member B	0002227 // innate immune response in mucosa // not recorded // 0006412 // translation // inferred from electronic annotation // 0001973 // antibacterial humoral response // not
1422617_a	0.006230	-1.03	1.11	NM_026055 // XM_0065005	LOC102634681 // LOC1026426	60S ribosomal protein L39-like // ribosomal protein L39	0007155 // cell adhesion // inferred from electronic annotation // 0001466 // negative regulation of peptidase activity // inferred from electronic annotation // 0001951 // negative regulation of
1428269_a	0.002610	-1.03	1.41	NM_007738 // NM_0065119	Col7a1	collagen, type VII, alpha 1	0006629 // lipid metabolic process // inferred from electronic annotation // 0006659 // phosphatidylserine biosynthetic process // inferred from electronic annotation // 0008654 //
1422598_a	0.004565	-1.04	1.11	NM_008959	Ptds1	phosphatidylserine synthase 1	
1433751_a	0.002538	-1.04	-1.44	NM_178625 // NM_0065051	Tmem209	transmembrane protein 209	
1422597_a	0.001133	-1.04	1.11	NM_009085	Polr1c	polymerase (RNA) I polypeptide C	
1449880_s	0.005753	-1.04	-1.22	NM_053075 // NM_0065356	Rheb	Ras homology enriched in brain	0006351 // transcription, DNA-templated // inferred from electronic annotation // 0006360 // transcription from RNA polymerase I promoter // not recorded // 0006383 // transcription from RNA
1437873_a	0.000782	-1.04	-1.54	NM_007861	Dld	dihydrolipoamide dehydrogenase	0006184 // GTP catalytic process // inferred from electronic annotation // 0007165 // signal transduction // inferred from electronic annotation // 0007264 // small GTPase mediated signal
1418745_a	0.001927	-1.04	1.35	NM_001163425 // NR_02810	Myev02	myeloma overexpressed 2	0006086 // acetyl-CoA biosynthetic process from pyruvate // not recorded // 0006103 // 2-oxoglutarate metabolic process // not recorded // 0006120 // mitochondrial electron transport,
1429209_a	0.001179	-1.04	-1.36	NM_027901 // NM_0065041	Gtf3c2	general transcription factor IIC, polypeptide 2, beta	
1420502_a	0.000893	-1.04	1.20	NM_027976 // NM_0065271	Ac3s	acyl-CoA synthetase long-chain family member 5	0006351 // transcription, DNA-templated // not recorded // 0006383 // transcription from RNA polymerase III promoter // not recorded
1437385_a	0.000796	-1.04	-1.53	NM_009700 // NR_002700 //	Btp3 // Gm734	B cell translocation gene 3 // B cell translocation gene 3 pseudogene	0001676 // long-chain fatty acid metabolic process // not recorded // 0006629 // lipid metabolic process // inferred from electronic annotation // 0006631 // fatty acid metabolic process //
1423070_a	0.000755	-1.04	1.09	NM_009082 // XM_030851	Gm10913 // Gm11449 // Gm12	predicted pseudogene 10913 // predicted gene 11449 // predicted gene	0004612 // translation // inferred from mutant phenotype // 0008283 // cell proliferation // inferred from mutant phenotype // 0001589 // cell-substrate adhesion // inferred from direct
1453063_a	0.000921	-1.04	-1.31	NM_00012309	Ccdc55	coiled-coil domain containing 55	0000381 // regulation of alternative mRNA splicing, via spliceosome // not recorded // 0006397 // mRNA processing // inferred from electronic annotation // 0006913 // nucleocytoplasmic
1423681_a	0.000228	-1.04	1.07	NM_027874 // NM_139059	Csnk1d	casein kinase 1, delta	0001934 // positive regulation of protein phosphorylation // not recorded // 0006468 // protein phosphorylation // inferred from direct assay // 0006468 // protein phosphorylation // inferred
1421070_a	0.007879	-1.04	1.17	NM_145469 // NM_0065200	Nipa2	NIPA-like domain containing 2	0015693 // magnesium ion transport // inferred from electronic annotation
1423003_a	0.000725	-1.05	1.10	NM_019883 // NM_029366	Kxd1 // Uba52	Kxdl motif containing 1 // ubiquitin A-52 residue ribosomal protein fusion	0006412 // translation // inferred from electronic annotation // 0010992 // ubiquitin homeostasis // inferred from genetic interaction // 0016192 // vesicle-mediated transport // inferred from
1439527_a	0.008157	-1.05	-1.58	NM_025776	Rbm22	RNA binding motif protein 22	000060 // protein import into nucleus, translocation // not recorded // 0006397 // mRNA processing // inferred from electronic annotation // 0006810 // transport // inferred from electronic
1418237_s	0.001409	-1.05	1.42	NM_025983	Atp5e	ATP synthase, H ⁺ transporting, mitochondrial F1 complex, epsilon subunit	0006200 // ATP catalytic process // not recorded // 0006754 // ATP biosynthetic process // inferred from electronic annotation // 0006810 // transport // inferred from electronic
1436300_a	0.009192	-1.05	-1.14	NM_001171003 // XM_0065	Mgom	malate-glucosylase	0005975 // carbohydrate metabolic process // inferred from electronic annotation // 0008152 // metabolic process // inferred from electronic annotation
1446875_a	0.004748	-1.05	-1.81	NM_021557 // NM_0065155	Rdh11	retinol dehydrogenase 11	0006281 // DNA repair // inferred from electronic annotation // 0006281 // DNA repair // inferred from sequence or structural similarity // 0006325 // chromatin organization // inferred from
1418174_a	0.004037	-1.05	1.43	NM_011694 // NM_0065331	Vdac1 // AK201917	voltage-dependent anion channel 1 // Mus musculus cDNA,	0001662 // behavioral fear response // inferred from mutant phenotype // 0006810 // transport // inferred from electronic annotation // 0006811 // ion transport // inferred from electronic
1418842_a	0.004632	-1.05	1.33	NM_172682 // NM_0065013	Fom160a1	family with sequence similarity 160, member A1	
1429579_a	0.000681	-1.05	-1.38	NM_008466	Kpna3	karyopherin (importin) alpha 3	00066

Table S7

Gene ID	p (Corr)	FC-RSV 1 d	FC-RSV 5 d	RefSeq Transcript ID	Gene Symbol	Gene Title	Gene Ontology Biological Process
1420562_a	0.007365	-1.05	1.20	NM_027949//XM_0065195	Phf7	PHD finger protein 7	
1433272_a	0.006170	-1.05	-1.43	NM_001164578//NM_1751	Tsr2	TSR2 205 rRNA accumulation	0006364 // rRNA processing // inferred from electronic annotation
1421657_a	0.004594	-1.05	1.15	NM_025919//XM_0065391	Rpl11//Gm5093	ribosomal protein L11//predicted gene 5093	0006364 // rRNA processing // not recorded//0006412 // translation // inferred from electronic annotation//0006605 // protein targeting // not recorded//0034504 // protein localization to
1422068_a	0.007698	-1.05	1.13	NM_001160400//XR_39106	Megf8	multiple EGF-like domains 8	0003143 // embryonic heart tube morphogenesis // inferred from mutant phenotype//0007275 // multicellular organismal development // inferred from electronic annotation//0010468 //
1418131_a	0.002903	-1.05	1.44	NM_010686//XM_0065369	Laptm5	lysosomal-associated protein transmembrane 5	0006810 // transport // inferred from electronic annotation
1438475_a	0.001347	-1.05	-1.56	NM_009007//XM_0065046	Rac1	RAS-related G3 botulinum substrate 1	0001934 // positive regulation of protein phosphorylation // not recorded//0002093 // auditory receptor cell morphogenesis // inferred from mutant phenotype//0002551 // mast cell
1419638_a	0.003011	-1.05	1.24	NM_172268//XM_0064979	Nup214	nucleoporin 214	0006406 // mRNA export from nucleus // inferred from mutant phenotype//0006606 // protein import into nucleus // inferred from mutant phenotype//0006611 // protein export from
1419658_a	0.000469	-1.05	1.24	NM_015740//NM_134006	Bloc1s1//Rdh5	biogenesis of lysosomal organelles complex-1, subunit 1//retinol	0007601 // visual perception // inferred from electronic annotation//0008089 // anterograde axon cargo transport // inferred from mutant phenotype//0008151 // metabolic process //
1423062_a	0.000469	-1.06	1.10	NM_019883//NM_029366	Kpl1//Uba52	Kdo1, notf containing 1//ubiquitin A-S2 residue ribosomal protein fusion	0006412 // translation // inferred from electronic annotation//0001992 // ubiquitin homeostasis // inferred from genetic interaction//0016192 // vesicle-mediated transport // inferred from
1420046_s	0.008977	-1.06	1.22	NM_025849	Tmem261	transmembrane protein 261	
1429198_a	0.008781	-1.06	-1.09	NM_001253805//NM_0012	Yuhwz	tyrosine 3-monoxygenase/tryptophan 5-monoxygenase activation	0002553 // histamine secretion by mast cell // not recorded//0006605 // protein targeting // inferred from direct assay//0006626 // protein targeting to mitochondrion // not
1434960_a	0.002359	-1.06	-1.47	NM_001042671//NM_0010	Gcpcd1	glycerophosphocholine phosphodiesterase GDE1 homolog (S. cerevisiae)	0006071 // glycerol metabolic process // inferred from electronic annotation//0006629 // lipid metabolic process // inferred from electronic annotation
1448584_a	0.004200	-1.06	-1.18	NM_011137//NM_198932	Pou2f1	POU domain, class 2, transcription factor 1	0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 // regulation of transcription, DNA-templated // inferred from electronic annotation//0006366 //
1421366_a	0.000404	-1.06	1.16	NM_001134383//NM_0011	Iqsec1	IQ motif and Sec7 domain 1	0030036 // actin cytoskeleton organization // not recorded//0032012 // regulation of ARF protein signal transduction // inferred from electronic annotation//0043087 // regulation of GTPase
1421086_a	0.005209	-1.06	1.17	NM_001127378//NM_0206	Atp5c1	ATP synthase, H+ transporting, mitochondrial F1 complex, gamma	0006172 // ADP biosynthetic process // not recorded//0006200 // ATP catabolic process // not recorded//0006754 // ATP biosynthetic process // inferred from electronic
1420011_s	0.003779	-1.06	1.22	NM_134006//XM_0065133	Rdh5//Bloc1s1	retinol dehydrogenase 5//biogenesis of lysosomal organelles complex-1,	0007601 // visual perception // inferred from electronic annotation//0008152 // metabolic process // inferred from electronic annotation//0042572 // retinol metabolic process //
1418162_a	0.000679	-1.06	1.43	NM_028116	Pgylg1	pygopus 1	0001822 // kidney development // inferred from genetic interaction//0006244 // hematopoietic progenitor cell differentiation // inferred from mutant phenotype//0007286 // spermatid
1430455_a	0.008579	-1.06	-1.40	NM_026157//XM_0065261	Mtpap	mitochondrial poly(A) polymerase	0006351 // transcription, DNA-templated // inferred from electronic annotation//0006378 // mRNA polyadenylation // not recorded//0006397 // mRNA processing // inferred from electronic
1424293_s	0.004478	-1.06	1.04	NM_001198998//NM_0116	Vdac3	voltage-dependent anion channel 3	0001662 // behavioral fear response // inferred from mutant phenotype//0006810 // transport // inferred from electronic annotation//0006811 // ion transport // inferred from electronic
1420741_x	0.000475	-1.06	1.19	NM_001277113//NM_0012	Rpl22	ribosomal protein L22	0006412 // translation // inferred from electronic annotation//0046632 // alpha-beta T cell differentiation // inferred from mutant phenotype
1417343_a	0.009494	-1.06	1.67	NM_001289593//NM_0012	Kynu	kyureninase (L-kyurenine hydrolase)	0006569 // tryptophan catabolic process // not recorded//0008152 // metabolic process // inferred from electronic annotation//0009435 // NAD biosynthetic process // inferred from
1435401_a	0.002583	-1.06	-1.48	NM_008255//XM_0065175	Hmgcr	3-hydroxy-3-methylglutaryl-Coenzyme A reductase	0006629 // lipid metabolic process // inferred from electronic annotation//0006694 // steroid biosynthetic process // inferred from electronic annotation//0006695 // cholesterol biosynthetic
1419968_a	0.002056	-1.07	1.22	NM_078479//XM_0065018	Mrps21	mitochondrial ribosomal protein S21	0006412 // translation // inferred from electronic annotation
1423152_a	0.005416	-1.07	1.09	NM_024214//XM_0065313	Tomm20	translocase of outer mitochondrial membrane 20 homolog (yeast)	0006605 // protein targeting // inferred from electronic annotation//0006626 // protein targeting to mitochondrion // not recorded//0006810 // transport // inferred from electronic
1418203_a	0.003043	-1.07	1.43	NM_178045//XM_0065058	Rassj94	Ras association (RalGDS/AF-6) domain family member 4	0007049 // cell cycle // inferred from electronic annotation//0007165 // signal transduction // inferred from electronic annotation//0010466 // negative regulation of peptidase activity //
1420927_a	0.000280	-1.07	1.18	NM_001164259//NM_0540	Fgf11	fibroblast growth factor receptor-like 1	001501 // skeletal system development // inferred from mutant phenotype//0003179 // heart valve morphogenesis // inferred from mutant phenotype//0007166 // cell surface receptor
1420376_a	0.007569	-1.07	1.21	NM_011293	Polr2j	polymerase (RNA) II (DNA directed) polypeptide j	0006351 // transcription, DNA-templated // inferred from electronic annotation//0006366 // transcription from RNA polymerase II promoter // not recorded
1456715_a	0.007378	-1.07	-2.08	NM_008542//NM_0065108	Smad6	SMAD family member 6	0001657 // ureteric bud development // inferred from expression pattern//0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 // regulation of
1422998_a	0.008165	-1.07	1.10	NM_024243	Fuca1	fucosidase, alpha-L-1, tissue	0005975 // carbohydrate metabolic process // inferred from electronic annotation//0006004 // fucose metabolic process // not recorded//0008152 // metabolic process // inferred from
1417073_a	0.002136	-1.07	1.82	NM_009910	Cacr3	chemokine (C-X-C motif) receptor 3	001525 // angiogenesis // inferred from electronic annotation//0001937 // negative regulation of endothelial cell proliferation // not recorded//0002685 // regulation of leukocyte migration
1422348_a	0.003119	-1.07	1.12	NM_026528	2700060E02Rik	RIKEN cDNA 2700060E02 gene	0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 // regulation of transcription, DNA-templated // inferred from electronic annotation//0045944 //
1430763_a	0.006602	-1.07	-1.41	NM_010302	Gna12	guanine nucleotide binding protein, alpha 12	0001701 // in utero embryonic development // inferred from genetic interaction//0006184 // GTP catabolic process // not recorded//0007165 // signal transduction // inferred from
1433920_a	0.003788	-1.08	-1.44	NM_026949//XM_0065341	Cnot8	CCR4-NOT transcription complex, subunit 8	0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 // regulation of transcription, DNA-templated // inferred from electronic annotation//0006417 //
1423226_a	0.005987	-1.08	1.09	NM_028419	Glxr5	glutaredoxin 5 homolog (S. cerevisiae)	0030097 // hemopoiesis // inferred from sequence or structural similarity//0045454 // cell redox homeostasis // inferred from electronic annotation//0055114 // oxidation-reduction process
1420387_a	0.002058	-1.08	1.21	NM_013765	Rps26	ribosomal protein S26	0006412 // translation // inferred from electronic annotation//0033119 // negative regulation of RNA splicing // not recorded
1429344_a	0.000960	-1.08	-1.37	NM_008996	Rob1	RAB1, member RAS oncogene family	0000045 // autophagic vacuole assembly // not recorded//0006184 // GTP catabolic process // not recorded//0006810 // transport // inferred from electronic annotation//0006886 //
1423235_a	0.001733	-1.08	-1.09	NM_009169	Shfm1	split hand/foot malformation (ectrodactyly) type 1	0007724 // double-strand break repair via homologous recombination // inferred from mutant phenotype//0006508 // proteolysis // not recorded
1417193_a	0.000408	-1.08	1.76	NM_022004//XM_0065105	Fxyd6	FXYD domain-containing ion transport regulator 6	0006810 // transport // inferred from electronic annotation//0006811 // ion transport // inferred from electronic annotation//0034220 // ion transmembrane transport // inferred from
1443871_a	0.006771	-1.08	-1.72	NM_026386//XM_0065261	Snx2	sorting nexin 2	0006810 // transport // inferred from electronic annotation//0006886 // intracellular protein transport // not recorded//0006897 // endocytosis // inferred from electronic
1417946_a	0.007277	-1.08	1.50	NM_009593	Abcg1	ATP-binding cassette, sub-family G (WHITE), member 1	0006200 // ATP catabolic process // not recorded//0006355 // regulation of transcription, DNA-templated // inferred from mutant phenotype//0006810 // transport // inferred from
1421394_a	0.006367	-1.08	1.16	XM_006528656//XM_0065	LOC101055948	FERM and PDZ domain-containing protein 3-like	
1422114_a	0.003286	-1.08	1.13	NM_026347	Rps20	ribosomal protein S20	0006412 // translation // inferred from electronic annotation
1447396_a	0.004007	-1.08	-1.84	NM_019930//XR_382234	Ranbp9	RAN binding protein 9	
1423266_a	0.002209	-1.08	1.09	NM_025918//XM_0065337	Ccdc43	coiled-coil domain containing 43	
1449106_a	0.002510	-1.08	-1.20	NM_001177874//NM_1453	Gps1	G protein pathway suppressor 1	
1439670_a	0.000584	-1.08	-1.59	NM_008513//XR_388250	Lrp5	low density lipoprotein receptor-related protein 5	
1436920_a	0.002452	-1.09	-1.52	NM_026377//XM_0065273	Sfr1	SWI5 dependent recombination repair 1	
1433565_a	0.004550	-1.09	-1.11	NM_009225//XM_0064990	Snrpb	small nuclear ribonucleoprotein B	
1434477_a	0.003151	-1.09	-1.46	NM_001141931//NM_0011	Rbms1	RNA binding motif, single stranded interacting protein 1	
1428579_a	0.000350	-1.09	-1.35	NM_183146	AS30054K11Rik	RIKEN cDNA AS30054K11 gene	
1436100_a	0.006011	-1.09	-1.50	NM_001146690//NM_1448	Chpt1	choline phosphotransferase 1	
1417859_a	0.002508	-1.09	1.52	NM_001291041//NM_0217	il21	interleukin 21	
1454622_a	0.000537	-1.09	-1.31	NM_023311	Yipf5	Yip1 domain family, member 5	
1439106_a	0.000734	-1.09	-1.57	NM_172429//XM_0065274	Smndc1	survival motor neuron domain containing 1	
1420853_a	0.002401	-1.09	1.18	NM_027862//XM_0065342	Atp5b	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit D	
1429370_a	0.001205	-1.09	-1.09	NM_001285489//NM_0012	Nap14	nucleosome assembly protein 1-like 4	
1449277_a	0.000545	-1.09	-1.21	NM_025859//XM_0065130	Ar1l	ADP-ribosylation factor-like 1	
1418340_a	0.000586	-1.09	1.40	NM_001146351//NM_0076	Ephb6	Eph receptor B6	
1425398_a	0.002771	-1.09	1.00	NM_009096//XM_0010039	Rps6//Rps6-	ribosomal protein S6//ribosomal protein S6, pseudogene 4//405	
1436423_a	0.007868	-1.09	-1.51	NM_026934	Zc3h15	zinc finger CCH-type containing 15	
1416868_a	0.000472	-1.09	2.02	NM_026507//XR_379477//	Zw1ch	zw1ch kinetochore protein	
1420971_a	0.002902	-1.10	1.17	NM_008248	Hint1	histidine triad nucleotide binding protein 1	
1455144_s	0.000126	-1.10	-1.98	NM_027571//XM_0065020	P2y212	purinergic receptor P2Y, G protein coupled 12	
1422631_a	0.001954	-1.10	1.11	NM_001134692//NM_0244	Ost4	oligosaccharyltransferase 4 homolog (S. cerevisiae)	
1429953_a	0.000490	-1.10	-1.39	NM_145542//XM_0065014	Ahcy1l	S-adenosylhomocysteine hydrolase-like 1	
1421217_a	0.000052	-1.10	1.16	NM_001289782//NM_0012	Cryab	crystallin, alpha B	
1418219_a	0.0004525	-1.10	1.42	NM_001168693//NM_0089	Endou	endonuclease, polyU-specific	
1428980_a	0.000508	-1.10	-1.36	NM_001008238//NM_0167	Bnip2	BCI2/adenovirus E1B interacting protein 2	
1422135_a	0.005297	-1.10	1.13	NM_026533//XM_0014808	Gm15483//LOC102642137//	predicted gene 15483//405 ribosomal protein S13-like//ribosomal protein	
1423456_a	0.001573	-1.10	1.08	NM_053266//XM_0065043	Gt2ird2	GTF2 repeat domain containing 2	
1424442_a	0.007129	-1.10	1.04	NM_013762//NM_0014757	Gm1281//Gm5879//Rpl3	predicted gene 12816//predicted gene 5879//ribosomal protein L3	
1420093_s	0.000646	-1.10	1.22	NM_031248	Lamtor2	late endosomal/lysosomal adaptor, MAPK and MTOR activator 2	
1426545_a	0.006217	-1.11	-1.03	NM_024212	Rpl4	ribosomal protein L4	
1420844_a	0.001594	-1.11	1.18	NM_139308//XM_0065004	Stard7	START domain containing 7	
1436545_a	0.003217	-1.11	-1.51	NM_026719//XM_0064962	Lbrd1	LMBR1 domain containing 1	
1419061_a	0.001470	-1.11	1.31	NM_001287514//NM_0012	Cebp	CCAAT/enhancer binding protein (C/EBP), alpha	
1434841_a	0.007928	-1.11	-1.47	NM_009721	Atp1b1	ATPase, Na+/K+ transporting, beta 1 polypeptide	
1424518_a	0.000096	-1.11	1.04	NM_011297//NM_207634	Rps24	ribosomal protein S24	
1451233_a	0.000369	-1.11	-1.27	XR_387732//XR_387723//	Zfp626//7637040204Rik	zinc finger protein 626//RIKEN cDNA 763040204 gene	
1440488_a	0.002410	-1.11	-1.62	NM_001081225//NM_1726	Fam178a	family with sequence similarity 178, member A	
1442023_a	0.005864	-1.11	-1.66	NM_001293672//NM_0288	Ctbs	chitinase, N-acetyl-	
1424424_a	0.004659	-1.11	1.04	NM_010193	Fem1b	feminization 1 homolog b (C. elegans)	
1446748_a	0.000787	-1.11	-1.80	NM_001277219//NM_0012	Crk	v-crk sarcoma virus CT10 oncogene homolog (avian)	
1437879_a	0.003800	-1.11	-1.54	NM_001159635//NM_0264	Rbm18	RNA binding motif protein 18	
1449678_a	0.005333	-1.11	-1.22	NM_001081019//NM_0082	Gm10257//Gm12657//Gm67	predicted gene 10257//predicted gene 12657//predicted pseudogene	
1433747_a	0.001105	-1.12	-1.44	NM_001168578//NM_0257	Tceo18	transcription elongation factor A (SII)-like 18	
1424936_a	0.000166	-1.12	-1.69	NM_001144987//NM_0011	Spg20	spastic paraplegia 20, spartin (Troyer syndrome) homolog (human)	
1416622_a	0.009365	-1.12	2.39	NM_010251//XM_0065037	Gabra4	gamma-aminobutyric acid (GABA) A receptor, subunit alpha 4	

Table S7

Gene ID	p (Corr)	FC-RSV 1 d	FC-RSV 5 d	RefSeq Transcript ID	Gene Symbol	Gene Title	Gene Ontology Biological Process
1425183_a	0.006063	-1.12	1.01	NM_001288578//NM_0074	<i>Adh5</i>	alcohol dehydrogenase 5 (class III), ch polypeptide	0001523 // retinoid metabolic process // inferred from mutant phenotype//0003016 // respiratory system process // inferred from mutant phenotype//0006068 // ethanol catabolic process
1422879_a	0.002021	-1.12	1.10	NM_009478//XM_0065029	<i>Urad</i>	uroporphyrinogen decarboxylase	0006779 // porphyrin-containing compound biosynthetic process // not recorded//0006782 // protoporphyrinogen IX biosynthetic process // inferred from electronic annotation//0006783 //
1427875_a	0.000086	-1.12	-1.06	NM_027425//XM_0065140	<i>Rufy2</i>	RUN and FVVE domain-containing 2	
1420197_a	0.000036	-1.12	1.22	NM_001159907//NM_1749	<i>Coa6</i> //Gm17296	cytochrome c oxidase assembly factor 6//predicted gene, 17296	0001510 // RNA methylation // inferred from electronic annotation//0006396 // RNA processing // inferred from electronic annotation//1902600 // hydrogen ion transmembrane transport
1440579_a	0.009643	-1.12	-1.62	NM_001290807//NM_0012	<i>Haus2</i>	HAUS augmin-like complex, subunit 2	0007049 // cell cycle // inferred from electronic annotation//0007067 // mitotic nuclear division // inferred from electronic annotation//0031023 // microtubule organizing center
1439336_a	0.005792	-1.12	-1.57	NM_009049//XR_373538	<i>Resp18</i>	regulated endonuclease-specific protein 18	0001701 // in utero embryonic development // inferred from mutant phenotype
1425276_a	0.009491	-1.12	-1.01	NM_010946//XM_0065218	<i>Ntan1</i> //Ilt2	N-terminal AS amidase//interleukin 2	0006113 // memory // inferred from mutant phenotype//0008152 // metabolic process // inferred from direct assay//0008152 // metabolic process // inferred from electronic
1426539_a	0.007587	-1.12	-1.02	NM_025736//XM_0065212	<i>Emc2</i>	ER membrane protein complex subunit 2	
1422606_a	0.008200	-1.12	1.11	NM_011299//XM_0014733	<i>Gm21571//Rps12//Rps12</i>	predicted gene, 21571//ribosomal protein S12//ribosomal protein S12,	0006412 // translation // inferred from electronic annotation
1423077_a	0.000887	-1.12	1.07	NM_183256//XM_0039453	<i>Cox14</i> //LOC101055854	cytochrome c oxidase assembly protein 14//cytochrome c oxidase	003617 // mitochondrial respiratory chain complex IV assembly // not recorded
1417929_a	0.000021	-1.12	1.50	NM_001264008//NM_0012	<i>Fni1</i>	fibronectin 1	0001525 // angiogenesis // inferred from electronic annotation//0001775 // cell activation // not recorded//0006953 // acute-phase response // inferred from electronic
1450473_a	0.001425	-1.13	-1.24	NM_001081019//NM_0082	<i>Gm10257//Gm12657//Gm67</i>	predicted gene 10257//predicted gene 12657//predicted pseudogene	0001649 // osteoblast differentiation // inferred from genetic interaction//0006334 // nucleosome assembly // inferred from electronic annotation//0006997 // nucleus organization //
1421415_a	0.008924	-1.13	1.15	NM_001161816//NM_0011	<i>Gm15455//Rbm10</i>	predicted gene 15455//RNA binding motif protein 10	0001122 // negative regulation of transcription from RNA polymerase II promoter // inferred from direct assay//0008285 // negative regulation of cell proliferation // inferred from direct
1426668_a	0.003650	-1.13	-1.03	NM_053207//XM_0065305	<i>Egl1n</i>	egl-9 family hypoxia-inducible factor 1	0001666 // response to hypoxia // not recorded//0018401 // peptidyl-proline hydroxylation to 4-hydroxy-L-proline // not recorded//0030821 // negative regulation of cAMP catabolic process
1422230_s	0.008277	-1.13	1.13	NM_009077//XM_0065407	<i>Rpl18</i>	ribosomal protein L18	0006412 // translation // inferred from electronic annotation
1427330_a	0.000137	-1.13	-1.05	NM_019755	<i>Plp2</i>	proteolipid protein 2	
1422587_a	0.001431	-1.13	1.11	NM_009752//NR_108101	<i>Glb1</i>	galactosidase, beta 1	0005975 // carbohydrate metabolic process // inferred from electronic annotation//0008152 // metabolic process // inferred from electronic annotation//0019388 // galactose catabolic
1420649_a	0.004478	-1.13	1.19	NM_026943//XM_0065024	<i>Gm5848//Snrpd2</i>	predicted pseudogene 5848//small nuclear ribonucleoprotein D2	0000387 // spliceosomal snRNP assembly // not recorded//0006397 // mRNA processing // inferred from electronic annotation//0008380 // RNA splicing // inferred from electronic
1421473_a	0.000323	-1.13	1.15	NM_028238	<i>Rob38</i>	RAB38, member RAS oncogene family	0006184 // GTP catalytic process // inferred from electronic annotation//0006810 // transport // inferred from electronic annotation//0006886 // intracellular protein transport // inferred
1451782_a	0.005983	-1.13	-1.28	NM_028138//XM_0065249	<i>Thump2</i>	THUMP domain containing 2	0008152 // metabolic process // inferred from electronic annotation//0008610 // lipid biosynthetic process // inferred from electronic annotation//0032259 // methylation // inferred from
1428057_a	0.007908	-1.14	-1.07	NM_153144//XM_0065329	<i>Ggnbp2</i>	gametogenin binding protein 2	0007275 // multicellular organismal development // inferred from electronic annotation//0007283 // spermatogenesis // inferred from electronic annotation//0030154 // cell differentiation
1460638_a	0.002795	-1.14	-1.34	NM_001080974//NM_0256	<i>Sri</i>	sorcin	0006508 // proteolysis // not recorded//0006816 // calcium ion transport // inferred from physical interaction//0010459 // negative regulation of heart rate // not recorded//0035774 //
1424509_a	0.001210	-1.14	1.04	NM_001037741//NM_0081	<i>Gpx4</i>	glutathione peroxidase 4	0006325 // chromatin organization // inferred from direct assay//0006749 // glutathione metabolic process // not recorded//0006979 // response to oxidative stress // inferred from
1422263_a	0.002366	-1.14	1.13	NM_027430	<i>Mpc2</i>	mitochondrial pyruvate carrier 2	0006090 // pyruvate metabolic process // inferred from genetic interaction//0008610 // transport // inferred from electronic annotation//0008650 // mitochondrial pyruvate transport //
1435990_a	0.001373	-1.14	-1.50	NM_175325//XM_0065107	<i>Bbs4</i>	Bardet-Biedl syndrome 4 (human)	0000226 // microtubule cytoskeleton organization // inferred from mutant phenotype//0000281 // mitotic cytokinesis // not recorded//0001843 // neural tube closure // inferred from
1448118_a	0.002673	-1.14	-1.17	NM_007589//NM_0079590	<i>Calm1</i> //Calm2//Calm3	calmodulin 1//calmodulin 2//calmodulin 3	0000086 // G2/M transition of mitotic cell cycle // inferred from direct assay//0001975 // response to amphetamine // inferred from electronic annotation//0000207 // regulation of heart
1454779_s	0.007957	-1.14	-1.32	NM_001163301//NM_0011	<i>Pea2</i>	peroxisomal biogenesis factor 2	0000038 // very-long-chain fatty acid metabolic process // not recorded//0000122 // negative regulation of transcription from RNA polymerase I promoter // not recorded//0001764 //
1422403_a	0.001313	-1.14	1.12	NM_001047158//NM_1979	<i>Uqcrl0</i>	ubiquinol-cytochrome c reductase, complex III subunit X	0006122 // mitochondrial electron transport, ubiquinol to cytochrome c // inferred from electronic annotation//0006810 // transport // inferred from electronic annotation//0055114 //
1449983_a	0.002065	-1.14	-1.23	NM_001293693//NM_1533	<i>Adam32</i>	a disintegrin and metalloproteinase domain 32	0006508 // proteolysis // inferred from electronic annotation//0007229 // integrin-mediated signaling pathway // inferred from electronic annotation
1421603_a	0.000727	-1.14	1.15	NM_025319//XM_0065339	<i>061009822Rik</i>	RIKEN cDNA 061009822Rik gene	0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 // regulation of transcription, DNA-templated // inferred from sequence or structural
1422459_a	0.006453	-1.14	1.12	NM_001033865//NM_0242	<i>Gm8430//Rps27a</i>	predicted pseudogene 8430//ribosomal protein S27A	0006412 // translation // inferred from electronic annotation//0010992 // ubiquitin homeostasis // inferred from genetic interaction
1448562_a	0.001156	-1.14	-1.18	NM_001145977//NM_1787	<i>Cadm2</i>	cell adhesion molecule 2	0007155 // cell adhesion // inferred from electronic annotation//0007420 // brain development // inferred from electronic annotation
1421887_a	0.008776	-1.14	1.14	NM_00101561//NM_1720	<i>Gm6251//Rpl32</i>	predicted gene 6251//ribosomal protein L32	0006412 // translation // inferred by curator
1420276_a	0.006428	-1.14	-1.34	NM_013499//XM_0064972	<i>Cr1l</i>	complement component (3b/4b) receptor 1-like	0001701 // in utero embryonic development // inferred from genetic interaction//0002376 // immune system process // inferred from electronic annotation//0006958 // complement
1428555_a	0.007326	-1.14	-1.35	NM_010418//XM_0065406	<i>Herc2</i>	hect (homologous to the E6-AP (UBE3A) carboxy terminus) domain and	0006281 // DNA repair // not recorded//0006974 // cellular response to DNA damage stimulus // not recorded//0007283 // spermatogenesis // inferred from mutant phenotype//0016567
1435829_a	0.007336	-1.14	-1.49	NM_001045515//NM_0011	<i>Synj1</i>	synaptotagmin 1	0006836 // neurotransmitter transport // inferred from mutant phenotype//0006897 // endocytosis // inferred from electronic annotation//0007612 // learning // inferred from mutant
1427334_s	0.003797	-1.14	-1.05	NM_028015	<i>Cers5</i>	ceramide synthase 5	0006355 // regulation of transcription, DNA-templated // inferred from electronic annotation//0006629 // lipid metabolic process // inferred from electronic annotation//0006665 //
1434228_a	0.002957	-1.15	-1.45	NM_001162989//NM_0199	<i>Phax</i>	phosphorylated adaptor for RNA export	0006408 // snRNA export from nucleus // inferred from direct assay//0006810 // transport // inferred from electronic annotation//0015031 // protein transport // inferred from electronic
1419834_x	0.003604	-1.15	1.23	NM_001160203//NM_0011	<i>Fau</i>	Finkel-Biskis-Reilly murine sarcoma virus (FBR-MuSV) ubiquitously	0002227 // innate immune response in mucosa // not recorded//0006412 // translation // inferred from electronic annotation//0019731 // antibacterial humoral response // not
1422014_a	0.002282	-1.15	1.13	NM_025933	<i>Higd2a</i>	HIG1 domain family, member 2A	0006810 // transport // inferred from electronic annotation//004306 // negative regulation of apoptotic process // not recorded//0055114 // oxidation-reduction process // inferred from
1451790_a	0.003761	-1.15	-1.28	NM_028923	<i>Gle1</i>	GLE1 RNA export mediator (yeast)	0006810 // transport // inferred from electronic annotation//0015031 // protein transport // inferred from electronic annotation//0016973 // poly(A) mRNA export from nucleus // inferred from
1419716_a	0.007803	-1.15	1.24	NM_023495//XM_0065193	<i>Xpo7</i>	exportin 7	0006611 // protein export from nucleus // not recorded//0006810 // transport // inferred from electronic annotation//0016973 // poly(A) mRNA export from nucleus // inferred from electronic
1422699_a	0.005587	-1.15	1.11	NM_001160256	<i>A1662493</i>	expressed sequence A1662493	0016310 // phosphorylation // inferred from electronic annotation
1419722_a	0.002564	-1.15	1.24	NM_026506	<i>Snrpg</i>	small nuclear ribonucleoprotein polypeptide G	000387 // spliceosomal snRNP assembly // inferred from sequence or structural similarity//0006397 // mRNA processing // inferred from electronic annotation//0008380 // RNA splicing //
1439647_a	0.006469	-1.15	-1.59	NM_172679//NM_172680	<i>4932438A13rik</i>	RIKEN cDNA 4932438A13 gene	0001558 // regulation of cell growth // non-traceable author statement//0006629 // lipid metabolic process // non-traceable author statement//0007283 // spermatogenesis // non-traceable
1420033_s	0.001039	-1.15	1.22	NR_003145	<i>Shng10</i>	small nuclear RNA host gene 10	
1422403_a	0.001179	-1.15	1.12	NM_009092//XR_141401	<i>Gm14586//Rps17</i>	predicted gene 14586//ribosomal protein S17	0000028 // ribosomal small subunit assembly // not recorded//0006364 // rRNA processing // not recorded//0006412 // translation // not recorded//0006414 // translational elongation //
1435897_a	0.004063	-1.15	-1.50	NM_007896	<i>Mapre1</i>	microtubule-associated protein, RP/EB family, member 1	0007049 // cell cycle // inferred from electronic annotation//0007067 // mitotic nuclear division // inferred from electronic annotation//0031113 // regulation of microtubule polymerization
1423817_s	0.007740	-1.15	1.06	NM_008366//NM_010946	<i>Ilt2//Ntnn1</i>	interleukin 2//N-terminal AS amidase	0001933 // negative regulation of protein phosphorylation // not recorded//0001934 // positive regulation of protein phosphorylation // not recorded//0002376 // immune system process //
1422975_a	0.000679	-1.15	1.10	NM_022891//XM_0036887	<i>LOC100044627//LOC1008624</i>	60S ribosomal protein L23-like//ribosomal protein L23	0006412 // translation // not recorded
1421129_a	0.001963	-1.15	1.17	NM_011481	<i>Srms</i>	src-related kinase lacking C-terminal regulatory tyrosine and N-terminal	0006468 // protein phosphorylation // inferred from electronic annotation//0016310 // phosphorylation // inferred from electronic annotation//0038083 // peptidyl-tyrosine
1429113_a	0.004727	-1.15	-1.36	NM_010273	<i>Gdi1</i>	guanine dinphosphate (GDP) dissociation inhibitor 1	0015031 // protein transport // inferred from electronic annotation//0032482 // Rab protein signal transduction // inferred from sequence or structural similarity//0043547 // positive
1424096_a	0.002002	-1.15	1.05	NM_001252200//NM_0012	<i>Map4k4</i>	mitogen-activated protein kinase kinase kinase kinase 4	0006468 // protein phosphorylation // not recorded//0006468 // protein phosphorylation // inferred from direct assay//0006950 // response to stress // inferred from direct assay//0010977
1424323_a	0.008157	-1.15	-1.04	NM_030561//XM_0065251	<i>BC004004//LOC102639688</i>	cDNA sequence BC004004//keratin-associated protein 16-1-like	0042060 // wound healing // not recorded//0045787 // positive regulation of cell cycle // not recorded//00050673 // epithelial cell proliferation // not recorded
1460351_a	0.000982	-1.15	1.33	NM_001110239//NM_0213	<i>Acpi1</i>	acid phosphatase 1, soluble	0006470 // protein dephosphorylation // inferred from electronic annotation//0016311 // dephosphorylation // inferred from direct assay//0035335 // peptidyl-tyrosine dephosphorylation
1419561_a	0.000220	-1.15	1.25	NM_026418//XM_0065081	<i>Rgs10</i>	regulator of G-protein signalling 10	0009968 // negative regulation of signal transduction // inferred from electronic annotation//0038032 // termination of G-protein coupled receptor signaling pathway // inferred from
1422868_s	0.003983	-1.15	1.10	NM_009082//XM_0030851	<i>Gm10913//Gm12447//Gm12</i>	predicted pseudogene 10913//predicted gene 12447//predicted gene	0006412 // translation // inferred from mutant phenotype//0008283 // cell proliferation // inferred from mutant phenotype//0031589 // cell-substrate adhesion // inferred from direct
1424267_a	0.008924	-1.15	1.04	NM_016755//XM_0065228	<i>Atp5f3</i>	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit F	0006200 // ATP catabolic process // not recorded//0006810 // transport // inferred from electronic annotation//0006811 // ion transport // inferred from electronic annotation//0015986 //
1435809_a	0.004006	-1.15	-1.93	NM_00117793//NM_0011	<i>Snap23</i>	synaptosomal-associated protein 23	0006461 // protein complex assembly // not recorded//0006810 // transport // inferred from electronic annotation//0006887 // exocytosis // inferred from mutant phenotype//0015031 //
1448866_a	0.003541	-1.16	-1.19	NM_027212	<i>Med30</i>	mediator complex subunit 30	0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 // regulation of transcription, DNA-templated // inferred from electronic annotation//0006357 //
1424873_a	0.004738	-1.16	1.02	NM_010150//XM_0065095	<i>Nr2f6</i>	nuclear receptor subfamily 2, group F, member 6	0001122 // negative regulation of transcription from RNA polymerase II promoter // not recorded//0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355
1425958_a	0.000111	-1.16	-1.01	NM_001159392//NM_0093	<i>Tnfrsf1</i>	tumor necrosis factor, alpha-induced protein 1 (endothelial)	0006260 // DNA replication // not recorded//0006955 // immune response // inferred from sequence or structural similarity//0006955 // immune response // inferred from electronic
1428735_a	0.004120	-1.16	-1.35	NM_001165989//NM_0294	<i>Kkap5</i>	cytoskeleton associated protein 5	0007049 // cell cycle // inferred from electronic annotation//0007051 // spindle organization // not recorded//0007067 // mitotic nuclear division // inferred from electronic
1425734_a	0.000751	-1.16	-1.30	NM_008810	<i>Pdh1a</i>	pyruvate dehydrogenase E1 alpha 1	0005975 // carbohydrate metabolic process // inferred from electronic annotation//0006006 // glucose metabolic process // inferred from electronic annotation//0006086 // acetyl-CoA
1421587_a	0.004391	-1.16	1.15	NM_001010930//NM_0102	<i>Mpr33</i>	mitochondrial ribosomal protein S33	
1423159_a	0.005014	-1.16	1.09	NM_009092//XR_141401	<i>Gm14586//Rps17</i>	predicted gene 14586//ribosomal protein S17	0000028 // ribosomal small subunit assembly // not recorded//0006364 // rRNA processing // not recorded//0006412 // translation // not recorded//0006414 // translational elongation //
1455979_a	0.009835	-1.16	-2.04	NM_025436	<i>Msmo1</i>	methylsterol monooxygenase 1	0006629 // lipid metabolic process // inferred from electronic annotation//0006633 // fatty acid biosynthetic process // inferred from electronic annotation//0006694 // steroid biosynthetic
1431367_a	0.003494	-1.16	-1.42	NM_001025438//NM_0010	<i>Camk2d</i>	calcium/calmodulin-dependent protein kinase II, delta	0000082 // G1/S transition of mitotic cell cycle // inferred from mutant phenotype//0001666 // response to hypoxia // not recorded//0002028 // regulation of sodium ion transport //
1430526_a	0.009997	-1.16	-1.10	NM_030109//XM_0065317	<i>Sj3b2</i>	splicing factor 3b, subunit 2	0000413 // protein peptidyl-prolyl isomerization // inferred from electronic annotation//0006457 // protein folding // inferred from electronic annotation
1430143_a	0.000975	-1.16	-1.39	NM_010918//XM_0065119	<i>Nktr</i>	natural killer tumor recognition sequence	0006998 // nuclear envelope organization // not recorded//0030335 // positive regulation of cell migration // inferred from mutant phenotype//0031022 // nuclear migration along
1421997_s	0.000657	-1.17	1.14	NM_001205345//NM_0012	<i>Sun2</i>	SaD1 and UNC84 domain containing 2	0007723 // telomere maintenance // inferred from mutant phenotype//0000723 // telomere maintenance // not recorded//0001701 // in utero embryonic development // inferred from
1427027_a	0.009307	-1.17	-1.04	NM_001083118//NM_0012	<i>Terf2</i>	telomeric repeat binding factor 2	0016447 // cell migration // inferred from mutant phenotype//0034446 // substrate adhesion-dependent cell spreading // inferred from mutant phenotype//0045600 // positive regulation of
1436338_a	0.006333	-1.17	-1.51	NM_173182//XM_0065355	<i>Frd3b</i>	fibronectin type III domain containing 3B	0001649 // osteoblast differentiation // not recorded//0006184 // GTP catalytic process // inferred from electronic annotation//0006886 // intracellular protein transport // inferred from
1435264_a	0.009194	-1.17	-1.48	NM_025846//XM_0065081	<i>Ras2</i>	predicted RAS viral (r-ras) oncogene homolog 2	0006412 // translation // inferred from electronic annotation//0042391 // regulation of membrane potential // inferred from genetic interaction
1424074_a	0.007736	-1.17	1.05	NM_001002239//XM_0065	<i>Gm10362//LOC101056140//</i>	predicted gene 10362//G0S ribosomal protein L17-like//ribosomal protein	0006919 // activation of cysteine-type endopeptidase activity involved in apoptotic process // inferred from electronic annotation//0032355 // response to estradiol // inferred from electronic
1420438_a	0.000021	-1.17	1.21	NM_026790//NM_194066	<i>Ifi27</i>	interferon, alpha-inducible protein 27	
1434067_a	0.002863	-1.17	-1.14	NM_001159609//NM_0011	<i>Lnc57</i>	leucine rich repeat containing 57	
1422156_a	0.001702	-1.17	1.13	NM_001285429//NM_0012	<i>Eef1d</i>	eukaryotic translation elongation factor 1 delta [guanine nucleotide	0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 // regulation of transcription, DNA-templated // inferred from electronic annotation//0006412 //
1431335_a	0.000018	-1.17	-1.10	NM_001199242//NM_0011	<i>Kcnp4</i>	Kv channel interacting protein 4	0006810 // transport // inferred from electronic annotation//0006811 // ion transport // inferred from electronic annotation//0006813 // potassium ion transport // inferred from electronic
1422348_a	0.002677	-1.17	1.12	NM_011287//XM_0065239	<i>Rpl10a</i>	ribosomal protein L10A	0006412 // translation // inferred from electronic annotation
1434245_a	0.001880	-1.17	-1.45	NM_019927//XM_0065111	<i>Arlh1</i>	arriadne ubiquitin-conjugating enzyme E2 binding protein homolog 1	0006511 // ubiquitin-dependent protein catabolic process // inferred from physical interaction//0016567 // protein ubiquitination // not recorded
1425825_a	0.005986	-1.17	-1.01	NM_001164729//NM_0012	<i>Prickle4//Tomm6</i>	prickle homolog 4 (Drosophila)//translocase of outer mitochondrial	0006810 // transport // inferred from electronic annotation//0015031 // protein transport // inferred from electronic annotation
1419353_a	0.003970	-1.17	1.27	NM_025592	<i>Rpl35</i>	ribosomal protein L35	0006412 // translation // inferred from electronic annotation
1422954_a	0.003736	-1.18					

Table S7

Gene ID	p (Corr)	FC-RSV 1 d	FC-RSV 5 d	RefSeq Transcript ID	Gene Symbol	Gene Symbol	Gene Ontology Biological Process
1454771_a	0.009263	-1.18	-1.32	NM_133780//XM_0065290	<i>Tpr</i>	translocated promoter region, nuclear basket protein	0000122 // negative regulation of transcription from RNA polymerase II promoter // not recorded//0000189 // MAPK import into nucleus // not recorded//0006404 // RNA import into nucleus
1429122_a	0.005323	-1.18	-1.09	NM_025279//XM_0065171	<i>Hnnpk</i>	heterogeneous nuclear ribonucleoprotein K	0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 // regulation of transcription, DNA-templated // inferred from electronic annotation//0006366 //
1439204_a	0.000324	-1.18	-1.57	NM_001130169//NM_0011	<i>Zfp207</i>	zinc finger protein 207	0000070 // mitotic sister chromatid segregation // not recorded//0007049 // cell cycle // inferred from electronic annotation//0007059 // chromosome segregation // inferred from
1447937_a	0.006613	-1.18	-1.86	NM_001177669//NM_0011	<i>Golph3</i>	golgi phosphoprotein 3-like	0007030 // Golgi organization // not recorded//00050714 // positive regulation of protein secretion // not recorded
1419132_a	0.000122	-1.18	1.30	NM_009662	<i>Alox5</i>	arachidonate 5-lipoxygenase	0002526 // acute inflammatory response // not recorded//0002540 // leukotriene production involved in inflammatory response // inferred from mutant phenotype//0006691 // leukotriene
1430373_a	0.000755	-1.18	-1.40	NM_026217//XM_0065261	<i>Atg12</i>	autophagy related 12	0000045 // autophagic vacuole assembly // inferred from mutant phenotype//0000422 // mitochondrial degradation // --//0002376 // immune system process // inferred from electronic annotation
1423102_a	0.006775	-1.18	-1.09	NM_029023	<i>Scp1</i>	serine carboxypeptidase 1	0006508 // proteolysis // inferred from electronic annotation//0042573 // retinoic acid metabolic process // inferred from electronic annotation//0004576 // negative regulation of blood
1419708_a	0.004415	-1.19	1.24	NM_001040631//NM_0010	<i>C1qtnf5//Mfpr</i>	C1q and tumor necrosis factor related protein 5//membrane-type frizzled-adaptor-related protein complex 5, mu 1 subunit	0007601 // visual perception // inferred from mutant phenotype//0009306 // protein secretion // inferred from mutant phenotype//0042462 // eye photoreceptor cell development //
1438532_a	0.000652	-1.19	-1.56	NM_144533//XM_0065196	<i>Ap5m1</i>	N-4-adenine-specific DNA methyltransferase 2 (putative)	0008319 // transport // inferred from electronic annotation//0006886 // intracellular protein transport // inferred from electronic annotation//0015031 // protein transport // inferred from
1423803_a	0.001425	-1.19	1.10	NM_026526//XM_0065194	<i>N6m2</i>	CD42 guanine nucleotide exchange factor (GEF) 9	0032259 // methylation // inferred from electronic annotation
1425673_a	0.001547	-1.19	-1.00	NM_001033329//NM_0012	<i>Arhgef9</i>	small GTPase mediated signal transduction // traceable author statement//0032321 // positive regulation of Rho GTPase activity // inferred from electronic annotation//0035023	
1423210_a	0.003827	-1.19	1.09	NM_024438	<i>Dusp19</i>	dual specificity phosphatase 19	0000188 // inactivation of MAPK activity // inferred from direct assay//0006469 // negative regulation of protein kinase activity // inferred from direct assay//0006470 // protein
1432588_a	0.000795	-1.19	-1.43	NM_007437//XM_0065320	<i>Aldh3a2</i>	aldehyde dehydrogenase family 3, subfamily A2	0000302 // response to reactive oxygen species // not recorded//0006081 // cellular aldehyde metabolic process // not recorded//0006714 // sesquiterpene metabolic process // not
1424590_a	0.000219	-1.19	1.03	NM_134255//XM_0065113	<i>Elov5</i>	ELOVL family member 5, elongation of long chain fatty acids (yeast)	0006629 // lipid metabolic process // inferred from electronic annotation//0006631 // fatty acid metabolic process // inferred from electronic annotation//0006633 // fatty acid biosynthetic
1445571_a	0.003027	-1.19	-1.76	NM_001291059//NM_0012	<i>Elf2</i>	E74-like factor 2	0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 // regulation of transcription, DNA-templated // inferred from electronic annotation//0006357 //
1420671_x	0.000099	-1.19	1.19	NM_025641	<i>Uqcrr</i>	ubiquinol-cytochrome c reductase heme protein	0006122 // mitochondrial electron transport, ubiquinol to cytochrome c // inferred from electronic annotation//0006810 // transport // inferred from electronic annotation//00051291 //
1430989_a	0.002770	-1.19	-1.10	NM_031185	<i>Akap12</i>	A kinase (PKA) anchor protein (gravin) 12	0006605 // protein targeting // inferred from electronic annotation//0007165 // signal transduction // not recorded//0007165 // signal transduction // traceable author statement//0010739
1436792_a	0.001972	-1.19	-1.52	NM_009072//XM_0065150	<i>Rock2</i>	Rho-associated coiled-coil containing protein kinase 2	0001843 // neural tube closure // inferred from genetic interaction//0006468 // protein phosphorylation // not recorded//0007165 // signal transduction // inferred from electronic
1436501_a	0.006063	-1.19	-1.51	NM_053089	<i>Naa15</i>	N(alpha)-acetyltransferase 15, Nalpha auxiliary subunit	0001525 // angiogenesis // inferred from electronic annotation//0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 // regulation of transcription, DNA-
1421592_a	0.001365	-1.19	1.15	NM_024266//XM_0065430	<i>Rps25//Gm4963//Gm6988</i>	ribosomal protein S25//predicted gene 4963//predicted gene 6988	0000028 // ribosomal small subunit assembly // not recorded
1426724_a	0.002985	-1.19	-1.02	NM_010860//XM_0065133	<i>Gm5526//Gm8894//LOC102</i>	myosin, light polypeptide 6, alkali, smooth muscle and non-muscle	0006200 // ATP catabolic process // inferred from sequence or structural similarity//0006936 // muscle contraction // traceable author statement//0007519 // skeletal muscle tissue
1423625_a	0.005734	-1.19	1.07	NM_080635//XM_0065213	<i>Elf3</i>	eukaryotic translation initiation factor 3, subunit H	0001731 // formation of translation preinitiation complex // inferred from electronic annotation//0006412 // translation // inferred from electronic annotation//0006413 // translational
1422020_a	0.004225	-1.19	1.13	NM_001005859//NM_0011	<i>Gm4705//Gm6404//Rpl34//</i>	predicted gene 4705//predicted gene 6404//ribosomal protein	0006412 // translation // inferred from electronic annotation
1450779_a	0.003423	-1.19	-1.25	NM_001103165//NM_0011	<i>Pcbp2</i>	poly(C) binding protein 2	0000186 // activation of MAPK activity // inferred from electronic annotation//0002376 // immune system process // inferred from electronic annotation//0006468 // protein
1418154_a	0.000708	-1.19	1.43	NM_173030//XM_0064980	<i>Goln13</i>	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-ribosomal protein S4, X-linked	0006486 // protein glycosylation // inferred from electronic annotation//0006493 // protein O-linked glycosylation // inferred from direct assay
1425810_a	0.0009878	-1.20	-1.01	NM_009094	<i>Rps4a</i>	solute carrier family 25, member 30	0006412 // translation // not recorded//0007275 // multicellular organismal development // not recorded//0008284 // positive regulation of cell proliferation // inferred from electronic
1457507_a	0.000299	-1.20	-2.21	NM_026323//XM_0065194	<i>Sk25a30</i>	cysteine carrier family 25, member 30	0006810 // transport // inferred from electronic annotation//0005508 // transmembrane transport // inferred from electronic annotation
1426858_a	0.000829	-1.20	-1.04	NM_007791	<i>Csrp1</i>	cytoskeleton anchoring protein 1	0030036 // actin cytoskeleton organization // traceable author statement
1423164_a	0.000622	-1.20	1.09	NM_009837	<i>Cct4</i>	chaperonin containing Tcp1, subunit 4 (delta)	0006457 // protein folding // inferred from electronic annotation//0007339 // binding of sperm to zona pellucida // inferred from direct assay//0044267 // cellular protein metabolic process
1426240_a	0.000436	-1.20	-1.02	NM_010860//XM_0065133	<i>Gm5526//Gm8894//LOC102</i>	myosin, light polypeptide 6, alkali, smooth muscle and non-muscle	0006200 // ATP catabolic process // inferred from sequence or structural similarity//0006936 // muscle contraction // traceable author statement//0007519 // skeletal muscle tissue
1434737_a	0.001703	-1.20	-1.46	NM_001114119//NM_1751	<i>Orich1</i>	glutamine-rich 1	
1434013_a	0.001865	-1.20	-1.44	NM_080636//XM_0065262	<i>Hors2</i>	histidyl-tRNA synthetase 2, mitochondrial (putative)	0006412 // translation // inferred from electronic annotation//0006418 // tRNA aminoacylation for protein translation // inferred from electronic annotation//0006427 // histidyl-tRNA
1421879_a	0.000179	-1.20	1.14	NM_01159561//NM_0110	<i>P2rx6</i>	purinergic receptor P2X, ligand-gated ion channel, 6	0006810 // transport // inferred from electronic annotation//0006811 // ion transport // inferred from electronic annotation//0006812 // cation transport // not recorded//0034220 // ion
1443249_a	0.004741	-1.20	-1.70	NM_001167750//NM_0011	<i>Ccdc132</i>	coiled-coil domain containing 132	
1424356_a	0.002476	-1.20	1.04	NM_178802	<i>Trim65</i>	tripartite motif-containing 65	
1423740_a	0.000831	-1.20	1.06	NM_008784	<i>Igfbp1</i>	immunoglobulin (CD79A) binding protein 1	0000122 // negative regulation of transcription from RNA polymerase II promoter // not recorded//0009966 // regulation of signal transduction // inferred from electronic
1418579_a	0.001571	-1.20	1.37	NM_026844//XM_0065312	<i>Cmc2</i>	COX assembly mitochondrial protein 2	
1424612_a	0.007099	-1.20	1.03	NM_001079822//NM_0093	<i>Tcf7l1</i>	transcription factor 7 like 1 (T cell specific, HMG box)	0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 // regulation of transcription, DNA-templated // inferred from electronic annotation//0006357 //
1427932_s	0.003842	-1.20	-1.06	NM_172400//XM_0065391	<i>Dnajc8</i>	DnaI (Hsp40) homolog, subfamily C, member 8	
1422664_a	0.000826	-1.20	1.11	NM_009321	<i>Tbca</i>	tubulin complex assembly	0007021 // tubulin complex assembly // inferred from electronic annotation
1424660_s	0.000852	-1.20	1.03	NM_008924	<i>Pkrar2a</i>	protein kinase, cAMP dependent regulatory, type II alpha	0001932 // regulation of protein phosphorylation // inferred from electronic annotation//0007165 // signal transduction // inferred from electronic annotation//0016310 // phosphorylation
1418901_a	0.007221	-1.21	1.32	NM_001159297//NM_0080	<i>Gscam</i>	germinal center associated, signaling and motility	0005855 // regulation of B cell receptor signaling pathway // not recorded//0004042 // negative regulation of lymphocyte migration // not recorded
1455014_a	0.006196	-1.21	-1.97	NM_025478	<i>Iscd1</i>	isochromatidase domain containing 1	0008152 // metabolic process // inferred from electronic annotation
1418552_a	0.001348	-1.21	1.40	NM_011353	<i>Serf1</i>	small EDRK-rich factor 1	
1455213_a	0.002008	-1.21	-1.98	NM_146145//XM_0065028	<i>Jank1</i>	Janus kinase 1	0006468 // protein phosphorylation // inferred from electronic annotation//0007167 // enzyme linked receptor protein signaling pathway // inferred from direct assay//0016310 //
1423591_a	0.001608	-1.21	1.07	NM_001040491//NM_0012	<i>Anapc5</i>	anaphase-promoting complex subunit 5	0007049 // cell cycle // inferred from electronic annotation//0007067 // mitotic nuclear division // inferred from electronic annotation//00016567 // protein ubiquitination // inferred from
1419681_a	0.001801	-1.21	1.24	NM_025337//XR_390721	<i>Akr7a5</i>	aldo-keto reductase family 7, member A5 (afatoxin aldehyde reductase)	0004597 // daunorubicin metabolic process // not recorded//0004598 // doxorubicin metabolic process // not recorded//00055114 // oxidation-reduction process // not recorded
1421260_a	0.004194	-1.21	1.16	NM_001130484//NM_0011	<i>Gm10029//LOC102377//Gm11</i>	predicted gene 10029//predicted gene 10237//predicted gene	0000070 // mitotic sister chromatid segregation // not recorded//0000724 // double-strand break repair via homologous recombination // not recorded//0006200 // ATP catabolic process //
1433727_a	0.002038	-1.21	-1.44	NM_028148//XM_0065214	<i>Scaf11</i>	SR-related CTD-associated factor 11	0000245 // spliceosomal complex assembly // not recorded//0000375 // RNA splicing, via transesterification reactions // not recorded//0008380 // RNA splicing // not recorded
1440465_a	0.004912	-1.21	-1.62	NM_010067//XM_0064973	<i>Trdm1</i>	tRNA aspartic acid methyltransferase 1	0001975 // response to amphetamine // inferred from electronic annotation//0006306 // DNA methylation // inferred from electronic annotation//0008033 // tRNA processing // inferred
1419215_a	0.000188	-1.21	1.29	NM_018796	<i>Eef1b2</i>	eukaryotic translation elongation factor 1 beta 2	0006412 // translation // inferred from sequence or structural similarity//0006414 // translational elongation // inferred from sequence or structural similarity
1437844_x	0.008882	-1.21	-1.16	NM_001252645//NM_0012	<i>RIKEN cDNA 4833439L19Rik</i>	RIKEN cDNA 4833439L19 gene	0055114 // oxidation-reduction process // inferred from electronic annotation
1424041_s	0.000369	-1.21	1.05	NM_001242580//NM_0120	<i>Nit1</i>	nitric oxide synthase 1	0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 // regulation of transcription, DNA-templated // inferred from electronic annotation//0006807 //
1418899_a	0.007479	-1.21	1.32	NM_027342	<i>Fam162a</i>	family with sequence similarity 162, member A	0006915 // apoptotic process // inferred from electronic annotation//0006919 // activation of cysteine-type endopeptidase activity involved in apoptotic process // not recorded//0006927 //
1426523_a	0.008606	-1.21	-1.02	NM_029012//XM_0065304	<i>Sppl3</i>	signal peptide peptidase 3	0006508 // proteolysis // not recorded//0006509 // membrane protein ectodomain proteolysis // inferred from sequence or structural similarity
1418508_a	0.006277	-1.21	1.38	NM_181394//XM_0065118	<i>Anapc13</i>	anaphase promoting complex subunit 13	0007049 // cell cycle // inferred from electronic annotation//0007067 // mitotic nuclear division // inferred from electronic annotation//00016567 // protein ubiquitination // inferred from
1424007_a	0.000815	-1.21	1.05	NM_024220//XM_0065432	<i>LOC102641347//Nduf1c</i>	NADH dehydrogenase (ubiquinone) 1 subunit C2-like//NADH	0006412 // translation // inferred from electronic annotation
1423134_a	0.002714	-1.21	1.09	NM_009076//XM_0064963	<i>LOC102635048//LOC1026356</i>	60S ribosomal protein L12-like//uncharacterized	0006412 // translation // inferred from electronic annotation//0007266 // rho protein signal transduction // not recorded//0008285 // negative regulation of cell proliferation // inferred
1424594_a	0.009657	-1.21	1.03	NM_016738//XM_0014746	<i>Gm10071//Rpl33//Ttx1b3p3</i>	predicted gene 10071//ribosomal protein L13//Tax1 (human T cell	000546 // glycine catabolic process // inferred from electronic annotation//0019464 // glycine decarboxylation via glycine cleavage system // not recorded//0032259 // methylation // not
1426037_a	0.000706	-1.21	-1.01	NM_026577//XM_0065313	<i>Gsh</i>	glycine cleavage system protein H (aminomethyl carrier)	0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 // regulation of transcription, DNA-templated // inferred from electronic annotation//0006366 //
1428910_a	0.007621	-1.22	-1.36	NM_001003898//NM_0010	<i>Tardbp</i>	TAR DNA binding protein	0001963 // synaptic transmission, dopaminergic // inferred from mutant phenotype//0006469 // negative regulation of protein kinase activity // not recorded//0006508 // proteolysis // not
1422672_a	0.003754	-1.22	1.11	NM_020569//XM_0065390	<i>Park7</i>	Parkinson disease (autosomal recessive, early onset) 7	0000165 // MAPK cascade // not recorded//0001505 // regulation of neurotransmitter levels // not recorded//0001933 // negative regulation of protein phosphorylation // not
1423063_a	0.008940	-1.22	1.10	NM_018858//NM_008021	<i>Pebp1//4933413G19Rik//Pro</i>	phosphatidylethanolamine binding protein 1//RIKEN cDNA 4933413G19	
1438148_a	0.004021	-1.22	-1.54	NM_175507	<i>Sk35g1</i>	solute carrier family 35, member G1	
1420377_a	0.002457	-1.22	1.21	NM_026674//NM_177583	<i>Aph1b//Aph1c</i>	anterior pharynx defective 1b homolog (C. elegans)//anterior pharynx	0001656 // metanephros development // inferred from mutant phenotype//0006508 // proteolysis // inferred from genetic interaction//0007219 // Notch signaling pathway // inferred from
1426937_a	0.005716	-1.22	-1.04	NM_134010//XM_0065130	<i>Nup107</i>	nucleoporin 107	0006406 // mRNA export from nucleus // not recorded//0006810 // transport // inferred from electronic annotation//0015031 // protein transport // inferred from electronic
1440831_a	0.005534	-1.22	-1.17	NM_007520//XM_0065228	<i>Bach1</i>	BTF and CNC homology 1	0000083 // regulation of transcription involved in G1/S transition of mitotic cell cycle // not recorded//0000117 // regulation of transcription involved in G2/M transition of mitotic cell cycle
1422555_s	0.002042	-1.22	1.12	NM_011434	<i>Sod1</i>	superoxide dismutase 1, soluble	0000187 // activation of MAPK activity // inferred from direct assay//0000302 // response to reactive oxygen species // inferred from mutant phenotype//0000303 // response to superoxide
1448699_a	0.006878	-1.22	-1.19	NM_145393	<i>Ythdf2</i>	YTH domain family 2	0043488 // regulation of mRNA stability // not recorded
1421921_a	0.002476	-1.22	1.14	NM_030717//XM_0065115	<i>Lactb</i>	lactamase, beta	0008152 // metabolic process // inferred from electronic annotation
1421184_a	0.004038	-1.22	1.16	NM_001130484//NM_0011	<i>Gm10029//Gm10237//Gm11</i>	predicted gene 10029//predicted gene 10237//predicted gene	0000070 // mitotic sister chromatid segregation // not recorded//0000724 // double-strand break repair via homologous recombination // not recorded//0006200 // ATP catabolic process //
1432048_a	0.001019	-1.22	-1.42	NM_001114334//NM_0282	<i>Rps6kb1</i>	ribosomal protein S6 kinase, polypeptide 1	0000082 // G1/S transition of mitotic cell cycle // not recorded//0003009 // skeletal muscle contraction // inferred from electronic annotation//0006417 // regulation of translation // inferred
1420697_a	0.000415	-1.22	1.19	NM_025294	<i>Natd1</i>	N-acetyltransferase domain containing 1	
1420091_s	0.000819	-1.22	1.22	NM_172911	<i>DBErd82e</i>	DBA segment, Chr 8, ERATO D01 82, expressed	0006468 // protein phosphorylation // inferred from electronic annotation//0016310 // phosphorylation // inferred from electronic annotation//0018108 // peptidyl-tyrosine phosphorylation
1448277_a	0.000545	-1.22	-1.21	NM_001164607//NM_0011	<i>Mafj</i>	MAF1 homolog (S. cerevisiae)	0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 // regulation of transcription, DNA-templated // inferred from electronic annotation//0016480 //
1455006_a	0.004825	-1.22	-1.32	NM_001038633//NM_0119	<i>Mpk4</i>	mitogen-activated protein kinase 4	0000165 // MAPK cascade // inferred from direct assay//0000165 // MAPK cascade // inferred from mutant phenotype//0000165 // MAPK cascade // not recorded//0000189 // MAPK
1424113_a	0.000220	-1.22	1.05	NM_001002939//XM_0065	<i>Nup85</i>	nucleoporin 85	0000226 // microtubule cytoskeleton organization // inferred from sequence or structural similarity//0001701 // in utero embryonic development // inferred from mutant
1437483_a	0.005915	-1.22	-1.53	NM_001256115//NM_0012	<i>Sun1</i>	Sad1 and UNC84 domain containing 1	0006998 // nuclear envelope organization // not recorded//0009028 // cytoskeletal anchoring at nuclear membrane // not recorded//0009029 // nuclear matrix anchoring at nuclear
1421120_a	0.008786	-1.22	1.17	NM_023312//XM_0065097	<i>Ndufa13//Yjefn3</i>	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 13//Yjef N-	0006915 // apoptotic process // inferred from electronic annotation//0017148 // negative regulation of translation // inferred from electronic annotation//0003262 // apoptotic nuclear
1426589_a	0.004677	-1.22	-1.03	NM_001113564//NM_0011	<i>Serbp1</i>	serpine1 mRNA binding protein 1	0042981 // regulation of apoptotic process // inferred from electronic annotation
1418808_a	0.001360	-1.23	1.34	NM_001243792//NM_0119	<i>Esrrg</i>	estrogen-related receptor gamma	0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 // regulation of transcription, DNA-templated // not recorded//0006355 // regulation of
1421935_a	0.002388	-1.23	1.14	NM_053162	<i>Mpl34</i>	mitochondrial ribosomal protein L34	0006412 // translation // not recorded
1426784_a	0.009278	-1.23	-1.03	NM_025939//XM_0065351	<i>Paics</i>	phosphoribosylaminoimidazole carboxylase, maternal embryonic leucine zipper kinase	0006164 // purine nucleotide biosynthetic process // inferred from electronic annotation//0006189 // "de novo" IMP biosynthetic process // inferred from electronic annotation//0008152 //
1416730_a	0.005868	-1.23	2.13	NM_010790//XM_0065376	<i>Melk</i>	maternal embryonic leucine zipper kinase	0006468 // protein phosphorylation // inferred from sequence or structural similarity//0006915 // apoptotic process // not recorded//0007049 // cell cycle // inferred from electronic
1427896_a	0.006743	-1.23	-1.06	NM_008112	<i>Gd12</i>	guanine dinucleotide (GDP) disphosphorylation inhibitor	

Table S7

Gene ID	p (Corr)	FC-RSV 1 d	FC-RSV 5 d	RefSeq Transcript ID	Gene Symbol	Gene Title	Gene Ontology Biological Process
1422437_a	0.002202	-1.23	1.12	NM_009098//XM_0065005	Gm15501//LOC101055915//	ribosomal protein S8 pseudogene//405 ribosomal protein S8-	0000462 // maturation of SSU-rRNA from tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA) // not recorded//0006412 // translation // inferred from electronic
1432322_a	0.007777	-1.23	-1.11	NM_146057	Dap	death-associated protein	0006914 // autophagy // inferred from electronic annotation//0006915 // apoptotic process // not recorded//0006919 // activation of cysteine-type endopeptidase activity involved in
1422541_a	0.006197	-1.23	1.12	NM_027891//XM_0065044	Lrw1d	leucine-rich repeats and WD repeat domain containing 1	0000080 // mitotic G1 phase // inferred from sequence or structural similarity//0006260 // DNA replication // inferred from electronic annotation//0006325 // chromatin organization // not
1425330_a	0.003426	-1.23	1.00	NM_023514//XM_0064962	Mrps9	mitochondrial ribosomal protein S9	0006412 // translation // inferred from electronic annotation
1460722_a	0.000574	-1.23	-1.34	NM_001159595//NM_1781	Ints8	integrator complex subunit 8	0016180 // snRNA processing // not recorded
1451139_a	0.000181	-1.24	-1.26	NM_001290995//NM_0084	Kif1b	kinesin family member 1B	0006200 // ATP catalytic process // inferred from direct assay//0007018 // microtubule-based movement // inferred from direct assay//0007270 // neuron-neuron synaptic transmission //
1426340_a	0.009480	-1.24	-1.02	NM_001101501//NM_0011	Zfp703	zinc finger protein 703	0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 // regulation of transcription, DNA-templated // not recorded//0008284 // positive regulation of
1424813_a	0.007812	-1.24	-1.02	NM_008197	H1FO	H1 histone family, member 0	0006334 // nucleosome assembly // inferred from electronic annotation
1434362_a	0.007882	-1.24	-1.45	NM_001435947//NM_0012	Dnm1l	dynamitin 1-like	0002266 // mitochondrial fission // inferred from mutant phenotype//0000266 // mitochondrial fission // not recorded//0001836 // release of cytochrome c from mitochondria // not
1424221_a	0.001820	-1.24	-1.03	NM_011291	Rpl7	ribosomal protein L7	0006364 // rRNA processing // not recorded//0006412 // translation // inferred by curator//0042273 // ribosomal large subunit biogenesis // not recorded
1422017_a	0.007972	-1.24	1.13	NM_025597	Ndufb3	NADH dehydrogenase (ubiquinone) 1 beta subcomplex 3	0006810 // transport // inferred from electronic annotation//0022900 // electron transport chain // inferred from electronic annotation//0055114 // oxidation-reduction process // inferred
1425269_a	0.003568	-1.24	1.01	NM_001289656//NM_0012	Aagl3l	ATP/GTP binding protein-like 3	0006508 // proteolysis // not recorded
1452451_a	0.001961	-1.24	-1.29	NM_145541//XM_0065009	Rap1a	RAS-related protein-1a	0006184 // GTP catalytic process // inferred from direct assay//0006886 // intracellular protein transport // inferred from electronic annotation//0006913 // nucleocytoplasmic transport //
1424268_a	0.000087	-1.24	1.04	NM_026988	Ptms	parathyrimosin	0002376 // immune system process // inferred from electronic annotation//0006452 // translational frameshifting // inferred from electronic annotation//0008612 // peptidyl-lysine
1451550_a	0.006333	-1.24	-1.27	NM_008972//XM_0030853	Gm15466//LOC102632565//	predicted gene 15466//[uncharacterized LOC102632565]//prothymosin	0043486 // histone exchange // inferred from direct assay//0043486 // histone exchange // inferred from mutant phenotype
1423482_a	0.009460	-1.24	1.08	NM_001002239//XM_0065	Gm10362//LOC101056140//	predicted gene 10362//605 ribosomal protein L17-like//ribosomal protein	0006412 // translation // inferred from electronic annotation//0042391 // regulation of membrane potential // inferred from genetic interaction//0001678 // cellular glucose homeostasis //
1435355_a	0.009571	-1.24	-1.48	NM_010306//XM_0065010	Gna13	guanine nucleotide binding protein (G protein), alpha inhibiting 3	0006184 // GTP catalytic process // not recorded//0006906 // vesicle fusion // not recorded//0007049 // cell cycle // inferred from electronic annotation//0007165 // signal transduction //
1424776_a	0.001348	-1.24	1.03	NM_026348//XM_0065033	Itgb3bp	integrin beta 3 binding protein (beta3-endonexin)	0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 // regulation of transcription, DNA-templated // inferred from electronic annotation//0006915 //
1454129_a	0.007972	-1.24	-1.94	NM_001099624//XM_0065	Rapgef2	Rap guanine nucleotide exchange factor (GEF) 2	0001568 // blood vessel development // inferred from mutant phenotype//0001764 // neuron migration // inferred from mutant phenotype//0007165 // signal transduction // inferred from
1440388_a	0.001547	-1.24	-1.61	NM_178376	Rraga	Ras-related GTP binding A	0006915 // apoptotic process // inferred from electronic annotation//0007264 // small GTPase mediated signal transduction // inferred from electronic annotation//0008219 // cell death //
1445128_a	0.003807	-1.24	-1.75	NM_019425//XM_0065192	Gnpnat1	glucosamine-phosphate N-acetyltransferase 1	0001889 // liver development // inferred from electronic annotation//0006041 // glucosamine metabolic process // not recorded//0006044 // N-acetylglucosamine metabolic process //
1418879_a	0.001961	-1.24	1.32	NM_008940//XM_0065409	Kik8	kallikrein related-peptide 8	0006508 // proteolysis // not recorded//0007613 // memory // inferred from mutant phenotype//0008219 // cell death // inferred from mutant phenotype//0009611 // response to
1423695_a	0.003480	-1.25	1.07	NM_009076//XM_0065346	LOC102635048//Rpl121//LOC	605 ribosomal protein L12-like//ribosomal protein L12//[uncharacterized	0006412 // translation // inferred from electronic annotation
1423430_a	0.005512	-1.25	-1.08	NM_013812	Cdk2p1	CDK2 (cyclin-dependent kinase 2)-associated protein 1	0001701 // in utero embryonic development // inferred from mutant phenotype//0007049 // cell cycle // inferred from electronic annotation//0060325 // face morphogenesis // inferred
1434872_x	0.000369	-1.25	-1.13	NM_001029850//NM_0010	Magi1	membrane-associated guanlylate kinase, WW and PDZ domain containing 1	0070997 // neuron death // not recorded
1456064_a	0.001902	-1.25	-1.32	NM_023565//XR_374389	Cae11	chromosome segregation 1-like (S. cerevisiae)	0006810 // transport // inferred from electronic annotation//0006886 // intracellular protein transport // inferred from electronic annotation//0015031 // protein transport // inferred from
1423317_a	0.002452	-1.25	1.08	NM_011975//XM_0030862	Rpl27a//Gm13981//Gm1440	ribosomal protein L27A//[predicted gene 13981]//[predicted gene	0006412 // translation // inferred from genetic interaction
1442323_a	0.007489	-1.25	-1.67	NM_021158//XM_0065381	Rab2a	RAB2a, member RAS oncogene family	0006184 // GTP catalytic process // not recorded//0006810 // transport // inferred from electronic annotation//0006886 // intracellular protein transport // traceable author
1425194_a	0.004455	-1.25	1.01	NM_025652	Gtf3a	general transcription factor III A	0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 // regulation of transcription, DNA-templated // inferred from electronic annotation
1423543_a	0.002034	-1.25	1.07	NM_011975//XM_0030862	Gm13981//Gm14407//Gm14	predicted gene 13981//[predicted gene 14407]//[predicted gene	0006412 // translation // inferred from genetic interaction
1430103_a	0.000304	-1.25	-1.39	NM_025709//XM_0064982	Gapv1	GTPase activating protein and VP59 domains 1	0006897 // endocytosis // inferred from electronic annotation//0007165 // signal transduction // inferred from electronic annotation//0043087 // regulation of GTPase activity // inferred
1423669_a	0.009298	-1.25	1.07	NM_009076//XM_0065346	LOC102635048//Rpl121//LOC	605 ribosomal protein L12-like//ribosomal protein L12//[uncharacterized	0006412 // translation // inferred from electronic annotation
1449024_a	0.000447	-1.25	-1.20	NM_001081191//XM_0065	Emi5	echinoderm microtubule associated protein like 5	0046856 // phosphatidylinositol dephosphorylation // not recorded
1427368_x	0.003064	-1.25	-1.05	NM_030692	Sacm1	SAC1 (suppressor of actin mutations 1, homolog-1 like (S. cerevisiae)	0000055 // ribosomal large subunit export from nucleus // inferred from mutant phenotype//0000056 // ribosomal small subunit export from nucleus // inferred from direct assay//0006281
1435394_x	0.000628	-1.25	-1.13	NM_001252260//NM_0012	Npm1	nucleophosmin 1	0006200 // ATP catalytic process // inferred from electronic annotation//0006397 // mRNA processing // inferred from electronic annotation//0008152 // metabolic process // inferred from
1450501_a	0.007451	-1.25	-1.24	NM_001042620//NM_0078	Dhx15	DEAH (Arg-Glu-Ala-His) box polypeptide 15	0001937 // negative regulation of endothelial cell proliferation // not recorded//0006783 // heme biosynthetic process // inferred from mutant phenotype//0006783 // heme biosynthetic
1423455_a	0.001733	-1.25	-1.08	NM_007512//XM_0065385	Atpf1	ATPase inhibitory factor 1	0001525 // angiogenesis // inferred from mutant phenotype//0007399 // nervous system development // inferred from direct assay//0007413 // axonal fasciculation // inferred from mutant
1450784_a	0.006367	-1.25	-1.25	NM_024226//NM_194051/	Rtn4	reticulon 4	0002376 // immune system process // inferred from electronic annotation//0007275 // multicellular organismal development // inferred from electronic annotation//0043368 // positive T
1418888_a	0.004856	-1.25	1.32	NM_178666//XM_0065126	Themis	thymocyte selection associated	0006810 // transport // inferred from electronic annotation//0055114 // oxidation-reduction process // inferred from electronic annotation
1421179_a	0.007987	-1.25	1.16	NM_019435//XM_0065275	Ndufb11	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 11	0035092 // sperm chromatin condensation // not recorded//0051084 // de novo posttranslational protein folding // traceable author statement//0055114 // oxidation-reduction process //
1450363_a	0.003823	-1.25	-1.24	NM_053102	A2628	PDZ and LIM domain 1 (elfin)	0001666 // response to hypoxia // inferred from electronic annotation//0006355 // regulation of transcription, DNA-templated // inferred from direct assay
1424757_a	0.005322	-1.26	1.03	NM_016861	Pdlim1	polymerase (RNA) II (DNA directed) polypeptide E	0006351 // transcription, DNA-templated // inferred from electronic annotation//0006360 // transcription from RNA polymerase I promoter // not recorded//0006366 // transcription from RNA
1425161_a	0.005474	-1.26	1.01	NM_025554	Polr2c	differentially expressed in B16F10 1	0006750 // glutathione biosynthetic process // inferred from electronic annotation//0032225 // regulation of synaptic transmission, dopaminergic // inferred from mutant
1421488_a	0.001277	-1.26	1.15	NM_026794	Deb1	paroxysmal nonkinetogenic dyskinesia	0006629 // lipid metabolic process // inferred from electronic annotation//0006694 // steroid biosynthetic process // inferred from electronic annotation//0006695 // cholesterol biosynthetic
1423285_a	0.000683	-1.26	1.08	NM_001039509//NM_0199	Pnkld	cytochrome B5 reductase 3	0006457 // protein folding // not recorded//0006457 // protein folding // traceable author statement//0006662 // glycerol ether metabolic process // inferred from electronic
1428869_a	0.003901	-1.26	-1.08	NM_025787//XM_0065202	Cyb5r3	protein disulfide isomerase associated 2	0006412 // translation // inferred from electronic annotation//0006417 // inference of translation // inferred from electronic annotation//0007148 // negative regulation of translation //
1428144_a	0.009122	-1.26	-1.07	NM_001081070//XM_0065	Pdia2	ribosomal protein L13A//FMS-like tyrosine kinase 3 ligand//605 ribosomal	0000070 // mitotic sister chromatid segregation // not recorded//0000226 // microtubule cytoskeleton organization // inferred from electronic annotation//0000281 // mitotic cytokinesis //
1427021_x	0.000679	-1.26	-1.04	NM_009438//NM_013520/	Rpl3aa//Frl3//Gm11478	nucleolar and spindle associated protein 2	0006605 // protein targeting // inferred from direct assay//00018345 // protein palmitoylation // inferred from direct assay//00018345 // protein palmitoylation // not recorded
1454531_a	0.002828	-1.26	1.03	NM_026917//XM_0065122	Zdhc3	zinc finger, DHHC domain containing 3	0006417 // regulation of translation // inferred from electronic annotation//0004572 // positive regulation of translation // not recorded
1449277_a	0.000545	-1.26	-1.21	NM_172585//XM_0065164	Larp4b	La ribonucleoprotein domain family, member 4B	0006749 // glutathione metabolic process // inferred from direct assay//00010243 // response to organonitrogen compound // not recorded//0032496 // response to lipopolysaccharide // not
1430590_a	0.007460	-1.26	-1.40	NM_019946//XM_0065064	Mgst1	microsomal glutathione S-transferase 1	0006915 // apoptotic process // inferred from electronic annotation//0030262 // apoptotic nuclear changes // not recorded//0007194 // execution phase of apoptosis // inferred from
1428279_a	0.000933	-1.26	-1.07	NM_175414//XM_0065053	Tspan9	tetraspanin 9	0010265 // SCF complex assembly // not recorded//0016567 // protein ubiquitination // not recorded//0030154 // cell differentiation // not recorded//0043086 // negative regulation of
1454402_a	0.005264	-1.26	-1.76	NM_001025582//NM_0012	Dram2	DNA-damage regulated autophagy modulator 2	0001678 // cellular glucose homeostasis // not recorded//0002931 // response to ischemia // not recorded//0005975 // carbohydrate metabolic process // inferred from electronic
1455271_a	0.000564	-1.26	-1.32	NM_027994	Cand1	cullin associated and neddylation dissociated 1	0006468 // protein phosphorylation // inferred from electronic annotation//0016310 // phosphorylation // inferred from electronic annotation//0035556 // intracellular signal transduction //
1416832_a	0.002496	-1.26	2.05	NM_028443	Fam101a	family with sequence similarity 101, member A	0007169 // transmembrane receptor protein tyrosine kinase signaling pathway // inferred from genetic interaction//0007399 // nervous system development // inferred from mutant
1422156_a	0.001702	-1.26	1.13	NM_001146100//NM_0104	Hkl1//Gm10362//Gm6133//	hexokinase 1//[predicted gene 10362]//605 ribosomal protein L17	0001525 // angiogenesis // inferred from mutant phenotype//0001570 // vasculogenesis // inferred from mutant phenotype//0001763 // morphogenesis of a branching structure // inferred
1420936_s	0.001697	-1.26	1.18	NM_172928	Dcl3	doublecortin-like kinase 3	0000002 // mitochondrial genome maintenance // traceable author statement//0006412 // translation // not recorded
1418809_s	0.001996	-1.26	1.34	NM_008115//XM_0065185	Gfra2	glial cell line derived neurotrophic factor family receptor alpha 2	0006810 // transport // inferred from electronic annotation//0006886 // intracellular protein transport // inferred from electronic annotation//0006888 // ER to Golgi vesicle-mediated
1422617_a	0.006320	-1.26	1.11	NM_008115//XM_0065185	Gfra2	glial cell line derived neurotrophic factor family receptor alpha 2	0001843 // neural tube closure // inferred from mutant phenotype//0002181 // cytoplasmic translation // not recorded//0006364 // rRNA processing // not recorded//0006412 //
1422403_a	0.001179	-1.27	1.12	NM_001271590//NM_0012	Gm13826//Rpl37	ribosomal protein S11	0006412 // translation // inferred from electronic annotation
1430312_a	0.009008	-1.27	-1.40	NM_028731//XM_0065160	Eys2	extended synaptotagmin-like protein 2	0006810 // transport // inferred from electronic annotation//0006869 // lipid transport // inferred from electronic annotation//0006897 // endocytosis // inferred from electronic annotation
1429475_a	0.001045	-1.27	-1.38	NM_016716//XM_0064964	Cul3	cullin 3	0000900 // mitotic anaphase // not recorded//0000209 // protein polyubiquitination // not recorded//0000902 // cell morphogenesis // inferred from mutant phenotype//0000910 //
1428050_a	0.007736	-1.27	-1.07	NM_001113199//NM_0012	Naco	nascent polypeptide-associated complex alpha polypeptide	0003231 // cardiac ventricle development // inferred from mutant phenotype//0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 // regulation of
1440840_a	0.007524	-1.27	-1.63	NM_001110204//NM_0011	Acrv1	activin A receptor, type 1	0000082 // G1/S transition of mitotic cell cycle // not recorded//0001569 // patterning of blood vessels // inferred from mutant phenotype//0001655 // urogenital system development // not
1426605_a	0.009043	-1.27	-1.03	NM_016959	Rps3a1	ribosomal protein S3A1	0002181 // cytoplasmic translation // not recorded//0006412 // translation // inferred from electronic annotation//00030154 // cell differentiation // inferred from electronic
1438407_a	0.000646	-1.27	-1.55	NM_133815//XM_0064970	Lbr	lamin B receptor	0055114 // oxidation-reduction process // inferred from electronic annotation
1417538_a	0.005291	-1.27	1.61	NM_010421//XR_373937	Hexa	hexosaminidase A	0001501 // skeletal system development // inferred from genetic interaction//0005975 // carbohydrate metabolic process // inferred from electronic annotation//0006689 // ganglioside
1418076_a	0.002879	-1.27	1.46	NM_009230//XM_0064967	Soat1	sterol O-acetyltransferase 1	0006629 // lipid metabolic process // inferred from electronic annotation//0008202 // steroid metabolic process // inferred from electronic annotation//0008203 // cholesterol metabolic
1421815_a	0.000552	-1.27	1.14	NM_001037798//NM_0076	Cbx3//Gm5792//Gm6901//	chromobox 3//[predicted pseudogene 5792]//[predicted gene	0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 // regulation of transcription, DNA-templated // inferred from electronic annotation//0001658 //
1422064_a	0.003826	-1.27	1.11	NM_172397//XM_0065340	Lmd2	LIM domain containing 2	0001967 // sucking behavior // inferred from genetic interaction//0006878 // cellular copper ion homeostasis // inferred from mutant phenotype//0007176 // regulation of epidermal growth
1427510_a	0.002118	-1.27	-1.06	NM_001102455//NM_0011	Asp2	amyloid beta (A4) precursor-like protein 2	0006486 // protein glycosylation // inferred from electronic annotation//0006506 // GPI anchor biosynthetic process // inferred from mutant phenotype//0006506 // GPI anchor biosynthetic
1451631_a	0.005761	-1.27	-1.28	NM_010072//NM_009628	Dpm1//Adnp	dolichol-phosphate (beta-D) mannosyltransferase 1//activity-dependent	0006397 // mRNA processing // inferred from electronic annotation//0008380 // RNA splicing // inferred from electronic annotation
1450729_a	0.000648	-1.27	-1.25	NM_001081183//XM_0065	1110037F02Rik	ribosomal protein S3A1	0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 // regulation of transcription, DNA-templated // inferred from electronic annotation//0001658 //
1421832_a	0.003699	-1.27	1.14	NM_001037798//NM_0076	Cbx3//Gm5792//Gm6901//	chromobox 3//[predicted pseudogene 5792]//[predicted gene	0000090 // mitotic anaphase // not recorded//0000209 // protein polyubiquitination // not recorded//0000902 // cell morphogenesis // inferred from mutant phenotype//0000910 //
1426289_a	0.000623	-1.27	-1.02	NM_026554	Ncbp2	nuclear cap binding protein subunit 2	0003231 // cardiac ventricle development // inferred from mutant phenotype//0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 // regulation of
1424067_a	0.004060	-1.27	-1.05	NM_025277	Gng10	guanine nucleotide binding protein (G protein), gamma 10	0007165 // signal transduction // inferred from electronic annotation//0007186 // G-protein coupled receptor signaling pathway // inferred from electronic annotation
1449511_a	0.004661	-1.27	1.22	NM_207302//XM_0065079	Zranb1	zinc finger, RAN-binding domain containing 1	0006508 // proteolysis // inferred from electronic annotation//0007010 // cytoskeleton organization // not recorded//0001605 // Wnt signaling pathway // inferred from electronic
1423935_x	0.000372	-1.27	1.06	NM_008033	Fnta	farnesyltransferase, CAAX box, alpha	0007528 // neuromuscular junction development // inferred from mutant phenotype//0008284 // positive regulation of cell proliferation // not recorded//0010035 // response to inorganic
1420899_a	0.001953	-1.27	1.18	NM_001177402//NM_0011	Cebpzs	CCAAT/enhancer binding protein (C/EBP), zeta, opposite strand	0043066 // negative regulation of apoptotic process // not recorded//0048659 // smooth muscle cell proliferation // inferred from mutant phenotype
1434488_a	0.006917	-1.27	-1.70	NM_030153//XM_0065174	Nao35	N(Alpa)-acetyltransferase 35, NatC auxiliary subunit	0006184 // GTP catalytic process // not recorded//0006810 // transport // inferred from electronic annotation//0006886 // intracellular protein transport // inferred from electronic
1428492_a	0.004007	-1.28	-1.08	NM_019773//XM_0065289	Rab9	RAB9, member RAS oncogene family	
1419522_a	0.003696	-1.28	1.26	NM_145607//XM_0065309	Ttc13	tetratricopeptide repeat domain 13	

Table S7

Gene ID	p (Corr)	FC-RSV 1 d	FC-RSV 5 d	RefSeq Transcript ID	Gene Symbol	Gene Title	Gene Ontology Biological Process
1423087_a	0.002056	-1.28	1.09	NM_025587//NM_0065007	Gm5963//Rps21	predicted pseudogene 5963//ribosomal protein S21	0000447 // endonucleolytic cleavage in ITS1 to separate 5S rRNA and LSU rRNA from tritronic rRNA transcript (5S rRNA, 5.8S rRNA, LSU rRNA) // not recorded//0000461
1428544_a	0.001310	-1.28	-1.35	NM_009408	Top1	topoisomerase (DNA I)	0006200 // ATP catabolic process // inferred from electronic annotation//0006260 // DNA replication // inferred from mutant phenotype//0006265 // DNA topological change // inferred
1429008_a	0.002036	-1.28	-1.36	NM_080443//NM_178236	Asb7	ankryin repeat and SOCS box-containing 7	0016567 // protein ubiquitination // inferred from electronic annotation//0003556 // intracellular signal transduction // inferred from electronic annotation
1420683_a	0.002769	-1.28	1.19	NM_025823//NM_0065064	Pcyox1	peroxyl carrier family 5, member B3	0006200 // ATP catabolic process // not recorded//0006821 // chloride transport // not recorded//0030327 // prenylated protein catabolic process // not recorded//0030328 //
1423358_a	0.001909	-1.28	1.08	NM_001190258//NM_0270	Rps27//Rps27rt	ribosomal protein S27//ribosomal protein S27, retrogene	0006412 // translation // inferred from electronic annotation
1424417_a	0.008130	-1.28	1.04	NM_009438//XR_141061//	Gm11478//Rpl13a	60S ribosomal protein L13a-like//ribosomal protein L13A	0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 // regulation of transcription, DNA-templated // inferred from electronic annotation//0006412 //
1437514_a	0.000628	-1.28	-1.54	NM_001122963//NM_0284	Gpbp1	GC-rich promoter binding protein 1	0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 // regulation of transcription, DNA-templated // inferred from electronic annotation//0006593 //
1416767_a	0.002292	-1.28	2.09	NM_009185//NM_0065029	Sbl	Scf/Tal1 interrupting locus	0000578 // embryonic axis specification // inferred from mutant phenotype//0001701 // in utero embryonic development // inferred from mutant phenotype//0001843 // neural tube
1425496_a	0.000540	-1.28	1.00	NM_001127566//NM_0011	Dctn1	dyncytin 1	0006810 // transport // inferred from electronic annotation//0008152 // metabolic process // inferred from electronic annotation//0010970 // microtubule-based transport // inferred from
1438684_a	0.002575	-1.28	-1.56	NM_001190439//NM_0011	Slc35b3	solute carrier family 35, member B3	0006810 // transport // inferred from electronic annotation//0005508 // transmembrane transport // inferred from electronic annotation
1423335_a	0.000247	-1.28	1.08	NM_001190258//NM_0270	Rps27//Rps27rt	ribosomal protein S27//ribosomal protein S27, retrogene	0006412 // translation // inferred from electronic annotation
1460273_a	0.000101	-1.28	-1.33	NM_023733//NM_0065036	Crot	carnitine O-octanoyltransferase	0006091 // generation of precursor metabolites and energy // not recorded//0006629 // lipid metabolic process // inferred from electronic annotation//0006631 // fatty acid metabolic
1418442_a	0.006685	-1.28	1.39	NM_009368	Tgfb3	transforming growth factor, beta 3	0000187 // activation of MAPK activity // not recorded//0001666 // response to hypoxia // not recorded//0001701 // in utero embryonic development // inferred from mutant
1420896_a	0.002428	-1.28	1.18	NM_001282064//NM_0012	Cyb561a3	cytochrome b561 family, member A3	0006810 // transport // inferred from electronic annotation//0005514 // oxidation-reduction process // inferred from electronic annotation
1425374_a	0.000090	-1.28	1.00	NM_029537	Tmem98	transmembrane protein 98	
1434331_a	0.000591	-1.29	-1.45	NM_022997	Vps35	vacuolar protein sorting 35	0006624 // vacuolar protein processing // not recorded//0006810 // transport // inferred from electronic annotation//0015031 // protein transport // inferred from electronic
1423994_a	0.005154	-1.29	1.05	NM_001163749//NM_0271	Camsap3	calmodulin regulated spectrin-associated protein family, member 3	0000226 // microtubule cytoskeleton organization // not recorded//0010923 // negative regulation of phosphatase activity // not recorded//0033043 // regulation of organelle organization //
1457727_a	0.007364	-1.29	-2.22	NM_001033430	Kdm7a	lysine (K)-specific demethylase 7A	0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 // regulation of transcription, DNA-templated // inferred from electronic annotation//0007399 //
1456553_a	0.007940	-1.29	-2.07	NM_001005863//NM_0010	Mtus1	mitochondrial tumor suppressor 1	0007049 // cell cycle // inferred from electronic annotation//0010758 // regulation of macrophage chemotaxis // inferred from direct assay//0071375 // cellular response to peptide hormone
1423191_a	0.004555	-1.29	1.09	NM_011653//NR_033599	Tuba1a//Gm6682	tubulin, alpha 1A//tubulin, alpha 1C pseudogene	0006184 // GTP catabolic process // inferred from electronic annotation//0007017 // microtubule-based process // inferred from electronic annotation//00051258 // protein polymerization //
1426123_a	0.000465	-1.29	-1.01	NM_145488	Pex6	peroxisomal biogenesis factor 6	0006200 // ATP catabolic process // not recorded//0006625 // protein targeting to peroxisome // not recorded//0007031 // peroxisome organization // not recorded//0008152 // metabolic
1426661_a	0.005333	-1.29	-1.03	NM_016980//NM_0010048	Rpl5//Rpl5-ps2	ribosomal protein L5//ribosomal protein L5, pseudogene 2	0006364 // rRNA processing // not recorded//0006412 // translation // inferred from electronic annotation//0010922 // positive regulation of phosphatase activity // not recorded//0042273
1422668_a	0.006025	-1.29	1.11	NM_009930	Col3a1	collagen, type III, alpha 1	0001501 // skeletal system development // inferred from electronic annotation//0001568 // blood vessel development // inferred from mutant phenotype//0007160 // cell-matrix adhesion
1422572_a	0.006836	-1.29	-1.12	NM_001105667//NM_0231	Dtymk	deoxythymidylate kinase	0006233 // dTDP biosynthetic process // inferred from direct assay//0006233 // dTDP biosynthetic process // not recorded//0006235 // dTTP biosynthetic process // not recorded//0009165
1448942_a	0.000167	-1.29	-1.20	NM_001253867//NM_0012	Tmem205	transmembrane protein 205	
1434392_a	0.006605	-1.29	-1.12	NM_001030959//NM_0012	Ahnak	AHNK nucleoside protein (desmyokinin)	0043484 // regulation of RNA splicing // inferred from direct assay//00051259 // protein oligomerization // inferred from mutant phenotype//0001385 // regulation of voltage-gated calcium
1428526_a	0.007163	-1.29	-1.08	NM_011948//NM_0065233	Map3k4	mitogen-activated protein kinase kinase kinase 4	0000165 // MAPK cascade // not recorded//0000186 // activation of MAPK activity // not recorded//0001890 // placenta development // inferred from mutant phenotype//0006468 //
1418479_a	0.001963	-1.29	1.38	XR_387288//XR_398758	Panc2	pancreatic-associated noncoding transcript 2	0019827 // stem cell maintenance // inferred from mutant phenotype
1449937_a	0.005030	-1.30	-1.23	NM_001136260//NM_0011	Slc40a	solute carrier family 4 (anion exchanger), member 4	0006810 // transport // inferred from electronic annotation//0006811 // ion transport // inferred from electronic annotation//0006814 // sodium ion transport // inferred from direct
1428942_a	0.003823	-1.30	-1.08	NM_178377//NM_0065262	Comm1d10	COMM domain containing 10	
1452246_a	0.002800	-1.30	-1.29	NM_007564	Zfp361	zinc finger protein 36, C2H type-like 1	0000288 // nuclear-transcribed mRNA catabolic process, deadenylation-dependent decay // inferred from direct assay//00001570 // vasculogenesis // inferred from mutant
1421410_a	0.000970	-1.30	1.15	NM_001130187//NM_0318	Smarca2	SWI/SNF related, matrix associated, actin dependent regulator of	0006337 // nucleosome disassembly // not recorded//0006338 // chromatin remodeling // not recorded//0006351 // transcription, DNA-templated // inferred from electronic
1430640_a	0.006280	-1.30	-1.40	NM_001122758//NM_0187	Pcdh7	protodactherin 7	0007155 // cell adhesion // inferred from electronic annotation//0007156 // homophilic cell adhesion // inferred from electronic annotation
1425945_a	0.008443	-1.30	-1.01	NM_007415	Parp1	poly (ADP-ribose) polymerase family, member 1	0000723 // telomere maintenance // inferred from mutant phenotype//0006259 // DNA metabolic process // inferred from mutant phenotype//0006281 // DNA repair // traceable author
1437152_a	0.001748	-1.30	-1.53	NM_0161854//NM_1449	Csde1	cold shock domain containing E1, RNA binding	0006355 // regulation of transcription, DNA-templated // inferred from electronic annotation//0007096 // nuclear-transcribed mRNA catabolic process, no-go decay // not recorded
1448380_a	0.000137	-1.30	-1.18	NM_016721//NM_0065409	Iqgap1//LOC102641119	IQ motif containing GTPase activating protein 1//uncharacterized	0001817 // regulation of cytokine production // inferred from mutant phenotype//0007165 // signal transduction // inferred from electronic annotation//0007173 // epidermal growth factor
1428781_a	0.000512	-1.30	-1.08	NM_001160233//NM_0011	Fam168b	family with sequence similarity 168, member B	
1423494_a	0.000193	-1.30	1.08	NM_001013578//NM_0012	Thoc7	THO complex 7 homolog (Drosophila)	
1437820_a	0.008750	-1.30	-1.54	NM_007508//NM_0065217	Atp6v1a	ATPase, H ⁺ transporting, lysosomal V1 subunit A	0006397 // mRNA processing // inferred from electronic annotation//0006406 // mRNA export from nucleus // not recorded//0006810 // transport // inferred from electronic
1428966_a	0.001733	-1.30	-1.08	NM_011804//NM_0064969	Creg1	cellular repressor of E1A-stimulated genes 1	0006810 // transport // inferred from electronic annotation//0006811 // ion transport // inferred from electronic annotation//00015991 // ATP hydrolysis coupled proton transport // inferred
1435572_a	0.000370	-1.30	-1.14	NM_001199105//NM_0218	Trp53inp1	transformation related protein 53 inducible nuclear protein 1	0006355 // regulation of transcription, DNA-templated // inferred from direct assay//0004008 // regulation of growth // inferred from electronic annotation//00055114 // oxidation-reduction
1422327_a	0.002246	-1.30	-1.12	NM_0110325//NM_0065074	Pnk1	p21 protein (Cdc42/Rac)-activated kinase 1	0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 // regulation of transcription, DNA-templated // inferred from electronic annotation//0006914 //
1448492_a	0.003224	-1.30	-1.18	NM_001128202//NM_0012	Spn1	spindlin 1	0001666 // response to hypoxia // not recorded//0001334 // positive regulation of protein phosphorylation // not recorded//0006468 // protein phosphorylation // not recorded//0006468 //
1450142_a	0.000603	-1.30	-1.23	NM_026697	Rab14	RAB14, member RAS oncogene family	0007049 // cell cycle // inferred from electronic annotation//0007126 // meiotic nuclear division // inferred from electronic annotation//0007143 // female meiotic division // inferred by
1420763_a	0.004521	-1.30	1.19	NM_053273	Ttyh2	Ttyh2, homolog 2 (Drosophila)	0006194 // GTP catabolic process // not recorded//0006810 // transport // inferred from electronic annotation//0006886 // intracellular protein transport // inferred from electronic
1428876_a	0.003615	-1.30	-1.36	NM_013865//NM_180956	Ndrp3	N-myc downstream regulated gene 3	0006810 // transport // inferred from electronic annotation//0006811 // ion transport // inferred from electronic annotation//0006821 // chloride transport // inferred from electronic
1423571_a	0.006348	-1.31	1.07	NM_009080//NR_003373	Gm15772//Rpl26	ribosomal protein L26 pseudogene//ribosomal protein L26	0006364 // rRNA processing // not recorded//0006412 // translation // inferred from electronic annotation//0042273 // ribosomal large subunit biogenesis // not recorded
1431491_a	0.001885	-1.31	-1.42	NM_001285507//NM_0012	Cops2	COP9 (constitutive photomorphogenic) homolog, subunit 2 (Arabidopsis	0000122 // negative regulation of transcription from RNA polymerase II promoter // not recorded//0008283 // cell proliferation // inferred from mutant phenotype//0010388 // cullin
1448555_a	0.004508	-1.31	-1.18	NM_025948//NM_0065402	Lsm14a	LSM14 homolog A (SCDS, S. cerevisiae)	0006417 // regulation of translation // inferred from electronic annotation//0007275 // multicellular organismal development // inferred from electronic annotation//0003962 // cytoplasmic
1429457_a	0.000055	-1.31	-1.09	NM_001081113//NM_0065	Ipo8	importin 8	0006200 // ATP catabolic process // not recorded//0006810 // transport // not recorded//0006886 // intracellular protein transport // inferred from electronic annotation//00015031 //
1427883_a	0.001668	-1.31	-1.06	NM_008251//NM_0065229	Hmgm1	high mobility group nucleosomal binding domain 1	0000720 // pyrimidine dimer repair by nucleotide-excision repair // inferred from mutant phenotype//0006283 // transcription-coupled nucleotide-excision repair // inferred from mutant
1439485_a	0.001533	-1.31	-1.58	NM_001146323//NM_0011	Hps3	Hermansky-Pudlak syndrome 3 homolog (human)	0006996 // organelle organization // inferred from mutant phenotype//0004373 // pigmentation // inferred from mutant phenotype
1451049_a	0.000756	-1.31	-1.26	NM_177390//NM_0065335	Myo1d	myosin ID	0006200 // ATP catabolic process // not recorded//0008152 // metabolic process // not recorded//0010923 // negative regulation of phosphatase activity // not recorded//00061502 // early
1426482_a	0.007684	-1.31	-1.02	NM_146094//NM_0065274	Fads1	fatty acid desaturase 1	0006629 // lipid metabolic process // inferred from electronic annotation//0006631 // fatty acid metabolic process // inferred from electronic annotation//0006633 // fatty acid biosynthetic
1434316_a	0.005983	-1.31	-1.45	NM_001164424//NM_0011	Prpsap2	phosphoribosyl pyrophosphate synthetase-associated protein 2	0009165 // nucleotide biosynthetic process // inferred from electronic annotation//0006348 // bone development // inferred from mutant phenotype
1433135_a	0.003575	-1.31	-1.43	NM_016898	Cd164	CD164 antigen	0007155 // cell adhesion // not recorded//0007157 // heterophilic cell-cell adhesion // not recorded//0007517 // muscle organ development // inferred from electronic annotation
1448790_a	0.008940	-1.31	-1.19	NM_009906//NM_0065072	Tpp1	tripeptidyl peptidase I	0006508 // proteolysis // not recorded//0006508 // proteolysis // inferred from sequence or structural similarity//0007040 // lysosome organization // inferred from mutant
1435639_a	0.000775	-1.31	-1.14	NM_001290792//NM_0012	Wdr45	WD repeat domain 45	0000045 // autophagic vacuole assembly // not recorded//0006914 // autophagy // not recorded//00050790 // regulation of catalytic activity // inferred from electronic annotation
1428775_a	0.008924	-1.31	-1.35	NM_153599//NM_181570	Cdk8	cyclin-dependent kinase 8	0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 // regulation of transcription, DNA-templated // inferred from electronic annotation//0006468 //
1448333_a	0.005146	-1.31	-1.51	NM_009282//NM_0065109	Stop1	stromal antigen 1	0007049 // cell cycle // inferred from electronic annotation//0007059 // chromosome segregation // inferred from electronic annotation//0007067 // mitotic nuclear division // inferred from
1428346_a	0.000085	-1.31	-1.08	NM_080289//XR_390349	Ghrpr	glyoxylate reductase/hydroxypyruvate reductase	0006098 // pentose-phosphate shunt // inferred from electronic annotation//0007588 // excretion // not recorded//0008152 // metabolic process // inferred from electronic
1446809_a	0.002359	-1.32	-1.81	NM_004475//NM_0065149	Ublcp1	ubiquitin-like domain containing CTD phosphatase 1	0008152 // metabolic process // inferred from electronic annotation//0016311 // dephosphorylation // inferred from electronic annotation
1422230_a	0.008277	-1.32	1.13	NM_001206335//NM_0272	Itfg3	integrin alpha FG-GAP repeat containing 3	
1428997_a	0.000125	-1.32	-1.08	NM_133685	Rab31	RAB31, member RAS oncogene family	0006184 // GTP catabolic process // inferred from electronic annotation//0006886 // intracellular protein transport // inferred from electronic annotation//0006913 // nucleocytoplasmic
1451066_a	0.002380	-1.32	-1.26	NM_175036	Leprot	leptin receptor overlapping transcript	0046426 // negative regulation of JAK-STAT cascade // not recorded//0006400 // negative regulation of growth hormone receptor signaling pathway // not recorded//0000009 // negative
1425475_a	0.000924	-1.32	1.00	NM_013822	Jag1	jagged 1	0001974 // blood vessel remodeling // inferred from mutant phenotype//0002011 // morphogenesis of an epithelial sheet // inferred from mutant phenotype//0002456 // T cell mediated
1434740_a	0.003533	-1.32	-1.46	NM_001004143	Usp22	ubiquitin specific peptidase 22	0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 // regulation of transcription, DNA-templated // inferred from electronic annotation//0006508 //
1442894_a	0.005166	-1.32	-1.69	NM_026734	Tmem126b	transmembrane protein 126b	
1450808_a	0.000495	-1.32	-1.25	NM_001252625//NM_0012	Ptgr2	prostaglandin reductase 2	0006693 // prostaglandin metabolic process // not recorded//00055114 // oxidation-reduction process // not recorded
1429117_a	0.008813	-1.32	-1.09	NM_001040187//NM_1528	Ddx17	DEAD (Asp-Glu-Ala-Asp) box polypeptide 17	0006200 // ATP catabolic process // inferred from electronic annotation//0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 // regulation of
1437534_a	0.000008	-1.32	-1.16	NM_001110228//NM_0011	Celf2	CUGBP, Elav-like family member 2	0006376 // mRNA splice site selection // inferred from direct assay//0006397 // mRNA processing // inferred from electronic annotation
1429219_a	0.007162	-1.32	-1.09	NM_0011294//NM_0065200	Sub1	SUB1 homolog (S. cerevisiae)	0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 // regulation of transcription, DNA-templated // inferred from electronic annotation//0006357 //
1428557_a	0.000511	-1.32	-1.35	NM_008098	Mtpn	myotrophin	0006584 // catecholamine metabolic process // inferred from electronic annotation//00100557 // positive regulation of macromolecule biosynthetic process // not recorded//00010613 //
1426213_a	0.007732	-1.32	-1.01	NM_140684//NM_0065258	Fam13b	family with sequence similarity 13, member B	0007165 // signal transduction // inferred from electronic annotation//0004547 // positive regulation of GTPase activity // inferred from electronic annotation
1418621_a	0.000240	-1.32	1.36	NM_172471//NM_0064974	Ith5	inter-alpha (globulin) inhibitor H5	0006614 // SRP-dependent cotranslational protein targeting to membrane // inferred from electronic annotation//00010466 // negative regulation of peptidase activity // inferred from
1448881_a	0.007120	-1.32	-1.19	NM_001128922//NM_0011	Fnn	Fyn proto-oncogene	0001764 // neuron migration // inferred from genetic interaction//0001764 // neuron migration // inferred from mutant phenotype//0002376 // immune system process // inferred from
1435230_a	0.002527	-1.32	-1.48	NM_001081164//NM_0012	Otdud4	OTU domain containing 4	0006508 // proteolysis // not recorded//0007108 // protein K48-linked deubiquitination // not recorded
1436876_a	0.003750	-1.33	-1.52	NM_010028//NM_0065275	Ddx3x	DEAD/HD (Asp-Glu-Ala-Asp/His) box polypeptide 3, X-linked	0002376 // immune system process // inferred from electronic annotation//0006200 // ATP catabolic process // not recorded//0006351 // transcription, DNA-templated // inferred from
1435325_a	0.001266	-1.33	-1.48	NM_008540//NM_0065257	Smad5	SMAD family member 4	0006658 // branching involved in uterine bud morphogenesis // inferred from genetic interaction//0001666 // response to hypoxia // not recorded//0001701 // in utero embryonic
1448855_a	0.002930	-1.33	-1.19	NM_146096//NM_0065269	Ahhb17b	ahbhydrolase domain containing 17b	0008152 // metabolic process // inferred from electronic annotation//0006508 // proteolysis // inferred from electronic annotation
1419088_a	0.003403	-1.33	1.30	NM_033373	Krt23	keratin 23	
1425732_a	0.009810	-1.33	-1.01	NM_001145780//NM_0259	Use1	unconventional SNARE in the ER 1 homolog (S. cerevisiae)	0006810 // transport // inferred from electronic annotation//0006888 // ER to Golgi vesicle-mediated transport // inferred from mutant phenotype//0007029 // endoplasmic reticulum
1448252_a	0.000854	-1.33	-1.17	NM_023402	Myl12b	myosin, light chain 12b, regulatory	0008360 // regulation of cell shape // inferred from mutant phenotype
1449108_a	0.000511	-1.33	-1.20	NM_001033474	Atn7b3b	ataxin 7-like 3b	
1436705_a	0.000793	-1.33	-1.52	NM_139227//NM_0065180	Atn7	ataxin 7	0000226 // microtubule cytoskeleton organization // not recorded//0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 // regulation of transcription,
1423148_a	0.000550	-1.33	1.09	NM_182841//NM_0065348	Tmem150c	transmembrane protein 150C	0006810 // transport // inferred from electronic annotation//0015031 // protein transport // inferred from electronic annotation//0042058 // regulation of epidermal growth factor receptor
1422878_a	0.001854	-1.33	1.10	NM_175184//NM_0064983	Mvb12b	multivesicular body subunit 12B	0000122 // negative regulation of transcription from RNA polymerase II promoter // inferred from mutant phenotype//0

Table S7

Gene ID	p (Corr)	FC-RSV 1 d	FC-RSV 5 d	RefSeq Transcript ID	Gene Symbol	Gene Title	Gene Ontology Biological Process
1440192_a	0.001305	-1.33	-1.17	NM_001168470//NM_0253	<i>Ermc6</i>	ER membrane protein complex subunit 6	
1448636_a	0.003183	-1.33	-1.18	NM_001112798//NM_0012	<i>Slc8a1</i>	solute carrier family 8 (sodium/calcium exchanger), member 1	0001666 // response to hypoxia // not recorded//0001892 // embryonic placenta development // inferred from mutant phenotype//0002026 // regulation of the force of heart contraction //
1438391_x	0.000570	-1.33	-1.16	NM_001077184//NM_0097	<i>Bsg</i>	basigin	0007566 // embryo implantation // inferred from electronic annotation//00042475 // odontogenesis of dentin-containing tooth // inferred from electronic annotation//00043434 // response to
1449455_a	0.000288	-1.33	-1.22	NM_001081436//NM_0011	<i>Ino80d</i>	INO80 complex subunit D	0006281 // DNA repair // inferred from electronic annotation//0006310 // DNA recombination // inferred from electronic annotation//0006351 // transcription, DNA-templated // inferred
1423823_a	0.002862	-1.33	1.06	NM_019953//XM_0065139	<i>Cnpy2</i>	canopy 2 homolog (zebrafish)	0010629 // negative regulation of gene expression // inferred from mutant phenotype//0010988 // regulation of low-density lipoprotein particle clearance // inferred from mutant
1431177_a	0.006740	-1.33	-1.10	NM_175095//XM_0065016	<i>Commid2</i>	COMMD domain containing 2	
1453523_a	0.000511	-1.33	-1.93	NM_001159382//NM_0011	<i>Gjc1</i>	gap junction protein, gamma 1	0001570 // vasculogenesis // inferred from mutant phenotype//0007154 // cell communication // inferred from electronic annotation//0007267 // cell-cell signaling // inferred from mutant
1439695_a	0.000511	-1.33	-1.59	NM_029949//XM_0065383	<i>Snappc3</i>	small nuclear RNA activating complex, polypeptide 3	0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 // regulation of transcription, DNA-templated // inferred from electronic annotation//0000395 //
1426739_a	0.006996	-1.33	-1.03	NM_001252489//NM_0012	<i>Ostbpl1a</i>	oxysterol binding protein-like 1A	0006351 // transport // inferred from electronic annotation//0006889 // lipid transport // inferred from electronic annotation
1437870_a	0.001027	-1.33	-1.54	NM_001286560//NM_0261	<i>Enp1c2</i>	ERGIC and golgi 2	0006810 // transport // inferred from electronic annotation//0006888 // ER to Golgi vesicle-mediated transport // inferred from sequence or structural similarity//0006192 // vesicle-
1436397_a	0.000521	-1.34	-1.51	NM_016978	<i>Oat</i>	ornithine aminotransferase	0008152 // metabolic process // inferred from electronic annotation//00042314 // protein hexamerisation // not recorded//00055129 // L-proline biosynthetic process // inferred from
1439814_a	0.003532	-1.34	-1.60	NM_001033746//NM_0214	<i>Prps13//Prps1</i>	phosphoribosyl pyrophosphate synthetase 1-like 3//phosphoribosyl	0006144 // purine nucleobase metabolic process // inferred from electronic annotation//0006164 // purine nucleotide biosynthetic process // inferred from electronic annotation//0006167
1424738_a	0.000825	-1.34	1.03	NM_001039581//NM_0138	<i>Abca3</i>	ATP-binding cassette, sub-family A (ABC1), member 3	0006200 // ATP catabolic process // inferred from electronic annotation//0006810 // transport // not recorded//0008152 // metabolic process // inferred from electronic
1450360_a	0.008946	-1.34	-1.24	NM_172120//NM_0065166	<i>Vps41</i>	vacuolar protein sorting 41 (yeast)	0006810 // transport // inferred from electronic annotation//0006886 // intracellular protein transport // inferred from electronic annotation//0015031 // protein transport // inferred from
1421103_a	0.005575	-1.34	1.17	NM_010657//XM_0065028	<i>Hivep3//LOC102640118</i>	human immunodeficiency virus type 1 enhancer binding protein	0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 // regulation of transcription, DNA-templated // inferred from electronic annotation//00035914 //
1438233_a	0.008012	-1.34	-1.16	NM_173423	<i>Fem1c</i>	fem-1 homolog C (C.elegans)	0016567 // protein ubiquitination // inferred from electronic annotation
1452348_s	0.001411	-1.34	-1.29	NM_009454//XM_0064991	<i>Ube2e3</i>	ubiquitin-conjugating enzyme E2E 3	0016567 // protein ubiquitination // inferred from electronic annotation//0040008 // regulation of growth // inferred from electronic annotation//00070534 // protein K63-linked
1429259_a	0.003487	-1.34	-1.36	NM_153572//XM_0065048	<i>Katnal1//S930430L01Rik</i>	katanin p60 subunit A-like 1//RIKEN cDNA S930430L01 gene	0006200 // ATP catabolic process // inferred from direct assay//0006281 // DNA repair // inferred from electronic annotation//0006310 // DNA recombination // inferred from electronic
1430666_a	0.009070	-1.34	-1.40	NM_010657//XM_0065028	<i>Hivep3</i>	human mobility group box transcription factor 1	0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 // regulation of transcription, DNA-templated // inferred from electronic annotation//0016055 //
1429300_a	0.007896	-1.34	-1.37	NM_008634//XM_0065175	<i>Map1b</i>	microtubule-associated protein 1B	0000226 // microtubule cytoskeleton organization // inferred from electronic annotation//0001578 // microtubule bundle formation // inferred from mutant phenotype//0001578 //
1425991_a	0.000852	-1.34	-1.01	NM_001166397//NM_0012	<i>Armcx2</i>	armadillo repeat containing, X-linked 2	
1422827_x	0.005074	-1.34	-1.10	NM_001048190//NM_0010	<i>Aagl5</i>	ATP/GTP binding protein-like 5	0006508 // proteolysis // inferred from direct assay//0035608 // protein deglutamylation // inferred from direct assay//0035611 // protein branching point deglutamylation // inferred from
1422201_a	0.000782	-1.34	1.13	NM_025974//NR_110499	<i>Rpl14//Rpl14-ps1</i>	ribosomal protein L14//ribosomal protein L14, pseudogene 1	0006364 // rRNA processing // not recorded//0006412 // translation // inferred from electronic annotation//0042273 // ribosomal large subunit biogenesis // not recorded
1429763_a	0.003797	-1.34	-1.09	NM_011279//XM_0065108	<i>Rnf7</i>	ring finger protein 7	0006819 // activation of cysteine-type endopeptidase activity involved in apoptotic process // inferred from direct assay//0008631 // intrinsic apoptotic signaling pathway in response to
1428890_a	0.007952	-1.34	-1.36	NM_011507//XM_0065058	<i>Succlg2</i>	succinate-Coenzyme A ligase, GDP-forming, beta subunit	0006099 // tricarboxylic acid cycle // not recorded//0006104 // succinyl-CoA metabolic process // not recorded//0006305 // succinate metabolic process // not recorded//0008152 //
1422190_a	0.000098	-1.34	1.13	NM_025974//NR_110499	<i>Rpl14//Rpl14-ps1</i>	ribosomal protein L14//ribosomal protein L14, pseudogene 1	0006364 // rRNA processing // not recorded//0006412 // translation // inferred from electronic annotation//0042273 // ribosomal large subunit biogenesis // not recorded
1426694_a	0.001134	-1.34	-1.03	NM_001162918//NM_0255	<i>Ccdc90b</i>	coiled-coil domain containing 90B	
1429621_a	0.009083	-1.34	-1.38	NM_144925//XM_0065077	<i>Tnrc6a</i>	trinucleotide repeat containing 6a	0006417 // regulation of translation // inferred from electronic annotation//0009267 // cellular response to starvation // inferred from direct assay//00031047 // gene silencing by RNA //
1421358_a	0.002944	-1.34	1.16	NM_146040//XM_0065157	<i>Cdca7l</i>	cell division cycle associated 7 like	0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 // regulation of transcription, DNA-templated // inferred from electronic annotation//00082824 //
1428171_a	0.009895	-1.34	-1.07	NM_001163485//NM_0090	<i>Gm12191//Gm5481//Gm610</i>	ribosomal protein L30 pseudogene//predicted gene S481//predicted	0006412 // translation // inferred from electronic annotation
1423830_a	0.007882	-1.34	1.06	NM_009084//NR_030451	<i>Rpl37a//Mir682</i>	ribosomal protein L37a//microRNA 682	0006412 // translation // inferred from electronic annotation
1452521_a	0.004392	-1.35	-1.30	NM_172380//XM_0065220	<i>Poglut1</i>	protein O-glucosyltransferase 1	0006486 // protein glycosylation // inferred from electronic annotation//0006493 // protein O-linked glycosylation // inferred from mutant phenotype//0006493 // protein O-linked
1425418_a	0.003927	-1.35	1.00	NM_198037	<i>Cachd1</i>	cache domain containing 1	0006810 // transport // inferred from electronic annotation//0006811 // ion transport // inferred from electronic annotation//0006816 // calcium ion transport // inferred from electronic
1433883_a	0.007030	-1.35	-1.12	NM_175383	<i>B3gnt1</i>	UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 1	0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 // regulation of transcription, DNA-templated // inferred from electronic annotation//0006486 //
1417779_a	0.007892	-1.35	1.54	NM_146171//XM_0065065	<i>Ncapd2</i>	non-SMC condensin I complex, subunit D2	0007049 // cell cycle // inferred from electronic annotation//0007067 // mitotic nuclear division // inferred from electronic annotation//0007076 // mitotic chromosome condensation // not
1425529_s	0.004482	-1.35	-1.00	NM_001047604//NM_0012	<i>Ttc21b</i>	tetratricopeptide repeat domain 21B	0006357 // regulation of transcription from RNA polymerase II promoter // not recorded//0007224 // smoothened signaling pathway // inferred from mutant phenotype//0005889 //
1428182_a	0.005875	-1.35	-1.07	NM_001163485//NM_0090	<i>Gm12191//Gm5481//Gm610</i>	ribosomal protein L30 pseudogene//predicted gene S481//predicted	0006412 // translation // inferred from electronic annotation
1451905_a	0.000101	-1.35	-1.28	NM_009628//NM_010072	<i>Adnp//Dpm1</i>	activity-dependent neuroprotective protein//dolichol-phosphate (beta-D)	0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 // regulation of transcription, DNA-templated // inferred from electronic annotation//0006486 //
1451441_a	0.009722	-1.35	-1.27	NM_026009	<i>Ccdc47</i>	coiled-coil domain containing 47	0001649 // osteoblast differentiation // not recorded//0006983 // ER overload response // inferred from mutant phenotype//0009790 // embryo development // inferred from mutant
1433922_a	0.000445	-1.35	-1.44	NM_001159516//NM_0011	<i>Qk</i>	quaking	0001570 // vasculogenesis // inferred from mutant phenotype//0006397 // mRNA processing // inferred from electronic annotation//0006417 // regulation of translation // inferred from
1425088_a	0.009241	-1.35	1.01	NM_018179	<i>Rb9</i>	retinitis pigmentosa 9 (human)	0001503 // ossification // inferred from mutant phenotype//0001649 // osteoblast differentiation // inferred from mutant phenotype//0003098 // lymphocyte differentiation // inferred from
1428028_a	0.000446	-1.35	-1.07	NM_001163485//NM_0011	<i>CgB</i>	core binding factor 2	0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 // regulation of transcription, DNA-templated // inferred from electronic annotation//0007399 //
1437808_x	0.000811	-1.35	-1.16	NM_024250//NM_0065249	<i>Phf10//LOC106740</i>	PHD finger protein 10//uncharacterized LOC106740	0000122 // negative regulation of transcription from RNA polymerase II promoter // inferred from direct assay//0006351 // transcription, DNA-templated // inferred from electronic
1424291_a	0.006602	-1.35	1.04	NM_178633//XM_0065161	<i>Ylpm1</i>	YLP motif containing 1	0006629 // lipid metabolic process // inferred from electronic annotation//0006661 // phosphatidylinositol biosynthetic process // not recorded//0008654 // phospholipid biosynthetic
1427495_a	0.000374	-1.35	-1.06	NM_0026638//XM_0065080	<i>Cdpt</i>	CDP-diacylglycerol--inositol 3-phosphatidytransferase (phosphatidylinositol)	0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 // regulation of transcription, DNA-templated // inferred from electronic annotation//0008284 //
1456043_a	0.005082	-1.35	-1.32	NM_01109745//NM_0011	<i>Cnbp</i>	cellular nucleic acid binding protein	0008283 // cell proliferation // not recorded//0003030 // cell projection organization // inferred from electronic annotation//0042384 // cilium assembly // not recorded
1438237_a	0.000139	-1.36	-1.55	NM_027740//XR_380415	<i>Poc1b</i>	POC1 nuclear protein homolog B (Chlamydomonas)	0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 // regulation of transcription, DNA-templated // inferred from electronic annotation//00045944 //
1425683_a	0.002326	-1.36	-1.30	NM_029885//NM_172512	<i>Gabpb2</i>	GA repeat binding protein, beta 2	0000122 // negative regulation of transcription from RNA polymerase II promoter // inferred from direct assay//0006306 // DNA methylation // inferred from direct assay//0006306 // DNA
1426892_a	0.002070	-1.36	-1.04	NM_001271753//NM_0078	<i>Dnmt3a</i>	DNA methyltransferase 3A	
1426813_a	0.006564	-1.36	-1.03	NM_008993	<i>Pxmp2</i>	peroxisomal membrane protein 2	
1420901_a	0.000755	-1.36	1.18	NM_001025602//NM_0012	<i>Il1r1</i>	interleukin 1 receptor-like 1	0002826 // negative regulation of T-helper 1 type immune response // inferred from genetic interaction//0007165 // signal transduction // inferred from electronic annotation//0008285 //
1425902_a	0.001702	-1.36	-1.01	NM_001159536//NM_0011	<i>Adcy3</i>	adenylylate cyclase 3	0006171 // cAMP biosynthetic process // not recorded//0006171 // cAMP biosynthetic process // traceable author statement//0007190 // activation of adenylylate cyclase activity // traceable
1448905_a	0.005665	-1.36	-1.19	NM_025812//XM_0065113	<i>Hmg20a</i>	high mobility group 20A	0000122 // negative regulation of transcription from RNA polymerase II promoter // inferred from mutant phenotype//0006351 // transcription, DNA-templated // inferred from electronic
1455465_a	0.007534	-1.36	-1.99	NM_007705//XM_0065131	<i>Cirp</i>	cold inducible RNA binding protein	0006950 // response to stress // inferred from electronic annotation//0009409 // response to cold // inferred from electronic annotation//0009411 // response to UV // not
1426733_a	0.002449	-1.36	-1.03	NM_017372	<i>Lyx2</i>	lysosome 2	0008152 // metabolic process // inferred from electronic annotation//0016998 // cell wall macromolecule catabolic process // inferred from electronic annotation//0019835 // cytolysis //
1460732_a	0.002706	-1.36	-1.34	NM_001035226//NM_1340	<i>Xpo1</i>	exportin 1, CRM1 homolog (yeast)	0000122 // negative regulation of transcription from RNA polymerase II promoter // not recorded//0006611 // protein export from nucleus // inferred from direct assay//0006611 // protein
1433478_a	0.000898	-1.36	-1.11	NM_009031	<i>Rbbp7</i>	retinoblastoma binding protein 7	0000122 // negative regulation of transcription from RNA polymerase II promoter // inferred from direct assay//0006260 // DNA replication // inferred from electronic annotation//0006338
1439647_a	0.006469	-1.36	-1.58	NM_028003	<i>Rpap3</i>	RNA polymerase II associated protein 3	
1430724_a	0.007411	-1.36	-1.41	NM_175344//NM_207515	<i>Mbn12</i>	muscleblind-like 2	0000381 // regulation of alternative mRNA splicing, via spliceosome // inferred from mutant phenotype//0000381 // regulation of alternative mRNA splicing, via spliceosome // not
1428381_a	0.002376	-1.36	-1.08	NM_001169576//NM_0011	<i>Ube2h</i>	ubiquitin-conjugating enzyme E2H	0008152 // metabolic process // inferred from electronic annotation//0016567 // protein ubiquitination // inferred from electronic annotation//0007936 // protein K48-linked ubiquitination
1426759_a	0.007888	-1.36	-1.03	NM_145625	<i>Ejfb</i>	eukaryotic translation initiation factor 4B	0006412 // translation // inferred from electronic annotation//0006413 // translational initiation // inferred from electronic annotation
1435120_a	0.004030	-1.36	-1.47	NM_145380	<i>Ejfm</i>	eukaryotic translation initiation factor 3, subunit M	0001731 // formation of translation preinitiation complex // inferred from electronic annotation//0002183 // cytoplasmic translational initiation // not recorded//0006412 // translation //
1417695_a	0.001903	-1.36	1.56	NM_001163501//NM_0084	<i>Kcnn4</i>	potassium intermediate/small conductance calcium-activated channel,	0002376 // immune system process // inferred from electronic annotation//0006810 // transport // inferred from electronic annotation//0006811 // ion transport // inferred from electronic
1429889_a	0.001444	-1.36	-1.39	NM_027332//NM_027371	<i>Rpl1</i>	ribosome production factor 1 homolog (S. cerevisiae)	0006364 // rRNA processing // inferred from electronic annotation//0042254 // ribosome biogenesis // inferred from electronic annotation
1440304_a	0.003323	-1.36	-1.61	NM_001008506//NM_0011	<i>Zc3h14</i>	zinc finger CCH type containing 14	
1434191_a	0.000808	-1.37	-1.45	NM_145575//XM_0065053	<i>Cald1</i>	caldesmon 1	
1427911_x	0.004120	-1.37	-1.06	NM_027373//XM_0065040	<i>Afp1</i>	actin filament associated protein 1	
1440815_a	0.001936	-1.37	-1.63	NM_001163029//NM_0011	<i>Cd97</i>	CD97 antigen	
1451596_a	0.000285	-1.37	-1.28	NM_001013380//XM_0065	<i>Dync1l2</i>	dynein, cytoplasmic 1 light intermediate chain 2	
1423271_a	0.000516	-1.37	1.09	NM_009801//XM_0065300	<i>Car2</i>	carbonic anhydrase 2	
1440346_a	0.000179	-1.37	-1.61	NM_033565//XM_0065345	<i>Aff4</i>	AF4/FMR2 family, member 4	
1457759_a	0.002449	-1.37	-1.24	NM_001025192//NM_0012	<i>Cvdr</i>	coccakievirus and adenovirus receptor	
1435157_a	0.005390	-1.37	-1.48	NM_001163018//NM_1991	<i>Suz12</i>	suppressor of zeste 12 homolog (Drosophila)	
1455727_a	0.003591	-1.37	-1.32	NM_008569//XM_0064988	<i>Anapc1</i>	anaphase promoting complex subunit 1	
1451468_s	0.003662	-1.37	-1.27	NM_001166553//NM_0012	<i>Zbed6//Zc3h11a</i>	zinc finger, BED domain containing 6//zinc finger CCH type containing	
1436351_a	0.000184	-1.37	-1.14	NM_011331//NM_045036	<i>Khrb1</i>	KH domain containing, RNA binding, signal transduction associated 1	
1427042_a	0.005399	-1.37	-1.04	NM_001177629//NM_0103	<i>Grb1</i>	growth factor receptor bound protein 10	
1452059_a	0.006341	-1.37	-1.29	NM_001166552//NM_0012	<i>Zbed6//Zc3h11a</i>	zinc finger, BED domain containing 6//zinc finger CCH type containing	
1449976_a	0.000785	-1.37	-1.23	NM_144880	<i>Ppp2r5a</i>	protein phosphatase 2, regulatory subunit B, alpha	
1460416_s	0.001373	-1.38	-1.34	NM_02424396//NM_2072	<i>Jmjd1c</i>	jumonji domain containing 1C	
1439121_a	0.002420	-1.38	-1.16	NM_001025375//NM_0010	<i>Wdr61</i>	WD repeat domain 61	
1417808_a	0.002078	-1.38	1.53	NM_181416	<i>Arhgap11a</i>	Rho GTPase activating protein 11A	
1421967_a	0.002485	-1.38	1.14	NM_009091//XM_0065133	<i>Rps15</i>	ribosomal protein S15	
1428421_a	0.008117	-1.38	-1.08	NM_025915	<i>Tmem88</i>	transmembrane protein 88	
1428922_a	0.001119	-1.38	-1.08	NM_001033167//XM_0065	<i>Scl22a23</i>	solute carrier family 22, member 23	
1424369_a	0.000529	-1.38	1.04	NM_010681	<i>Lama4</i>	laminin, alpha 4	
1426970_a	0.000531	-1.38	-1.04	NM_027192	<i>Tti</i>	tubulin tyrosine ligase	
1437510_x	0.003141	-1.38	-1.16	NM_009741//NM_177410	<i>Bcl2</i>	B cell leukemia/lymphoma 2	

Table S7

Gene ID	p (Corr)	FC-RSV 1 d	FC-RSV 5 d	RefSeq Transcript ID	Gene Symbol	Gene Title	Gene Ontology Biological Process
1421772_a	0.000511	-1.38	1.14	NM_001002239//NM_0011	Gm10362//Gm6133//Hk11	predicted gene 10362//60S ribosomal protein L17	0001678 // cellular glucose homeostasis // not recorded//0002931 // response to ischemia // not recorded//0005975 // carbohydrate metabolic process // inferred from electronic annotation
1443206_a	0.007388	-1.38	-1.70	NM_026470//XM_0065033	Spato6e	spermatogenesis associated 6	0007275 // multicellular organismal development // inferred from electronic annotation//0007283 // spermatogenesis // inferred from electronic annotation//0030154 // cell differentiation
1437634_a	0.004925	-1.38	-1.16	NM_021280	Pkg1	phospholipase C, gamma 1	001701 // in utero embryonic development // inferred from mutant phenotype//0006629 // lipid metabolic process // inferred from electronic annotation//0006816 // calcium ion transport
1427919_a	0.005868	-1.38	-1.06	NM_001130149//NM_0267	Drasha	drospha, ribonuclease type III	0006396 // RNA processing // inferred from electronic annotation//0010468 // regulation of gene expression // inferred from mutant phenotype//0010586 // miRNA metabolic process //
1426952_a	0.002092	-1.38	-1.04	NM_178681//XM_0065150	Dgkb	diacylglycerol kinase, beta	0007205 // protein kinase C-activating G-protein coupled receptor signaling pathway // inferred from electronic annotation//0008152 // metabolic process // inferred from electronic
1424101_a	0.000511	-1.38	1.05	NM_023645//XM_0064962	Kdelc1	KDEL (Lys-Asp-Glu-Leu) containing 1	
1438838_a	0.009049	-1.38	-1.56	NM_001282000//NM_0012	Rbl2	retinoblastoma-like 2	0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 // regulation of transcription, DNA-templated // inferred from electronic annotation//0006357 //
1421927_a	0.002544	-1.38	-1.14	NM_009976	Cst3	cystatin C	0001654 // eye development // inferred from electronic annotation//0001666 // response to hypoxia // inferred from electronic annotation//0001775 // cell activation // inferred from
1451229_a	0.008466	-1.38	-1.27	NM_025522	Dhrs7	dehydrogenase/reductase (SDR family) member 7	0008152 // metabolic process // inferred from electronic annotation//0055114 // oxidation-reduction process // inferred from electronic annotation
1451815_a	0.004239	-1.39	-1.28	NM_001290743//NM_2134	Cnot6	CCR4-NOT transcription complex, subunit 6	0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 // regulation of transcription, DNA-templated // inferred from electronic annotation//0006417 //
1417041_a	0.008046	-1.39	-1.85	NM_001025364//NM_0136	Rtn2	reticulon 2 (Z-band associated protein)	0046324 // regulation of glucose import // inferred from mutant phenotype//0065002 // intracellular protein transmembrane transport // inferred from mutant phenotype
1436829_a	0.009275	-1.39	-1.52	NM_057172//XM_0065016	Fubp1	far upstream element (FUSE) binding protein 1	0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 // regulation of transcription, DNA-templated // inferred from electronic annotation//0006366 //
1433549_a	0.001466	-1.39	-1.11	NM_025630	Aggl1	angiogenic factor with G patch and FHA domains 1	0001525 // angiogenesis // inferred from electronic annotation//0001938 // positive regulation of endothelial cell proliferation // not recorded//0007155 // cell adhesion // not
1428968_a	0.006075	-1.39	-1.36	NM_019973//NM_178880/	Son	Son DNA binding protein	0000226 // microtubule cytoskeleton organization // not recorded//0000910 // cytokinesis // not recorded//0006351 // transcription, DNA-templated // inferred from electronic
1436347_a	0.006230	-1.39	-1.51	NM_008133	Glud1	glutamate dehydrogenase 1	0006520 // cellular amino acid metabolic process // inferred from electronic annotation//0006537 // glutamate biosynthetic process // not recorded//0006538 // glutamate catabolic process
1427044_a	0.004548	-1.39	-1.04	NM_001085355//XM_0065	Arid1b	AT rich interactive domain 18 (SWI-like)	
1435574_a	0.004957	-1.39	-1.49	NM_001081045//XM_0065	Kansl1	KAT8 regulatory NSL complex subunit 1	0016568 // chromatin modification // inferred from electronic annotation//0043981 // histone H4-K5 acetylation // not recorded//0043982 // histone H4-K8 acetylation // not
1421240_a	0.004859	-1.39	1.16	NM_001160399	Ccdc112	coiled-coil domain containing 112	
1434991_a	0.000591	-1.39	-1.47	NM_001282055//NM_1459	Ddx46	DEAD (Asp-Glu-Ala-Asp) box polypeptide 46	0006200 // ATP catabolic process // inferred from electronic annotation//0006397 // mRNA processing // inferred from electronic annotation//0008152 // metabolic process // inferred from
1418345_a	0.008896	-1.39	1.40	NM_175406	Atp6Vdd2	ATPase, H+ transporting, lysosomal V0 subunit D2	0006810 // transport // inferred from electronic annotation//0006811 // ion transport // inferred from electronic annotation//0015991 // ATP hydrolysis coupled proton transport // inferred
1431591_a	0.000609	-1.39	-1.10	NM_145604//XM_0065308	Riken	cDNA D230025D16 gene	0043001 // Golgi to plasma membrane protein transport // not recorded
1435237_a	0.004429	-1.39	-1.48	NM_012024//XM_0065159	Ppp2r5e	protein phosphatase 2, regulatory subunit B', epsilon	0007165 // signal transduction // inferred from electronic annotation//0005790 // regulation of catalytic activity // inferred from electronic annotation
1428835_a	0.001560	-1.39	-1.08	NM_177171//XM_0065160	Heatr5a	HEAT repeat containing 5A	
1429030_a	0.008639	-1.39	-1.36	NM_001029895//NM_0011	Ate1	arginyltransferase 1	0016598 // protein arginylation // inferred from direct assay
1449366_a	0.000918	-1.39	-1.22	NM_146001//XM_0065044	Hsp1	huntingtin interacting protein 1	0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 // regulation of transcription, DNA-templated // inferred from electronic annotation//0006897 //
1421326_a	0.005740	-1.39	1.16	NM_175473//XM_0065348	Frs1	Fraser syndrome 1 homolog (human)	0002099 // morphogenesis of an epithelium // inferred from mutant phenotype//0003338 // metamorphosis morphogenesis // inferred from mutant phenotype//0007154 // cell
1435529_a	0.002373	-1.39	-1.49	NM_145507//NM_177445	Dars	aspartyl-tRNA synthetase	0006412 // translation // inferred from electronic annotation//0006418 // tRNA aminoacylation for protein translation // inferred from electronic annotation//0006422 // aspartyl-tRNA
1460716_a	0.001715	-1.39	-1.34	NM_181584	Gab3	growth factor receptor bound protein 2-associated protein 3	0030225 // macrophage differentiation // inferred from direct assay
1426350_a	0.006891	-1.39	-1.02	NM_001081213//NM_1460	Emp1	endoplasmic reticulum xoloopetide 1	0001541 // ovarian follicle development // not recorded//0006508 // proteolysis // inferred from electronic annotation//0008152 // metabolic process // inferred from electronic annotation
1418254_a	0.006513	-1.39	1.42	NM_181821//XM_0065244	Hcfc1r1	host cell factor C1 regulator 1 (XP01-dependent)	
1435518_a	0.007865	-1.39	-1.13	NM_177271	Samd5	sterile alpha motif domain containing 5	
1426716_a	0.000970	-1.40	-1.03	NM_001033399//XM_0065	Gfod1	glucose-fructose oxidoreductase domain containing 1	0008152 // metabolic process // inferred from electronic annotation//0055114 // oxidation-reduction process // inferred from electronic annotation
1450649_a	0.002126	-1.40	-1.24	NM_009105//XM_0064974	Rsu1	Ras suppressor protein 1	0007265 // Ras protein signal transduction // inferred from mutant phenotype//0000179 // positive regulation of neural precursor cell proliferation // inferred from genetic interaction
1433724_a	0.007340	-1.40	-1.11	NM_024198	Gpx7	glutathione peroxidase 7	0006979 // response to oxidative stress // inferred from electronic annotation//0055114 // oxidation-reduction process // not recorded
1448194_a	0.007268	-1.40	-1.17	NM_001026211//NM_0012	Dnajc19//Dnajc19-ps	Dna1 (Hsp40) homolog, subfamily C, member 19//Dna1 (Hsp40) homolog,	0006810 // transport // inferred from electronic annotation//0007601 // visual perception // not recorded//0015031 // protein transport // inferred from electronic annotation//0048806 //
1435930_a	0.002005	-1.40	-1.50	NM_146016//XM_0065146	Em16	echinoderm microtubule associated protein like 6	
1449880_a	0.005753	-1.40	-1.22	NM_199143//XM_0065063	Znf2	zinc and ring finger 2	0016567 // protein ubiquitination // inferred from electronic annotation//0016567 // protein ubiquitination // ...
1420614_a	0.000529	-1.40	1.19	NM_026376	Plexn1	plexin D1	0001525 // angiogenesis // inferred from mutant phenotype//0001569 // patterning of blood vessels // inferred from mutant phenotype//0003151 // outflow tract morphogenesis // inferred
1427294_a	0.006223	-1.40	-1.05	NM_001205082//NM_0012	Scarb1	scavenger receptor class B, member 1	0001935 // endothelial cell proliferation // inferred from mutant phenotype//0002221 // pattern recognition receptor signaling pathway // not recorded//0006702 // androgen biosynthetic
1430700_a	0.001930	-1.40	-1.10	NM_008661//NM_201600/	Myo5b	myosin VB	0006810 // transport // inferred from electronic annotation//0008152 // metabolic process // inferred from electronic annotation//0015031 // protein transport // not recorded//0016192
1423364_a	0.007364	-1.40	-1.08	NM_009658//NR_028271//	Akr1b3//Gm6644	aldo-keto reductase family 1, member B3 (aldose reductase)//Akr1b3	0001894 // tissue homeostasis // not recorded//0005996 // monosaccharide metabolic process // not recorded//0006061 // sorbitol biosynthetic process // not recorded//0009414 //
1438727_a	0.000885	-1.40	-1.56	NM_008891	Pnn	pilin	0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 // regulation of transcription, DNA-templated // inferred from electronic annotation//0006397 //
1421135_a	0.005360	-1.40	-1.17	NM_025793	Tmem223	transmembrane protein 223	0004005 // RNA export from nucleus // inferred from direct assay//0006406 // mRNA export from nucleus // not recorded//0006406 // mRNA export from nucleus // inferred from electronic
1421450_a	0.003093	-1.40	1.15	NM_001045489//NM_0085	Mlfg6	milk fat globule-EGF factor 8 protein	0001525 // angiogenesis // inferred from electronic annotation//0006910 // phagocytosis, recognition // inferred from direct assay//0006911 // phagocytosis, engulfment // inferred from
1423091_a	0.008300	-1.40	1.09	NM_001166597//NM_1383	Dgkz	diacylglycerol kinase zeta	0007205 // protein kinase C-activating G-protein coupled receptor signaling pathway // inferred from electronic annotation//0008152 // metabolic process // inferred from electronic
1439920_a	0.002257	-1.41	-1.60	NM_001101478	D3Erd254e	DNA segment, Chr 3, ERATO Doi 254, expressed	0006355 // regulation of transcription, DNA-templated // not recorded
1429485_a	0.007913	-1.41	-1.09	NM_020252//NM_177284/	Nrxn1	neurxin 1	0001525 // angiogenesis // inferred from electronic annotation//0006904 // vesicle docking involved in exocytosis // not recorded//0007155 // cell adhesion // inferred from electronic
1421225_a	0.006744	-1.41	1.16	NM_001291159//NM_0295	Rph3a1	rabphilin 3A-like (without C2 domains)	0006886 // intracellular protein transport // inferred from electronic annotation//0006887 // exocytosis // inferred from electronic annotation//0007158 // regulation of calcium ion-
1425927_a	0.001456	-1.41	-1.01	NM_009148//XM_0065058	Exoc4	exocyst complex component 4	0006612 // protein targeting to membrane // not recorded//0006810 // transport // inferred from electronic annotation//0006887 // exocytosis // inferred from electronic
1423155_a	0.001466	-1.41	1.09	NR_045265	Toposors	topoisomerase I binding, arginine/serine-rich, opposite strand	
1449909_a	0.008424	-1.41	-1.22	NM_001204915//NM_1786	Reep3	receptor accessory protein 3	0006998 // nuclear envelope organization // not recorded//0007049 // cell cycle // inferred from electronic annotation//0007067 // mitotic nuclear division // inferred from electronic
1438629_a	0.002058	-1.41	-1.16	NM_027168//XM_0065128	Hddc2	HD domain containing 2	0008152 // metabolic process // inferred from electronic annotation
1428231_a	0.007401	-1.41	-1.34	NM_133352	Tm9sf3	transmembrane 9 superfamily member 3	
1425298_a	0.002107	-1.41	-1.29	NM_028603//XM_0065370	Zbtb8a	zinc finger and BTB domain containing 8a	0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 // regulation of transcription, DNA-templated // inferred from electronic annotation
1421747_a	0.007645	-1.41	-1.14	NM_181072//XM_0065114	Myo1e	myosin IE	0001570 // vasculogenesis // inferred from mutant phenotype//0001701 // in utero embryonic development // inferred from mutant phenotype//0001822 // kidney development // inferred
1425398_a	0.007560	-1.41	-1.12	NM_007840//XM_0065321	Ddx5	DEAD (Asp-Glu-Ala-Asp) box polypeptide 5	0001022 // negative regulation of transcription by RNA polymerase II promoter // not recorded//0003381 // regulation of alternative mRNA splicing, via spliceosome // not
1422573_a	0.000465	-1.41	-1.29	NM_010189//XM_0065406	Fcgrt	Fc receptor, IgG, alpha chain transporter	0001916 // positive regulation of T cell mediated cytotoxicity // inferred from electronic annotation//0002416 // IgG immunoglobulin transcytosis in epithelial cells mediated by FcRn
1435304_a	0.006566	-1.41	-1.13	NM_028194//NM_177136/	Fryl	furry homolog-like (Drosophila)	
1422866_a	0.004525	-1.41	1.10	NM_001300//XR_140756//	Gm7285//Rps7	predicted gene 7285//ribosomal protein S7	0001843 // neural tube closure // inferred from mutant phenotype//0002181 // cytoplasmic translation // not recorded//0006364 // rRNA processing // not recorded//0006412 //
1446500_a	0.009433	-1.41	-1.78	NM_025698	Tmed7	transmembrane emp24 protein transport domain containing 7	0006810 // transport // inferred from electronic annotation
1427348_a	0.001018	-1.41	-1.05	NM_001038700//NM_0011	Fbnp1	formin binding protein 1	0006897 // endocytosis // inferred from electronic annotation//0007165 // signal transduction // inferred from electronic annotation//0007399 // nervous system development // not
1423523_a	0.007759	-1.41	1.08	NM_010729	Lwd1	lysyl oxidase-like 1	0055114 // oxidation-reduction process // inferred from direct assay
1424142_a	0.004408	-1.41	1.05	NM_023133//XM_0065396	Rps19//Rps19-ps3	ribosomal protein S19//ribosomal protein S19, pseudogene 3	0000028 // ribosomal small subunit assembly // not recorded//0004062 // maturation of SSU-rRNA from tritricrion rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA) // not
1417243_a	0.000726	-1.41	1.75	NM_001172092//NM_0011	Depdc1a	DEP domain containing 1A	0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 // regulation of transcription, DNA-templated // inferred from electronic annotation//0007165 //
1433612_a	0.000925	-1.41	-1.11	NM_00170694//NM_1340	Rcctb2	regulator of chromosome condensation (RCC1) and BTB (POZ) domain	
1450746_a	0.003105	-1.41	-1.25	NM_001024622//XM_0065	Pcnp	PEST proteolytic signal containing nuclear protein	0007049 // cell cycle // inferred from electronic annotation//0016567 // protein ubiquitination // not recorded//0043161 // proteasome-mediated ubiquitin-dependent protein catabolic
1452408_a	0.000215	-1.42	-1.29	NM_001190357//NM_0012	Carkd	carbohydrate kinase domain containing	0046496 // nicotinamide nucleotide metabolic process // inferred from electronic annotation
1439098_a	0.000770	-1.42	-1.57	NM_001160219//NM_0011	Pum2	pumilio RNA-binding family member 2	0006417 // regulation of translation // inferred from electronic annotation//0004063 // stress granule assembly // inferred from direct assay//0034063 // stress granule assembly // not
1439644_a	0.002796	-1.42	-1.58	NM_016700//XM_0065190	Mapk8	mitogen-activated protein kinase 8	0001503 // ossification // inferred from mutant phenotype//0006355 // regulation of transcription, DNA-templated // not recorded//0006468 // protein phosphorylation // inferred from
1430841_a	0.006744	-1.42	-1.41	NM_008774	Pabp1	poly(A) binding protein, cytoplasmic 1	0000184 // nuclear-transcribed mRNA catabolic process, nonsense-mediated decay // inferred from electronic annotation//0006397 // mRNA processing // inferred from electronic
1423665_a	0.00180	-1.42	1.07	NM_001277898//NM_0088	Prkaca	protein kinase, cAMP dependent, catalytic, alpha	0001707 // mesoderm formation // inferred from genetic interaction//0001843 // neural tube closure // inferred from genetic interaction//0006468 // protein phosphorylation // inferred
1428799_a	0.003305	-1.42	-1.36	NM_175380	Gpd1l	glycerol-3-phosphate dehydrogenase 1-like	0002027 // regulation of heart rate // not recorded//0005975 // carbohydrate metabolic process // inferred from electronic annotation//0006072 // glycerol-3-phosphate metabolic process
1431114_a	0.002037	-1.42	-1.41	NM_152809//XM_0065262	Csnk1g3	casein kinase 1, gamma 3	0006468 // protein phosphorylation // not recorded//0016055 // Wnt signaling pathway // inferred from electronic annotation//0016310 // phosphorylation // inferred from electronic
1426844_a	0.001748	-1.42	-1.04	NM_001128094//NM_0011	Atp13a3	ATPase type 13A3	0006200 // ATP catabolic process // inferred from electronic annotation//0006812 // cation transport // inferred from electronic annotation//0008152 // metabolic process // inferred from
1454268_a	0.003154	-1.42	-1.31	NM_015771//NM_153382/	Lmts2//Xpo4	large tumor suppressor 2//exportin 4	0000082 // G1/S transition of mitotic cell cycle // inferred from direct assay//0000082 // G1/S transition of mitotic cell cycle // not recorded//0006468 // protein phosphorylation // inferred
142715_a	0.006346	-1.42	1.11	NM_019730//NM_023260	Mtpp34//Nme3	mitochondrial ribosomal protein S34//NME/NUM23 nucleoside diphosphate	0006165 // nucleoside diphosphate phosphorylation // inferred from electronic annotation//0006163 // GTP biosynthetic process // inferred from electronic annotation//0006228 // UTP
1416939_a	0.006721	-1.43	1.91	NM_001012335//NM_0010	Mdk	midkine	0001662 // behavioral fear response // inferred from mutant phenotype//0007275 // multicellular organismal development // inferred from electronic annotation//0007614 // short-term
1420104_a	0.009239	-1.43	1.22	NM_001080967//NM_2072	Tmsb15b2//Tmsb15l	thymosin beta 15b2/thymosin beta 15b like	0007010 // cytoskeleton organization // inferred from electronic annotation//00030036 // actin cytoskeleton organization // inferred from electronic annotation//0030837 // negative
1439718_a	0.002164	-1.43	-1.59	NM_026218//XM_0065070	Fgfr1ap2	FGFR1 oncogene partner 2	0009611 // response to wounding // inferred from electronic annotation//0042060 // wound healing // inferred from mutant phenotype
1429564_a	0.000890	-1.43	-1.38	NM_177662	Ctso	cathepsin O	0006508 // proteolysis // inferred from electronic annotation
1445212_a	0.009205	-1.43	-1.76	NM_010485//XM_0065086	Elavl1	ELAV (embryonic lethal, abnormal vision)-like 1 (Hu antigen R)	0006417 // regulation of translation // not recorded//0045727 // positive regulation of translation // inferred from direct assay//0045727 // positive regulation of translation // inferred from
1428837_a	0.008191	-1.43	-1.36	NM_133710//XM_0065122	Ctdspl	CTD (carboxy-terminal domain, RNA polymerase II, polypeptide A) small	0008152 // metabolic process // inferred from electronic annotation//0016311 // dephosphorylation // inferred from electronic annotation
1435123_a	0.000764	-1.43	-1.47	NM_017381	Zranb2	zinc finger, RAN-binding domain containing 2	0006397 // mRNA processing // inferred from electronic annotation//0008380 // RNA splicing // inferred from electronic annotation
1451054_a	0.000195	-1.43	-1.26	NM_001039214	Mex3c	mex3 homolog C (C. elegans)	0003415 // chronodromy hypertrophy // inferred from mutant phenotype//0008152 // metabolic process // inferred from electronic annotation//0045598 // regulation of fat cell
1426861_a	0.001095	-1.43	-1.04	NM_026503	1110058L19Rik	RIKEN cDNA 1110058L19 gene	0045087 // innate immune response // inferred from mutant phenotype
1433846_a	0.001114	-1.43	-1.44	NM_020575//XM_0064999	42436	membrane-associated ring finger (C3HC4) 7	0016567 // protein ubiquitination // inferred from electronic annotation
1439151_a	0.005238	-1.43	-1.57	NM_007307//XM_0065126	Gprc6a	G protein-coupled receptor, family C, group 6, member A	0007165 // signal transduction // inferred from electronic annotation//0007186 // G-protein coupled receptor signaling pathway // inferred from direct assay//0019722 // calcium-mediated
1422764_a	0.002876	-1.43	1.10	NM_016763	Hsd17b10	hydroxysteroid (17-beta) dehydrogenase 10	0008033 // rRNA processing // inferred from electronic annotation//0008152 // metabolic process // inferred from electronic annotation//0051289 // protein homotrimerization // not

Table S7

Gene ID	p (Corr)	FC-RSV 1 d	FC-RSV 5 d	RefSeq Transcript ID	Gene Symbol	Gene Title	Gene Ontology Biological Process
1428221_a	0.002507	-1.43	-1.34	NM_009172//NM_009173	<i>Siah1a</i> // <i>Siah1b</i>	seven in absentia 1A//seven in absentia 1B	0006511 // ubiquitin-dependent protein catabolic process // not recorded//0006511 // ubiquitin-dependent protein catabolic process // inferred from electronic annotation//0006915 //
1424902_a	0.002126	-1.43	1.02	NM_001267710//NM_0012	<i>Eef2k</i>	eukaryotic elongation factor-2 kinase	0006414 // translational elongation // traceable author statement//0006468 // protein phosphorylation // inferred from direct assay//0016310 // phosphorylation // inferred from electronic
1442805_a	0.001733	-1.43	-1.69	NM_001039388//NM_0010	<i>Wdr37</i>	WD repeat domain 37	
1424235_a	0.001965	-1.43	1.05	NM_138743	<i>Smm11</i>	small integral membrane protein 11	
1423025_a	0.004058	-1.43	-1.10	NM_001146022//XM_0065	<i>Wdfy4</i>	WD repeat and FYVE domain containing 4	
1427944_a	0.008343	-1.43	-1.06	NM_027127//XM_0065177	<i>Gpx8</i>	glutathione peroxidase 8 (putative)	0006979 // response to oxidative stress // inferred from electronic annotation//0055114 // oxidation-reduction process // not recorded
1425225_a	0.002802	-1.43	1.01	NM_145853//XR_387565//	<i>Tpcn1</i>	two pore channel 1	0006810 // transport // inferred from electronic annotation//0006811 // ion transport // inferred from electronic annotation//0006816 // calcium ion transport // not recorded//0034220 //
1421127_a	0.004850	-1.43	1.17	NM_009933	<i>Col6a1</i>	collagen, type VI, alpha 1	0001649 // osteoblast differentiation // not recorded//0007155 // cell adhesion // inferred from electronic annotation//0007208 // protein heterotrimerization // not recorded//0071230 //
1423657_a	0.007859	-1.43	1.07	NM_008908	<i>Ppic</i>	peptidylprolyl isomerase C	0004113 // protein peptidyl-prolyl isomerization // inferred from electronic annotation//0006457 // protein folding // inferred from electronic annotation
1436095_a	0.002420	-1.43	-1.15	NM_019806	<i>Vspg</i>	vesicle-associated membrane protein, associated protein B and C	0006874 // cellular calcium ion homeostasis // not recorded//0006986 // response to unfolded protein // inferred from electronic annotation//0006987 // activation of signaling protein
1419155_a	0.000169	-1.44	1.30	NM_001167920//NM_0804	<i>Skba3</i>	solute carrier family 8 (sodium/calcium exchanger), member 3	0002244 // hematopoietic progenitor cell differentiation // inferred from mutant phenotype//0006814 // sodium ion transport // not recorded//0006816 // calcium ion transport // inferred
1436736_x	0.000198	-1.44	-1.15	NM_007711//NM_173873	<i>Ckn3</i>	chloride channel 3	0006810 // transport // inferred from electronic annotation//0006811 // ion transport // not recorded//0006821 // chloride transport // not recorded//0034220 // ion transmembrane
1426505_a	0.004618	-1.44	-1.02	NM_145580//NM_170760	<i>Igfr1</i> // <i>U2af1</i>	IGF-like family receptor 1//U2 small nuclear RNA auxiliary factor 1-like 4	0006397 // mRNA processing // inferred from electronic annotation//0008380 // RNA splicing // inferred from electronic annotation
1448609_a	0.009173	-1.44	-1.18	NM_011650	<i>Tsn</i>	translin	0008152 // metabolic process // inferred from electronic annotation//0090305 // nucleic acid phosphodiester bond hydrolysis // inferred from electronic annotation
1450043_a	0.000417	-1.44	-1.23	NM_018859//XM_0065164	<i>Akr1e1</i>	aldo-keto reductase family 1, member E1	0055114 // oxidation-reduction process // inferred from electronic annotation
1423612_a	0.009618	-1.44	1.07	NM_144796//XM_0064970	<i>Susd4</i>	sushi domain containing 4	
1427747_a	0.001119	-1.44	-1.06	NM_029564//NM_016738	<i>Tax1bp3</i> // <i>Rpl13</i>	Tax1 (human T cell leukemia virus type I) binding protein 3//ribosomal	0007266 // Rho protein signal transduction // not recorded//0008285 // negative regulation of cell proliferation // inferred from direct assay//0016055 // Wnt signaling pathway // inferred
1423131_a	0.002126	-1.44	1.09	NM_008492//XM_0065069	<i>Ldhb</i>	lactate dehydrogenase B	0005975 // carbohydrate metabolic process // inferred from electronic annotation//0006089 // lactate metabolic process // not recorded//0006096 // glycolytic process // inferred from
1420408_a	0.000224	-1.44	1.21	NM_010216//XM_0065287	<i>Fgf1</i>	c-fos induced growth factor	0001525 // angiogenesis // inferred from electronic annotation//0007275 // multicellular organismal development // inferred from electronic annotation//0008283 // cell proliferation //
1444668_a	0.006337	-1.44	-1.14	NM_145420//XM_0065134	<i>Ube2d1</i>	ubiquitin-conjugating enzyme E2D 1	0000209 // protein polyubiquitination // inferred from direct assay//0000209 // protein polyubiquitination // not recorded//0006511 // ubiquitin-dependent protein catabolic process // not
1420801_a	0.005989	-1.44	1.19	NM_001025310//NM_0010	<i>St6galnac6</i>	ST6 (alpha-N-acetyl-neuraminyl-2,3-beta-galactosyl-1,3)-N-	0001574 // ganglioside biosynthetic process // inferred from direct assay//0006486 // protein glycosylation // inferred from electronic annotation//0006677 // glycosylceramide metabolic
1435076_a	0.001982	-1.44	-1.47	NM_021510//XM_0065338	<i>Hmnp1</i>	heterogeneous nuclear ribonucleoprotein H1	0006397 // mRNA processing // inferred from electronic annotation//0008380 // RNA splicing // inferred from electronic annotation//0043484 // regulation of RNA splicing // not recorded
1428378_a	0.001297	-1.44	-1.34	NM_019739	<i>Foxo1</i>	forkhead box O1	0000122 // negative regulation of transcription from RNA polymerase II promoter // inferred from direct assay//0001568 // blood vessel development // inferred from mutant
1424942_a	0.008628	-1.44	1.02	NM_172145//XM_0065030	<i>Eva1b</i>	eva-1 homolog B (C. elegans)	
1448977_a	0.006469	-1.44	-1.23	NM_001290527//NM_1339	<i>Pwp1</i>	PC4 and SFRS1 interacting protein 1	0000395 // mRNA 5'-splice site recognition // not recorded//0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 // regulation of transcription, DNA-
1416921_x	0.008628	-1.44	1.94	NM_021790//NM_181051	<i>Cenpk</i>	centromere protein K	0045944 // positive regulation of transcription from RNA polymerase II promoter // inferred from direct assay
1460224_a	0.005861	-1.44	-1.33	NM_021299//XM_0065272	<i>Ak3</i>	adenylylate kinase 3	0006139 // nucleobase-containing compound metabolic process // inferred from electronic annotation//0006172 // ADP biosynthetic process // not recorded//0006756 // AMP
1423790_a	0.003613	-1.44	1.06	NM_175128//XM_0065140	4930430F08Rik	RIKEN cDNA 4930430F08 gene	0002244 // hematopoietic progenitor cell differentiation // inferred from genetic interaction
1425422_a	0.008511	-1.44	1.00	NM_030075//XM_0065118	<i>Klhdcb8</i>	kelch domain containing 8B	
1418448_a	0.005238	-1.44	1.39	NM_177688	<i>H2afj</i>	H2A histone family, member J	0006334 // nucleosome assembly // inferred from electronic annotation
1437028_a	0.004050	-1.44	-1.15	NM_198014//XM_0065183	<i>Slain1</i>	SLAIN motif family, member 1	
1441242_a	0.001831	-1.44	-1.64	NM_007610//XM_0065054	<i>Casp2</i>	caspase 2	
1430500_x	0.004599	-1.45	-1.10	NM_178772	<i>Nche1</i>	neutral cholesterol ester hydrolase 1	
1428711_a	0.007466	-1.45	-1.35	NM_009458//XM_0065331	<i>Ube2b</i>	ubiquitin-conjugating enzyme E2B	
1460196_a	0.002719	-1.45	-1.33	NM_017367//XM_0065347	<i>Ccni</i>	cyclin I	
1455134_a	0.004762	-1.45	-1.32	NM_011767//XM_0065200	<i>Zfr</i>	zinc finger RNA binding protein	
1436822_x	0.000963	-1.45	-1.15	NM_001081098	<i>Zfp362</i>	zinc finger protein 362	
1433850_a	0.009359	-1.45	-1.12	NM_001164497//NM_0011	<i>Popd5</i>	PAP associated domain containing 5	
1448244_a	0.008843	-1.45	-1.17	NM_033521	<i>Laptm4b</i>	lysosomal-associated protein transmembrane 4B	
1453486_a	0.000158	-1.45	-1.31	NM_001165902//NM_0076	<i>Ctnnb1</i>	catenin (cadherin associated protein), beta 1	
1450791_a	0.000657	-1.45	-1.25	NM_030708//XM_0065301	<i>Zfxv4</i>	zinc finger homeodomain 4	
1434006_a	0.005915	-1.45	-1.44	NM_027448//NM_029434	<i>Lcd3</i>	Leber congenital amaurosis 5 (human)	
1450744_a	0.002065	-1.45	-1.45	NM_029850	<i>Bcl7a</i>	B cell CLL/lymphoma 7A	
1428952_a	0.001179	-1.45	-1.36	NM_026375//XM_0064968	<i>Ahtc1</i>	AT hook containing transcription factor 1	
1430718_x	0.001963	-1.45	-1.10	NM_011943//XM_0065333	<i>Map2k6</i>	mitogen-activated protein kinase kinase 6	
1433461_a	0.007916	-1.45	-1.11	NM_144897//XM_0065015	<i>Apoa1bp</i>	apolipoprotein A1-binding protein	
1437408_a	0.003838	-1.45	-1.53	NM_011896//XM_0065354	<i>Spry1</i>	sprouty homolog 1 (Drosophila)	
1428847_a	0.000169	-1.45	-1.08	NM_028761//XM_0065226	<i>Parn</i>	poly(A)-specific ribonuclease (deadenylation nuclease)	
1450757_a	0.000361	-1.46	-1.25	NM_172448//XM_0065327	<i>Rnf43</i>	ring finger protein 43	
1457438_a	0.002724	-1.46	-2.20	NM_008222//XM_0065287	<i>Hccs</i>	holocytochrome c synthetase	
1453266_a	0.001509	-1.46	-1.48	NM_011277//XM_0065292	<i>Rnf2</i> // <i>LOC102640476</i>	ring finger protein 2//uncharacterized LOC102640476	
1454755_a	0.001054	-1.46	-1.96	NM_016985//XM_0065281	<i>Mtmr1</i>	myotubularin related protein 1	
1427982_x	0.005486	-1.46	-1.06	NM_178600//XM_0065079	<i>Vkar1</i>	vitamin K epoxide reductase complex, subunit 1	
1424783_a	0.004054	-1.46	1.02	NM_001081204//XM_0065	<i>Bglct1</i>	beta-3-glucosyltransferase	
1439647_a	0.006469	-1.46	-1.59	XR_387722//XR_387723//	763040204Rik// <i>Zfp626</i>	RIKEN cDNA 763040204 gene//zinc finger protein 626	
1449243_a	0.000726	-1.46	-1.21	NM_001291890//NM_0012	<i>Adam19</i>	a disintegrin and metalloproteinase domain 19 (meltrin beta)	
1440557_a	0.000020	-1.46	-1.62	NM_172827	<i>Lnppe</i>	leucyl/cystinyl aminopeptidase	
1421074_a	0.000252	-1.46	-1.17	NM_197999//XM_0065313	<i>Ces2g</i>	carboxylesterase 2G	
1430656_a	0.003699	-1.46	-1.10	NM_001036684//NM_0097	<i>Atp2b2</i>	ATPase, Ca++ transporting, plasma membrane 2	
1442214_a	0.008781	-1.46	-1.67	NM_007754	<i>Cpd</i>	carboxypeptidase D	
1423339_a	0.006931	-1.46	-1.42	NM_019635//XM_0065201	<i>Shk3</i>	serine/threonine kinase 3	
1425398_a	0.002771	-1.46	1.00	NM_144521//XM_0065340	<i>Snap47</i>	synaptosomal-associated protein, 47	
1452672_a	0.004652	-1.46	-1.87	NM_001172098//NM_0529	<i>Strn3</i>	stratin, calmodulin binding protein 3	
1432273_a	0.000768	-1.46	-1.11	NM_173379	<i>Leprel1</i>	leprecan-like 1	
1428667_a	0.002042	-1.46	-1.08	NM_010657//XM_0065028	<i>Hvep3</i> // <i>LOC102640118</i>	human immunodeficiency virus type I enhancer binding protein	
1451695_a	0.001760	-1.46	-1.28	NM_029148	<i>Tmx4</i>	thioredoxin-related transmembrane protein 4	
1451655_a	0.003002	-1.46	-1.28	NM_207659//XM_0065091	<i>Hook3</i>	hook homolog 3 (Drosophila)	
1433711_x	0.009722	-1.46	-1.11	NM_028242//NM_029371	<i>Httatf1</i>	HIV TAT specific factor 1	
1449118_a	0.006654	-1.46	-1.20	NM_001039179//NM_0010	<i>Bicd2</i>	bicaudal D homolog 2 (Drosophila)	
1451320_a	0.000680	-1.47	-1.27	NM_001164198//NM_0011	<i>Prkab</i>	protein kinase, cAMP dependent, catalytic, beta	
1423282_a	0.003991	-1.47	1.08	NM_001164216//NM_0011	<i>Romo1</i>	reactive oxygen species modulator 1	
1449540_a	0.000972	-1.47	-1.22	NM_001135577	<i>Smm13</i>	small integral membrane protein 13	
1418612_a	0.000972	-1.47	1.36	NM_023186	<i>Chia1</i>	chitinase, acidic 1	
1435903_a	0.002906	-1.47	-1.14	NM_009919//XM_0065185	<i>Cnih1</i>	cornichon homolog 1 (Drosophila)	
1455743_a	0.005290	-1.47	-2.02	NM_016966//XM_0065112	<i>Tromod3</i>	tropomodulin 3	
1433494_a	0.008220	-1.47	-1.11	NM_011001	<i>Prkca</i>	protein kinase C, alpha	
1417669_a	0.002543	-1.47	1.57	NM_173405	<i>Amn2</i>	archaelysin family metalloproteinase 1	
1434872_x	0.000369	-1.47	-1.13	NM_029979	<i>Trim35</i>	tripartite motif-containing 35	
1450476_a	0.006638	-1.47	-1.24	NM_001145952//NM_0011	<i>Lpp</i>	LIM domain containing preferred translocation partner in lipoma	
1450966_a	0.002192	-1.47	-1.25	NM_133648//NM_133649	<i>Slc12a6</i>	solute carrier family 12, member 6	
1444026_a	0.008022	-1.47	-1.72	NM_011894//XM_0065190	<i>Sh3bp5</i>	SH3 domain binding protein 5 (BTK-associated)	
1423911_a	0.006659	-1.47	1.06	NM_008437	<i>Napsa</i>	napsin A aspartic peptidase	
1436172_a	0.000525	-1.47	-1.14	NM_001253822//NM_0083	<i>Irx3</i>	Iroquois related homeobox 3	
1432235_a	0.002878	-1.48	-1.10	NM_009437	<i>Tst</i>	thiosulfate sulfurtransferase, mitochondrial	
1426210_x	0.000447	-1.48	-1.01	NM_025912//XM_0065000	<i>Fam210b</i>	family with sequence similarity 210, member B	
1426738_a	0.001667	-1.48	-1.03	NM_001081286//XM_0065	<i>Fat1</i>	FAT tumor suppressor homolog 1 (Drosophila)	
1451098_a	0.007107	-1.48	-1.26	NM_001099785//NM_0012	<i>D3Ertd751e</i>	DNA segment, Chr 3, ERATO Doi 751, expressed	
1453467_x	0.007064	-1.48	-1.31	NM_009260//NM_175836	<i>Sptbn1</i>	spectrin beta, non-erythrocytic 1	

Table S7

Gene ID	p (Corr)	FC-RSV 1 d	FC-RSV 5 d	RefSeq Transcript ID	Gene Symbol	Gene Title	Gene Ontology Biological Process
1423220_a	0.002604	-1.48	1.09	NM_194339//XM_0065058	Bms1	BMS1 homolog, ribosome assembly protein (yeast)	0006184 // GTP catabolic process // inferred from electronic annotation//0042254 // ribosome biogenesis // inferred from electronic annotation
1460351_a	0.009082	-1.48	-1.33	NM_001252313//NM_0113	Ncor1	nuclear receptor co-repressor 1	0001122 // negative regulation of transcription from RNA polymerase II promoter // inferred from genetic interaction//0000122 // negative regulation of transcription from RNA polymerase II
1449968_s	0.002543	-1.48	-1.23	NM_172630//XM_0065258	Mppe1	metallophosphoesterase 1	0006506 // GPI anchor biosynthetic process // inferred from electronic annotation//0006810 // transport // inferred from electronic annotation//0006888 // ER to Golgi vesicle-mediated
1423088_a	0.007210	-1.48	1.09	NM_001145884//NM_0105	Itgb5	integrin beta 5	0007155 // cell adhesion // inferred from electronic annotation//0007229 // integrin-mediated signaling pathway // inferred from electronic annotation//0007275 // multicellular organismal
1439519_a	0.007056	-1.48	-1.58	NM_001159349//NM_0272	Fyttd1	forty-two-three domain containing 1	0006406 // mRNA export from nucleus // not recorded//0006810 // transport // inferred from electronic annotation//00051028 // mRNA transport // inferred from electronic annotation
1428895_a	0.000311	-1.48	-1.08	NM_175268//NM_212473	Fams3b	family with sequence similarity 53, member B	
1427076_a	0.002933	-1.48	-1.05	NM_020031//NM_027044	Pfdn5	prefoldin 5	0006457 // protein folding // inferred from electronic annotation//00045892 // negative regulation of transcription, DNA-templated // not recorded//00060041 // retina development in camera-
1428728_a	0.003708	-1.49	-1.08	NM_022423	Rnf187	ring finger protein 187	0008284 // positive regulation of cell proliferation // inferred from mutant phenotype//0016567 // protein ubiquitination // inferred from electronic annotation//00043161 // proteasome-
1439529_a	0.007812	-1.49	-1.58	NM_008668//XM_0064954	Lyp1a1	lysophosphatase 1	0002084 // protein deamidation // inferred from mutant phenotype//0006629 // lipid metabolic process // inferred from electronic annotation//0006631 // fatty acid metabolic process
1431079_a	0.000255	-1.49	-1.41	NM_0012851//NM_0012	Cnot6l	CCR4-NOT transcription complex, subunit 6-like	0000288 // nuclear-transcribed mRNA catabolic process, deadenylation-dependent decay // inferred from mutant phenotype//0006351 // transcription, DNA-templated // inferred from
1426682_a	0.009281	-1.49	-1.03	NM_00115942//NM_0011	Ccdc58	coiled-coil domain containing 58	
1453238_s	0.006633	-1.49	-1.31	NM_001205367//NM_0098	42620	septin 7	0007049 // cell cycle // inferred from electronic annotation//0007067 // mitotic nuclear division // inferred from electronic annotation//0016476 // regulation of embryonic cell shape //
1437019_a	0.000008	-1.49	-1.53	NM_001289826//NM_0077	Clock	circadian locomotor output cycles kaput	0000077 // DNA damage checkpoint // not recorded//0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 // regulation of transcription, DNA-templated
1443154_a	0.001333	-1.49	-1.70	NM_025283//XM_0064957	Mob4	MOB family member 4, p40	0006810 // transport // inferred from electronic annotation
1430245_a	0.002056	-1.49	-1.39	NM_026499	Srsf6	serine/arginine-rich splicing factor 6	0003080 // alternative mRNA splicing, via spliceosome // not recorded//0000381 // regulation of alternative mRNA splicing, via spliceosome // not recorded//0006376 // mRNA splice site
1435280_a	0.000185	-1.49	-1.48	NM_027453//XM_0065093	Btf3l4	basic transcription factor 3-like 4	
1449517_a	0.002002	-1.49	-1.22	NM_001013392//NM_0010	Rreb1	ras responsive element binding protein 1	0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 // regulation of transcription, DNA-templated // inferred from electronic annotation//00045892 //
1459478_a	0.000238	-1.49	-1.33	NM_024189//NR_028315//	Yaf2	YY1 associated factor 2	0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 // regulation of transcription, DNA-templated // inferred from electronic annotation//00045892 //
1441987_a	0.005587	-1.49	-1.66	NM_008682//XM_0065133	Nedd1	neuronal precursor cell expressed, developmentally down-regulated gene 1	0007019 // microtubule depolymerization // not recorded//0007049 // cell cycle // inferred from electronic annotation//0007067 // mitotic nuclear division // inferred from electronic
1423780_a	0.006493	-1.49	1.06	NM_013535	Grcx10	gene rich cluster, C10 gene	
1439046_a	0.008738	-1.49	-1.57	NM_133832	Rdh10	retinol dehydrogenase 10 (all-trans)	0001656 // metanephros development // inferred from mutant phenotype//0001701 // in utero embryonic development // inferred from mutant phenotype//0002138 // retinoic acid
1451777_a	0.000161	-1.49	-1.28	NM_019995//XM_0065018	Supt20	suppressor of Ty 20	0007275 // multicellular organismal development // inferred from electronic annotation//0007369 // gastrulation // inferred from electronic annotation//0005948 // positive regulation of
1437628_s	0.004134	-1.49	-1.16	NM_001005847//NM_0012	Aga	aspartylglucosaminidase	0006508 // proteolysis // inferred from electronic annotation//0006517 // protein deglycosylation // not recorded//00051604 // protein maturation // inferred from direct assay
1420682_a	0.006526	-1.49	-1.19	NM_013902	Fkbp3	FK506 binding protein 3	0000413 // protein peptidyl-prolyl isomerization // not recorded//0006457 // protein folding // inferred from electronic annotation//0018208 // peptidyl-proline modification // not
1459557_a	0.001132	-1.49	2.74	NM_007714//XM_0065321	CK4	CDC like kinase 4	0006468 // protein phosphorylation // inferred from electronic annotation//0016310 // phosphorylation // inferred from electronic annotation//0018108 // peptidyl-tyrosine phosphorylation
1431689_a	0.000710	-1.49	-1.42	NM_009758//XM_0065184	Bmp1a	bone morphogenetic protein 1 receptor, type 1A	0001701 // in utero embryonic development // inferred from mutant phenotype//0001707 // mesoderm formation // inferred from mutant phenotype//0001756 // somitogenesis // inferred
1426901_s	0.007961	-1.50	-1.04	NM_001081981//NM_0010	Nfix	nuclear factor IX	0000122 // negative regulation of transcription from RNA polymerase II promoter // inferred from direct assay//0000122 // negative regulation of transcription from RNA polymerase II
1448106_a	0.001954	-1.50	-1.17	NM_001161369//NM_0011	Ss18	synovial sarcoma translocation, Chromosome 18	0000226 // microtubule cytoskeleton organization // inferred from direct assay//0000902 // cell morphogenesis // inferred from direct assay//0000902 // cell morphogenesis // inferred from
1428135_a	0.003043	-1.50	-1.07	NM_134052	Ad1l	acireductone dihydrogenase 1	0006355 // regulation of transcription, DNA-templated // inferred from electronic annotation//0008652 // cellular amino acid biosynthetic process // inferred from electronic
1454733_a	0.000861	-1.50	-1.96	NM_030257//XM_0065174	Lysmd3	LysM, putative peptidoglycan-binding, domain containing 3	0016998 // cell wall macromolecule catabolic process // inferred from electronic annotation
1448325_a	0.007191	-1.50	-1.17	NM_001122667//NM_1535	Mkl2	MKL/myocardin-like 2	0001701 // in utero embryonic development // inferred from mutant phenotype//0001889 // liver development // inferred from mutant phenotype//0003007 // heart morphogenesis //
1427512_a	0.000056	-1.50	-1.06	NM_019647//XM_0014802	Gm12045//Gm11703//Gm13	predicted pseudogene 10045//predicted gene 11703//predicted gene	0006412 // translation // inferred from electronic annotation
1437882_s	0.009844	-1.50	-1.16	NM_021552	Nso2	NSA2 ribosome biogenesis homolog (S. cerevisiae)	0006364 // rRNA processing // inferred from electronic annotation//0042254 // ribosome biogenesis // inferred from electronic annotation
1454862_a	0.009237	-1.50	-1.32	NM_001024512//NM_0011	Fam149b	family with sequence similarity 149, member B	
1434762_a	0.000684	-1.50	-1.46	NM_0011173//XM_0065029	Ybx1	Y box protein 1	0000122 // negative regulation of transcription from RNA polymerase II promoter // inferred from direct assay//0000122 // negative regulation of transcription from RNA polymerase II
1418191_a	0.000021	-1.50	1.43	NM_007737	Col5a2	collagen, type V, alpha 2	0001501 // skeletal system development // inferred from mutant phenotype//0003199 // collagen fibril organization // inferred from mutant phenotype//0003199 // collagen fibril
1442448_a	0.009770	-1.50	-1.68	NM_177806//XM_0065160	Prpf39	PRP39 pre-mRNA processing factor 39 homolog (yeast)	0006396 // RNA processing // inferred from electronic annotation//0006397 // mRNA processing // inferred from electronic annotation//0008380 // RNA splicing // inferred from electronic
1433992_a	0.008278	-1.50	-1.44	NM_001190322//NM_0011	Chchd7	coiled-coil-helix-coiled-coil-helix domain containing 7	
1498860_a	0.000218	-1.50	-1.22	NM_025314	Dtd1	D-tyrosyl-tRNA deacylase 1	0006260 // DNA replication // inferred from electronic annotation//0019478 // D-amino acid catabolic process // inferred from electronic annotation
1439493_a	0.002884	-1.50	-1.58	NM_001110327//NM_0118	Dmrtf1	cyclin D binding myb-like transcription factor 1	0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 // regulation of transcription, DNA-templated // inferred from electronic annotation//0007049 //
1430483_a	0.000628	-1.50	-1.18	NM_001042779//NM_0012	Sema3b	sema domain, immunoglobulin domain (lg), short basic domain, secreted,	0007275 // multicellular organismal development // inferred from electronic annotation//0007399 // nervous system development // inferred from electronic annotation//00030154 // cell
1448561_a	0.000935	-1.50	-1.10	NM_028572//XM_0065230	Vg1a3	vestigial like 3 (Drosophila)	0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 // regulation of transcription, DNA-templated // inferred from electronic annotation
1431749_a	0.000525	-1.50	-1.10	NM_019975//XM_0065193	Hsd1l	2-hydroxyacyl-CoA lyase 1	0001561 // fatty acid alpha-oxidation // not recorded//0006629 // lipid metabolic process // inferred from direct assay//0006631 // fatty acid metabolic process // inferred from electronic
1440562_a	0.008996	-1.50	-1.62	NM_007422//XM_0064966	Adis	adenylsuccinate synthetase, non muscle	0006164 // purine nucleotide biosynthetic process // inferred from direct assay//0006167 // AMP biosynthetic process // inferred from direct assay//0006167 // AMP biosynthetic process //
1439827_a	0.003572	-1.51	-1.60	NM_144825//XM_0065329	Tao1k1	TAD kinase 1	0000165 // MAPK cascade // not recorded//0000186 // activation of MAPK activity // not recorded//0006281 // DNA repair // inferred from electronic annotation//0006468 // protein
1438815_a	0.004659	-1.51	-1.56	NM_001199265//NM_0135	Epb4.1l2	erythrocyte protein band 4.1-like 2	0008360 // regulation of cell shape // inferred from sequence or structural similarity//0003036 // actin cytoskeleton organization // inferred from sequence or structural similarity//0003086
1425052_a	0.000555	-1.51	1.01	NM_029116//XM_0065089	Kbtbd11	kelch repeat and BTB (POZ) domain containing 11	
1406255_a	0.004143	-1.51	-1.33	NM_145494//XM_0065254	Me2	malic enzyme 2, NAD(+)-dependent, mitochondrial	0006108 // malate metabolic process // inferred from electronic annotation//0008152 // metabolic process // inferred from electronic annotation//0005114 // oxidation-reduction process //
1431705_a	0.000277	-1.51	-1.10	NM_201518//XM_0065160	Flrt2	fibronectin leucine rich transmembrane protein 2	0007411 // axon guidance // inferred from genetic interaction//0005919 // negative chemotaxis // inferred from direct assay//0001222 // regulation of neuron migration // inferred from
1451804_a	0.001111	-1.51	-1.28	NM_001190401//XM_0065	Usp34	ubiquitin specific peptidase 34	0006508 // proteolysis // not recorded//0006511 // ubiquitin-dependent protein catabolic process // inferred from electronic annotation//0016055 // Wnt signaling pathway // inferred from
1450318_a	0.008987	-1.51	-1.24	NM_146090//XM_0065264	Zadhd2	zinc binding alcohol dehydrogenase, domain containing 2	0005114 // oxidation-reduction process // inferred from electronic annotation
1426916_a	0.003779	-1.51	-1.04	NM_008388	Elf3e	eukaryotic translation initiation factor 3, subunit E	0000184 // nuclear-transcribed mRNA catabolic process, nonsense-mediated decay // not recorded//0006412 // translation // inferred from electronic annotation//0006413 // translational
1435741_a	0.001425	-1.51	-1.49	NM_025904	Yae1d1	Yae1 domain containing 1	
1423754_a	0.000087	-1.51	1.06	NM_010882	Ndn	neadin	0001558 // regulation of cell growth // traceable author statement//0001764 // neuron migration // inferred from mutant phenotype//0003016 // respiratory system process // inferred from
1424838_a	0.005254	-1.51	1.02	NM_018801//NM_173067//	Syt7	synaptotagmin VII	0001778 // plasma membrane repair // inferred from direct assay//0006810 // transport // inferred from electronic annotation//0006887 // exocytosis // inferred from electronic
1452595_a	0.00034	-1.51	-1.30	NM_022996//XM_0065261	Ndfip1	NEDD5 family interacting protein 1	0002761 // regulation of myeloid leukocyte differentiation // inferred from mutant phenotype//0002829 // negative regulation of type 2 immune response // inferred from mutant
1423068_a	0.003048	-1.51	-1.10	NM_025654//XM_0065339	Rdm1	RasD2 motif 1	0006281 // DNA repair // inferred from electronic annotation//0006310 // DNA recombination // inferred from electronic annotation
1453913_a	0.001650	-1.51	-1.31	NM_025797	Cy6b5a	cytochrome b5 type A (microsomal)	0006631 // fatty acid metabolic process // inferred by curator//0006810 // transport // inferred from electronic annotation//0006468 // response to cadmium ion // inferred from electronic
1451715_a	0.000016	-1.51	-1.28	NM_026417	Yipf4	Yip1 domain family, member 4	
1426983_a	0.003040	-1.51	-1.04	NM_008986	Prif	polymerase I and transcript release factor	0006351 // transcription, DNA-templated // inferred from electronic annotation//0006353 // DNA-templated transcription, termination // inferred from electronic annotation//0006355 //
1417552_a	0.002257	-1.52	1.61	NM_001290477//NM_0012	Khv4	kelch-like 4	
1449360_a	0.007489	-1.52	-1.22	NM_026420	Pap2	DNA segment, Chr 14, ERATO Del 725, expressed	
1423254_s	0.006583	-1.52	1.09	NM_172994//XM_0065039	Ppp2r2c	protein phosphatase 2, regulatory subunit B, gamma	0007165 // signal transduction // inferred from electronic annotation//00050790 // regulation of catalytic activity // inferred from electronic annotation
1429527_a	0.008066	-1.52	-1.09	NM_001145900//NM_2016	Btdb6	BTB (POZ) domain containing 6	
1436033_a	0.004652	-1.52	-1.50	NM_001033432//XM_0065	Heca	headcase homolog (Drosophila)	
1437741_a	0.002135	-1.52	-1.16	NM_029881//XM_0065129	Tmem200a	transmembrane protein 200A	
1440483_a	0.001594	-1.52	-1.62	NM_011399	Sks2a17	solute carrier family 25 (mitochondrial carrier, peroxisomal membrane	0006635 // fatty acid beta-oxidation // not recorded//0006810 // transport // inferred from electronic annotation//0015866 // ADP transport // not recorded//0015867 // ATP transport //
1424099_a	0.005185	-1.52	1.05	NM_001081071//NM_0011	Lclat1	lysate carrier family 25 (mitochondrial carrier, peroxisomal membrane	0006629 // lipid metabolic process // inferred from electronic annotation//0007275 // multicellular organismal development // inferred from electronic annotation//0008152 // metabolic
1400637_a	0.002825	-1.52	-1.40	NM_028848//NM_029067//	Spatol17	spermatogenesis associated 17	
1425907_s	0.003374	-1.52	-1.01	NM_001293641//NM_1461	Poa2	pyrophosphatase (inorganic)	0006796 // phosphate-containing compound metabolic process // inferred from electronic annotation//0016311 // dephosphorylation // inferred from direct assay
1430943_a	0.006417	-1.52	-1.41	NM_016796//XM_0064969	Vamp4	vesicle-associated membrane protein 4	0006887 // exocytosis // not recorded//0006897 // endocytosis // not recorded//0006906 // vesicle fusion // not recorded//00016192 // vesicle-mediated transport // inferred from
1452737_a	0.006655	-1.52	-1.87	NM_001164231//NM_0275	Pwmp2a	PWWP domain containing 2A	
1426239_s	0.003272	-1.52	-1.02	NM_021534//XM_0064999	Pxmp4	peroxisomal membrane protein 4	
1429310_a	0.003103	-1.52	-1.37	NM_026420	Pap2	polyadenylate-binding protein-interacting protein 2	0006417 // regulation of translation // inferred from mutant phenotype//0007283 // spermatogenesis // inferred from mutant phenotype//0007613 // memory // inferred from mutant
1428327_a	0.009068	-1.53	-1.08	NM_012044//XM_0065310	Brd7	bromodomain containing 7	0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 // regulation of transcription, DNA-templated // inferred from electronic annotation//0006357 //
1448781_a	0.008147	-1.53	-1.19	NM_010901//XM_0065307	Nfyc3	nuclear factor of activated T cells, cytoplasmic, calcineurin dependent 3	0001569 // patterning of blood vessels // inferred from genetic interaction//0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 // regulation of
1426302_a	0.007972	-1.53	-1.02	NM_207232//XM_0065169	Ptpdc1	protein tyrosine phosphatase domain containing 1	0006470 // protein dephosphorylation // inferred from electronic annotation//0007224 // smoothened signaling pathway // inferred from mutant phenotype//0016311 // dephosphorylation
1428905_a	0.008598	-1.53	-1.08	NM_144919//XM_0065059	Hdac11	histone deacetylase 11	0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 // regulation of transcription, DNA-templated // inferred from electronic annotation//0014003 //
1460348_a	0.000713	-1.53	-1.33	NM_001081050//XM_0064	Pard3b	par-3 family cell polarity regulator beta	0007049 // cell cycle // inferred from electronic annotation//00051301 // cell division // inferred from electronic annotation
1452362_a	0.004089	-1.53	-1.29	NM_025707//XM_0065161	Khv28	kelch-like 28	
1458943_a	0.000302	-1.53	-2.51	NM_006544168	LOC102643033	zinc finger protein OZF-like	0006355 // regulation of transcription, DNA-templated // not recorded//0006355 // regulation of transcription, DNA-templated // --
1453092_a	0.000021	-1.53	-1.31	NM_181322//XM_0065306	Ctcf	CCCTC-binding factor	0000122 // negative regulation of transcription from RNA polymerase II promoter // inferred from mutant phenotype//0006306 // DNA methylation // inferred from direct assay//0006306 //
1439528_a	0.001146	-1.53	-1.58	NM_145517	Ormd1	ORM1-like 1 (S. cerevisiae)	0006672 // ceramide metabolic process // not recorded
1449962_a	0.001733	-1.53	-1.23	NM_198295	Tmx3	thioredoxin-related transmembrane protein 3	0006457 // protein folding // not recorded//0006662 // glycerol ether metabolic process // inferred from electronic annotation//0034976 // response to endoplasmic reticulum stress // not
1422397_a	0.000270	-1.53	1.12	NM_001199357//NM_0011	Tmem164	transmembrane protein 164	
1444174_a	0.005672	-1.53	-1.72	NM_026665//NR_037622//	Cep57	centrosomal protein 57	0000060 // protein import into nucleus, translocation // inferred from mutant phenotype//0007286 // spermatid development // inferred from expression pattern//0008543 // fibroblast
1427994_a	0.000910	-1.53	-1.06	NM_198170//XM_0065030	Szt2	seizure threshold 2	0007417 // central nervous system development // inferred from mutant phenotype//0009790 // embryo development // inferred from mutant phenotype//0009791 // post-embryonic
1430801_a	0.003419	-1.53	-1.41	NM_144931//XM_0065308	Nae1	NEDB8 activating enzyme E1 subunit 1	0006915 // apoptotic process // inferred from electronic annotation//0007049 // cell cycle // inferred from electronic annotation//0008152 // metabolic process // inferred from electronic

Table S7

Gene ID	p (Corr)	FC-RSV 1 d	FC-RSV 5 d	RefSeq Transcript ID	Gene Symbol	Gene Title	Gene Ontology Biological Process
1451439_a	0.006670	-1.54	-1.27	NM_001013391//XM_0065	<i>Cpsf6</i>	cleavage and polyadenylation specific factor 6	0006378 // mRNA polyadenylation // not recorded//0006397 // mRNA processing // not recorded//0051262 // protein tetramerization // not recorded
1454042_a	0.000932	-1.54	-1.31	NM_001017955//XM_0065	<i>Zscan18</i>	zinc finger and SCAN domain containing 18	0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 // regulation of transcription, DNA-templated // inferred from electronic annotation//0006357 //
1449449_a	0.000265	-1.54	-1.22	NM_007496//XM_0065305	<i>Zfxh3</i>	zinc finger homeobox 3	0000122 // negative regulation of transcription from RNA polymerase II promoter // not recorded//0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355
1450672_a	0.000465	-1.54	-1.25	NM_001282967//NM_0135	<i>Elk3</i>	ELK3, member of ETS oncogene family	0001525 // angiogenesis // inferred from mutant phenotype//0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 // regulation of transcription, DNA-
1442270_a	0.008256	-1.54	-1.67	NM_007929//XM_0065217	<i>Emp2</i>	epithelial membrane protein 2	0001954 // positive regulation of cell-matrix adhesion // not recorded//2001046 // positive regulation of integrin-mediated signaling pathway // inferred from mutant phenotype//2001046 //
1436281_a	0.005980	-1.54	-1.50	NM_001039483//NM_0268	<i>Tmco1</i>	transmembrane and coiled-coil domains 1	
1452674_a	0.007532	-1.54	-1.30	NM_028058	<i>Fundc1</i>	FUN1 domain containing 1	0000422 // mitochondrion degradation // not recorded//0001666 // response to hypoxia // not recorded//0006914 // autophagy // inferred from electronic annotation
1425888_a	0.000628	-1.54	-1.01	NM_008211//XM_0065010	<i>Hadh</i>	hydroxyacyl-Coenzyme A dehydrogenase	0006629 // lipid metabolic process // inferred from electronic annotation//000663 // fatty acid metabolic process // inferred from electronic annotation//0006635 // fatty acid beta-
1450820_a	0.002160	-1.54	-1.25	NM_029333//XM_0065412	<i>Akap13</i>	A kinase (PRK) anchor protein 13	0006468 // protein phosphorylation // inferred from electronic annotation//0010611 // regulation of cardiac muscle hypertrophy // not recorded//0016310 // phosphorylation // inferred
1438930_a	0.006655	-1.54	-1.44	NM_177092//XM_0065137	<i>Mrb3</i>	methionine sulfinate oxidoreductase B3	0006979 // response to oxidative stress // inferred from electronic annotation//0030091 // protein repair // not recorded//0030091 // protein repair // inferred from sequence or structural
1451191_a	0.009656	-1.54	-1.26	NM_026029//XM_0065339	<i>Glod4//Gemin4//Gm6330</i>	glyoxalase domain containing 4//gem (nuclear organelle) associated	0000387 // spliceosomal snRNP assembly // not recorded
1432068_a	0.009281	-1.54	-1.10	NM_001277121//NM_0012	<i>Hmnp1</i>	heterogeneous nuclear ribonucleoprotein R	
1439999_a	0.008993	-1.54	-1.61	NM_001081975//NM_0262	<i>Mfap1a//Mfap1b//LOC1026</i>	microfibrillar-associated protein 1A//microfibrillar-associated protein	
1423133_a	0.007746	-1.54	1.09	NM_182805//XM_0065215	<i>Gpt</i>	glutamic pyruvic transaminase, soluble	0009058 // biosynthetic process // inferred from electronic annotation//0042853 // L-alanine catabolic process // inferred from electronic annotation
1448757_a	0.000931	-1.54	-1.19	NM_026817//XM_0065213	<i>Rab12</i>	RAB, member RAS oncogene family-like 2	0006184 // GTP catalytic process // inferred from electronic annotation//0006886 // intracellular protein transport // inferred from electronic annotation//0006913 // nucleocytoplasmic
1434848_a	0.002359	-1.54	-1.47	NM_019771	<i>Dstn</i>	desmin	0000910 // cytokinesis // inferred from mutant phenotype//0006928 // cellular component movement // inferred from mutant phenotype//0030042 // actin filament depolymerization //
1424965_a	0.009199	-1.54	1.02	NM_011359	<i>Sftpc</i>	surfactant associated protein C	0007585 // respiratory gaseous exchange // inferred from electronic annotation//0007623 // circadian rhythm // inferred from electronic annotation//0009725 // response to hormone //
1447983_a	0.001013	-1.54	-1.17	NM_001013026//XM_0065	<i>Tcf2</i>	transcription termination factor, RNA polymerase II	0006200 // ATP catalytic process // inferred from electronic annotation//0006351 // transcription, DNA-templated // inferred from electronic annotation//0006353 // DNA-templated
1426884_a	0.006921	-1.54	-1.04	NM_153103//XM_0065323	<i>Klf1c</i>	krasin family member 1C	0006890 // retrograde vesicle-mediated transport, Golgi to ER // inferred from direct assay//0007018 // microtubule-based movement // inferred from electronic annotation//0008152 //
1429195_a	0.000628	-1.54	-1.36	NM_008885//XM_0065324	<i>Pmp22</i>	peripheral myelin protein 22	0007049 // cell cycle // inferred from electronic annotation//0007050 // cell cycle arrest // inferred from electronic annotation//0008285 // negative regulation of cell proliferation // not
1448906_a	0.009487	-1.54	-1.19	NM_01159496//NM_0011	<i>Pom1b</i>	protein phosphatase 1B, magnesium dependent, beta isoform	0006470 // protein dephosphorylation // inferred from mutant phenotype//0006470 // protein dephosphorylation // not recorded//0006499 // N-terminal protein myristoylation // inferred
1429049_a	0.002746	-1.54	-1.36	NM_011630//XM_0065059	<i>Nr2c2</i>	nuclear receptor subfamily 2, group C, member 2	0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 // regulation of transcription, DNA-templated // inferred from electronic annotation//0007283 //
1433665_a	0.006155	-1.54	-1.11	NM_029022//XM_0065003	<i>Scn3</i>	scnecrin 3	0006508 // proteolysis // inferred from electronic annotation
1449091_a	0.007569	-1.55	-1.20	NM_139063//XM_0065165	<i>Bloc1s5</i>	biogenesis of lysosomal organelles complex-1, subunit 5, mutated	0008089 // anterograde axon cargo transport // inferred from mutant phenotype//0016192 // vesicle-mediated transport // inferred from mutant phenotype//0031175 // neuron projection
1438714_a	0.002095	-1.55	-1.16	NM_001081156//XM_0065	<i>Tmp1</i>	TMF1-regulated nuclear protein 1	0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 // regulation of transcription, DNA-templated // inferred from electronic annotation//0007049 //
1419963_a	0.004570	-1.55	1.23	NM_031877//XM_0065129	<i>Wajf1</i>	WAS protein family, member 1	0016601 // Rac protein signal transduction // not recorded//0030036 // actin cytoskeleton organization // inferred from electronic annotation//0072673 // lamellipodium morphogenesis //
1451172_a	0.003272	-1.55	-1.26	NM_001114338//NM_0012	<i>Ccp1</i>	cell cycle progression 1	0007049 // cell cycle // inferred from electronic annotation//0008284 // positive regulation of cell proliferation // not recorded//0045787 // positive regulation of cell cycle // not
1449152_a	0.007339	-1.55	-1.20	NM_008715//XM_0065186	<i>Ints6</i>	integrator complex subunit 6	0016180 // snRNA processing // not recorded
1424433_a	0.006163	-1.55	1.04	NM_025403	<i>Nop10</i>	NOP10 ribonucleoprotein	0001522 // pseudouridine synthesis // inferred from electronic annotation//0006364 // rRNA processing // inferred from electronic annotation//0042254 // ribosome biogenesis // inferred
1431225_a	0.001134	-1.55	-1.42	NM_016867	<i>Gipc2</i>	GPCR PDZ domain containing family, member 2	
1433549_a	0.001466	-1.55	-1.11	NM_001146222//NM_0011	<i>Dpy30</i>	dpy-30 homolog (C. elegans)	0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 // regulation of transcription, DNA-templated // inferred from electronic annotation//0016197 //
1426941_a	0.004800	-1.55	-1.04	NM_001163427//NM_0285	<i>Pradc1</i>	protease-associated domain containing 1	
1449127_a	0.007669	-1.55	-1.20	NM_198022//XM_0065331	<i>Tnrc6c</i>	trinucleotide repeat containing 6C	0001706 // endoderm formation // inferred from mutant phenotype//0006417 // regulation of translation // inferred from electronic annotation//0007492 // endoderm development //
1440406_a	0.002314	-1.55	-1.62	NM_009481//XM_0065275	<i>Usp9x</i>	ubiquitin specific peptidase 9, X chromosome	0001701 // in utero embryonic development // inferred from genetic interaction//0001764 // neuron migration // inferred from mutant phenotype//0006508 // proteolysis // inferred from
1438097_a	0.003039	-1.55	-1.16	NM_001252442//NM_1534	<i>Phldb2</i>	pleckstrin homology-like domain, family B, member 2	
1428034_a	0.002608	-1.55	-1.07	NM_001033298//XM_0064	<i>Kiz</i>	kizuna centrosomal protein	0007051 // spindle organization // not recorded
1436310_a	0.004084	-1.55	-1.50	NM_025822//XM_0065019	<i>Rsrc1</i>	arginine/serine-rich coiled-coil 1	0000380 // alternative mRNA splicing, via spliceosome // inferred from direct assay//0000398 // mRNA splicing, via spliceosome // not recorded//0006397 // mRNA processing // inferred
1451026_a	0.002047	-1.55	-1.26	NM_175465//XM_0064992	<i>Sest1</i>	SEC14 and spectrin domains 1	
1428530_a	0.001355	-1.55	-1.08	NM_011543//XM_0065327	<i>Skp1a</i>	S-phase kinase-associated protein 1A	0006511 // ubiquitin-dependent protein catabolic process // inferred by curator//0016567 // protein ubiquitination // inferred by curator//0016567 // protein ubiquitination // not
1448493_a	0.009355	-1.55	-1.18	NM_026079//XR_390319	<i>Ikbkap</i>	inhibitor of kappa light polypeptide enhancer in B cells, kinase complex-	0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 // regulation of transcription, DNA-templated // inferred from electronic annotation//0006357 //
1423474_a	0.002437	-1.55	-1.08	NM_001111016//NM_1752	<i>Nav2</i>	neuron navigator 2	0003025 // regulation of systemic arterial blood pressure by baroreceptor feedback // inferred from mutant phenotype//0007399 // nervous system development // not recorded//0007605
144586_a	0.002745	-1.55	-1.62	NM_009071//XM_0065257	<i>Rck1</i>	Rho-associated coiled-coil containing protein kinase 1	0003383 // apical constriction // inferred from genetic interaction//0006468 // protein phosphorylation // not recorded//0006915 // apoptotic process // inferred from electronic
1434743_a	0.007908	-1.55	-1.13	NM_026166//NM_027078	<i>Ikbip</i>	IKBKB interacting protein	
1452612_a	0.002309	-1.55	-1.31	NM_029665//XM_0065177	<i>Ipo11</i>	importin 11	0006610 // ribosomal protein import into nucleus // inferred from direct assay//0006810 // transport // inferred from electronic annotation//0006886 // intracellular protein transport //
1426563_a	0.005476	-1.56	-1.03	NM_0011339	<i>Cxcl15</i>	chemokine (C-X-C motif) ligand 15	0006935 // chemotaxis // inferred from direct assay//0006954 // inflammatory response // inferred from direct assay//0006955 // immune response // inferred from electronic
1451755_a	0.007879	-1.56	-1.28	NM_001048147//NM_0010	<i>Ghr</i>	growth hormone receptor	0000187 // activation of MAPK activity // not recorded//0000255 // allantoin metabolic process // inferred from mutant phenotype//0006301 // citrate metabolic process // inferred from
1428966_a	0.001733	-1.56	-1.08	NM_178651//XM_0065036	<i>Sica30a9</i>	solute carrier family 30 (zinc transporter), member 9	0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 // regulation of transcription, DNA-templated // inferred from electronic annotation//0006810 //
1444531_a	0.004479	-1.56	-1.73	NM_011895//XM_0065378	<i>Sic35a1</i>	solute carrier family 35 (CMP-sialic acid transporter), member 1	0006810 // transport // inferred from electronic annotation//0006843 // carbohydrate transport // inferred from electronic annotation//0015780 // nucleotide-sugar transport // inferred
1451537_a	0.000259	-1.56	-1.27	NM_001146707//NM_0157	<i>Nap11</i>	nucleosome assembly protein 1-like 1	0006334 // nucleosome assembly // inferred from electronic annotation
1425053_a	0.000932	-1.56	-1.18	NM_008229//XM_0065125	<i>Hdac2</i>	histone deacetylase 2	0000122 // negative regulation of transcription from RNA polymerase II promoter // inferred from genetic interaction//0000122 // negative regulation of transcription from RNA polymerase II
1425065_a	0.000336	-1.56	1.01	NM_010062//NR_103491	<i>Dnase2a//LOC100503676</i>	deoxyribonuclease II alpha//uncharacterized LOC100503676	0000737 // DNA catabolic process, endonucleolytic // inferred from direct assay//0006259 // DNA metabolic process // inferred from electronic annotation//0006308 // DNA catabolic process
1416055_a	0.001702	-1.56	6.94	NM_001290539//NM_1459	<i>Vstm2a</i>	V-set and transmembrane domain containing 2A	
1449277_a	0.000545	-1.56	-1.21	NM_031397//XM_0065143	<i>Bic1c</i>	bicaudal C homolog 1 (Drosophila)	
1450355_a	0.002072	-1.56	-1.24	NM_010629//XM_0064966	<i>Kifap3</i>	kinesin-associated protein 3	0007275 // multicellular organismal development // inferred from electronic annotation//0090090 // negative regulation of canonical Wnt signaling pathway // not recorded
1428314_a	0.008270	-1.56	-1.08	NM_145611	<i>Kank2</i>	KN motif and ankyrin repeat domains 2	0007017 // microtubule-based process // inferred from physical interaction//0007266 // Rho protein signal transduction // traceable author statement//0008104 // protein localization //
1429562_a	0.005841	-1.56	-1.09	NM_170779	<i>Wwc1</i>	WW, C2 and coiled-coil domain containing 1	0000122 // negative regulation of transcription from RNA polymerase II promoter // not recorded//0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 // regulation of transcription, DNA-templated // inferred from electronic annotation//0006357 //
1439831_a	0.007469	-1.56	-1.60	NM_001081193//XM_0065	<i>Lemd3</i>	LEM domain containing 3	0030512 // negative regulation of transforming growth factor beta receptor signaling pathway // not recorded//0030514 // negative regulation of BMP signaling pathway // not
1454528_a	0.000785	-1.56	-1.95	NM_133718//XR_379454	<i>Tmem30a</i>	transmembrane protein 30A	0006810 // transport // inferred from electronic annotation//0006889 // lipid transport // inferred from electronic annotation//0010976 // positive regulation of neuron projection
1426880_a	0.004503	-1.56	-1.04	NM_00111324//NM_0174	<i>Nedp9</i>	neuronal precursor cell expressed, developmentally down-regulated gene 9	0007049 // cell cycle // inferred from electronic annotation//0007067 // mitotic nuclear division // inferred from electronic annotation//0007155 // cell adhesion // inferred from electronic
1448939_a	0.009480	-1.57	-1.20	NM_011220//XM_0065101	<i>Pis</i>	6-pyruvyl-tetrahydropterin synthase	0006729 // tetrahydropterin biosynthetic process // inferred from direct assay
1454664_a	0.007745	-1.57	-1.77	NM_001289722//NM_0012	<i>Wif1</i>	WAS/WASL interacting protein family, member 1	0008154 // actin polymerization or depolymerization // inferred from electronic annotation//0030036 // actin cytoskeleton organization // not recorded//0030048 // actin filament-based
1451306_a	0.005988	-1.57	-1.27	NM_001290805//NM_0012	<i>Kif3a</i>	kinesin family member 3A	0001701 // in utero embryonic development // inferred from genetic interaction//0001822 // kidney development // inferred from mutant phenotype//0007018 // microtubule-based
1435582_a	0.003963	-1.57	-1.49	NM_016686//XM_0065364	<i>Vezf1</i>	vascular endothelial zinc finger 1	0001525 // angiogenesis // inferred from mutant phenotype//0001885 // endothelial cell development // inferred from mutant phenotype
1436507_a	0.000726	-1.57	-1.51	NM_009560//NM_029531	<i>Zfp60</i>	zinc finger protein 60	0006355 // regulation of transcription, DNA-templated // not recorded
1430796_a	0.000034	-1.57	-1.41	NM_010451	<i>Hoxa2</i>	homeobox A2	0000122 // negative regulation of transcription from RNA polymerase II promoter // not recorded//0001709 // cell fate determination // inferred from mutant
1434528_a	0.000726	-1.57	-1.13	NM_178060	<i>Thra</i>	thyroid hormone receptor alpha	0001502 // cartilage condensation // inferred from mutant phenotype//0001503 // ossification // inferred from mutant phenotype//0002155 // regulation of thyroid hormone mediated
1442506_a	0.008334	-1.57	-1.68	NM_177242//XM_0065303	<i>Pptc7</i>	PTC7 protein phosphatase homolog (S. cerevisiae)	0008152 // metabolic process // inferred from electronic annotation//0016311 // dephosphorylation // inferred from electronic annotation
1432498_a	0.006561	-1.57	-1.42	NM_001177843//NM_0011	<i>Frm4a4</i>	FERM domain containing 4A	0090162 // establishment of epithelial cell polarity // inferred from genetic interaction
1428119_a	0.006670	-1.57	-1.07	NM_009214//XM_0014734	<i>Gm14680//Sms</i>	predicted gene 14680//spermine synthase	0006596 // polyamine biosynthetic process // inferred from electronic annotation//0006597 // spermine biosynthetic process // not recorded//0008215 // spermine metabolic process //
1450647_a	0.008147	-1.57	-1.24	NM_009879//XM_0065301	<i>Ifj81</i>	intraflagellar transport 81	0007275 // multicellular organismal development // inferred from electronic annotation//0007283 // spermatogenesis // inferred from electronic annotation//0030030 // cell projection
1428577_a	0.006589	-1.57	-1.68	NM_173765//XM_0065348	<i>Aasdh</i>	aminoadipate-semialdehyde dehydrogenase	0006629 // lipid metabolic process // inferred from electronic annotation//0006631 // fatty acid metabolic process // inferred from electronic annotation//0008152 // metabolic process //
1441057_a	0.000114	-1.57	-1.04	NM_001081322//NM_0278	<i>Pds5a</i>	PD55, regulator of cohesion maintenance, homolog A (S. cerevisiae)	0007049 // cell cycle // inferred from electronic annotation//0007067 // mitotic nuclear division // inferred from electronic annotation//0008156 // negative regulation of DNA replication //
1442588_a	0.006063	-1.58	-1.68	NM_001033348//XM_0064	<i>Ralgap2</i>	Ral GTPase activating protein, alpha subunit 2 (catalytic)	0032484 // Ral protein signal transduction // inferred from mutant phenotype//0032859 // activation of Ral GTPase activity // inferred from genetic interaction//0032859 // activation of Ral
1449962_a	0.001733	-1.58	-1.23	NM_148938	<i>Sic1a3</i>	Salt Paser activity 1 (glial high affinity glutamate transporter), member 3	0006536 // glutamate metabolic process // inferred from mutant phenotype//0006537 // glutamate biosynthetic process // inferred from mutant phenotype//0008610 // transport //
1424051_a	0.002057	-1.58	1.05	NM_024188	<i>Oxcl1</i>	3-oxoadic CoA transferase 1	0007420 // brain development // inferred from electronic annotation//0007507 // heart development // inferred from electronic annotation//0007584 // response to nutrient // inferred
1429264_a	0.007036	-1.58	-1.36	NM_011739	<i>Ywhag</i>	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation	0006679 // protein targeting // inferred from direct assay//0007165 // signal transduction // traceable author statement//0007264 // small GTPase mediated signal transduction // inferred
1434227_a	0.000025	-1.58	-1.12	NM_001164041//NM_0011	<i>Smad5</i>	SMAD family member 5	0001503 // ossification // inferred from electronic annotation//0001525 // angiogenesis // inferred from electronic annotation//0001657 // ureteric bud development // inferred from
1456616_a	0.005122	-1.58	-1.33	NM_001276402//NM_0012	<i>Lef1</i>	lymphoid enhancer binding factor 1	0000122 // negative regulation of transcription from RNA polymerase II promoter // inferred from direct assay//0001569 // patterning of blood vessels // inferred from mutant
1451068_a	0.000726	-1.58	-1.26	NM_010828//XM_0065125	<i>Cited2</i>	Cbp/p300-interacting transactivator, with Glu/Asp-rich carboxy-terminal	0000122 // negative regulation of transcription from RNA polymerase II promoter // not recorded//0001568 // blood vessel development // inferred from mutant phenotype//0001570 //
1455197_a	0.000636	-1.58	-1.98	NM_001081092//XM_0065	<i>Taf4a</i>	TAF4A RNA polymerase II, TATA box binding protein (TBP)-associated factor	0001541 // ovarian follicle development // inferred from mutant phenotype//0006352 // DNA-templated transcription, initiation // not recorded//0006355 // regulation of transcription, DNA-
1438054_a	0.008175	-1.58	-1.54	NM_001081278//NM_1733	<i>Tbc1d4</i>	TBC1 domain family, member 4	0016192 // vesicle-mediated transport // not recorded//0031339 // negative regulation of vesicle fusion // not recorded//0032313 // regulation of Rab GTPase activity // inferred from
1436342_a	0.002511	-1.58	-1.14	NM_019826//XM_0064999	<i>Ivd</i>	isovaleryl coenzyme A dehydrogenase	0006552 // leucine catabolic process // not recorded//0008152 // metabolic process // inferred from electronic annotation//0055114 // oxidation-reduction process // not recorded
1432195_a	0.002791	-1.58	-1.10	NM_001164823//NM_0253	<i>Tmem42</i>	transmembrane protein 42	
1424306_a	0.000050	-1.58	1.04	NM_009388	<i>Tkt</i>	transketolase	0006098 // pentose-phosphate shunt // not recorded//0008152 // metabolic process // inferred from electronic annotation//0009052 // pentose-phosphate shunt, non-oxidative branch //
1430539_a	0.004221	-1.58	-1.40	NM_001205241//NM_0174	<i>Kat6b</i>	K(lysine) acetyltransferase 6B	0006334 // nucleosome assembly // inferred from electronic annotation//0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 // regulation of
1425833_a	0.005704	-1.58	-1.88	NM_015791	<i>Fbxo8</i>	F-box protein 8	0006511 // ubiquitin-dependent protein catabolic process // inferred from physical interaction//0030036 // actin cytoskeleton organization // not recorded//0032012 // regulation of ARF

Table S7

Gene ID	p (Corr)	FC-RSV 1 d	FC-RSV 5 d	RefSeq Transcript ID	Gene Symbol	Gene Title	Gene Ontology Biological Process
1435608_a	0.000736	-1.59	-1.49	NM_001093752//NM_0010	<i>Srsf11</i>	serine/arginine-rich splicing factor 11	0016567 // protein ubiquitination // inferred from electronic annotation//0032088 // negative regulation of NF-kappaB transcription factor activity // not recorded//0046600 // negative regulation of NF-kappaB transcription factor activity // not recorded//0007264 // self proteolysis // not recorded
1449289_a	0.000782	-1.59	-1.21	NM_179787//XM_0065340	<i>Trim37</i>	tripartite motif-containing 37	
1429676_a	0.003498	-1.59	-1.38	NM_009796//XM_0065185	<i>Cpn7</i>	calpain 7	
1449222_a	0.000303	-1.59	-1.21	NM_026178	<i>Mmd</i>	monocyte to macrophage differentiation-associated	
1451070_a	0.001483	-1.59	-1.26	NM_011327	<i>Scp2</i>	sterol carrier protein 2, liver	
1433028_a	0.009394	-1.59	-1.43	NM_001033270//XM_0065	<i>Slc4a7</i>	slc4 carrier family 4, sodium bicarbonate cotransporter, member 7	
1436785_a	0.001651	-1.59	-1.52	NM_001005868//NM_0012	<i>Erbp2ip</i>	Erbp2 interacting protein	
1433925_a	0.005207	-1.59	-1.44	NM_001166371//NM_0087	<i>Zfml</i>	zinc finger, matrix-like	
1433476_a	0.001162	-1.59	-1.13	NM_001166453//NM_0011	<i>Pk3</i>	plaxin 3 (T-isoform)	
1429159_a	0.001650	-1.59	-1.09	NM_138587//XM_0065051	<i>Fam3c</i>	family with sequence similarity 3, member C	
1416467_a	0.002167	-1.59	2.62	NM_020008	<i>Clec7a</i>	C-type lectin domain family 7, member A	0001878 // response to yeast // inferred from direct assay//0001879 // detection of yeast // inferred from direct assay//0002221 // pattern recognition receptor signaling pathway // not recorded//00051289 // positive regulation of transcription, DNA-templated // inferred from electronic annotation
1436643_x	0.009770	-1.59	-1.15	NM_001159616//NM_0011	<i>Pi3p</i>	phosphatidylinositol glycan anchor biosynthesis, class P	
1424645_a	0.005686	-1.59	1.03	NM_002821//XM_0065173	<i>Pcdh2</i>	pterin 4 alpha carbinolamine dehydratase/dimerization cofactor of	
1433936_a	0.006107	-1.60	-1.12	NM_001190449//NM_0167	<i>Ddah2</i>	dimethylarginine dimethylaminohydrolase 2	
1431206_a	0.002487	-1.60	-1.41	NM_020561	<i>Smpd3a</i>	sphingomyelin phosphodiesterase, acid-like 3A	
1428125_a	0.003427	-1.60	-1.07	NM_207301//XM_0065230	<i>Wrb</i>	tryptophan rich basic protein	
1424895_a	0.000283	-1.60	1.02	NM_019877	<i>Cop2</i>	coatamer protein complex, subunit zeta 2	
1452621_a	0.004999	-1.60	-1.30	NM_011221	<i>Purb</i>	purine rich element binding protein B	
1448543_a	0.001606	-1.60	-1.18	NM_031998//XM_0065052	<i>Cep41</i>	centrosomal protein 41	
1424133_a	0.000982	-1.60	1.05	NM_013813//XM_0065236	<i>Epb4.1l3</i>	erythrocyte protein band 4.1-like 3	
1425881_a	0.001177	-1.60	-1.01	NM_199446//XM_0065305	<i>Phk6</i>	phosphorylase kinase beta	0005975 // carbohydrate metabolic process // inferred from electronic annotation//0005976 // polysaccharide metabolic process // inferred from electronic annotation//0005977 // glycogen metabolism // inferred from electronic annotation//0005978 // negative regulation of transcription from RNA polymerase II promoter // inferred from genetic interaction//0000122 // negative regulation of transcription from RNA polymerase II promoter // inferred from electronic annotation//0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 // regulation of transcription, DNA-templated // inferred from electronic annotation
1424659_a	0.001035	-1.60	1.03	NM_001081125//XM_0065	<i>Gl2</i>	GLI-Kruppel family member GLI2	
1419653_a	0.005761	-1.60	1.24	NM_009036//XM_0064990	<i>Rbpjl</i>	recombination signal binding protein for immunoglobulin kappa 1 region	
1437349_a	0.000608	-1.61	-1.15	NM_001159634//NM_1726	<i>Prrc2b</i>	proline-rich coiled-coil 2B	
1460726_a	0.003678	-1.61	-1.34	NM_026388//XM_0065391	<i>Tgpl</i>	transformation related protein 63 regulated like	
1431894_a	0.002167	-1.61	-1.42	NM_001146010//NM_1990	<i>Fchs42</i>	FCH and double SH3 domains 2	
1460643_a	0.004525	-1.61	-1.34	NM_001252494//NM_0012	<i>Rapgef6</i>	Rap guanine nucleotide exchange factor (GEF) 6	
1417344_a	0.007649	-1.61	1.67	NM_0010337134//NM_0012	<i>Cnec2</i>	cyclin E2	
1440020_a	0.003861	-1.61	-1.61	NM_001033422//XM_0065	<i>Thoc2</i>	THO complex 2	
1450835_a	0.004428	-1.61	-1.25	NM_010771	<i>Matr3</i>	matrin 3	
1435894_a	0.008982	-1.61	-1.49	NM_001048250//XM_0065	<i>Smin15</i>	small integral membrane protein 15	0002376 // immune system process // inferred from electronic annotation//0002474 // antigen processing and presentation of peptide antigen via MHC class I // inferred from electronic annotation//0006162 // behavioral fear response // inferred from mutant phenotype//0006182 // cGMP biosynthetic process // not recorded//0006661 // phosphatidylinositol biosynthetic process // not recorded//0006182 // negative regulation of transcription from RNA polymerase II promoter // inferred from direct assay//0008285 // negative regulation of cell proliferation // inferred from mutant phenotype//0008285 // negative regulation of cell proliferation // inferred from mutant phenotype
1425039_a	0.002420	-1.61	1.01	NM_010378//XM_0065365	<i>H2-Aa</i>	histocompatibility 2, class II antigen A, alpha	
1422490_a	0.009486	-1.61	1.12	NM_008312//XM_0065287	<i>Htr2c</i>	5-hydroxytryptamine (serotonin) receptor 2C	
1436839_a	0.001994	-1.61	-1.15	NM_001168382//NM_0294	<i>Phf14</i>	PHD finger protein 14	
1439121_a	0.002240	-1.61	-1.16	NM_001165951//NM_1775	<i>Vangl1</i>	vang-like 1 (van gogh, Drosophila)	
1434157_a	0.002166	-1.61	-1.45	NM_173038//XM_0065103	<i>Tbcl</i>	tubulin folding cofactor E-like	
1423069_a	0.004776	-1.62	1.10	NM_026555//XM_0065409	<i>Rcn3</i>	reticulocalbin 3, EF-hand calcium binding domain	
1450311_a	0.000938	-1.62	-1.24	NM_175751//XM_0065259	<i>Zfp608</i>	zinc finger protein 608	
1433784_a	0.008280	-1.62	-1.12	NM_001165930//NM_0296	<i>Gltr41</i>	glycosyltransferase 8 domain containing 1	
1430329_a	0.000297	-1.62	-1.40	NM_175266	<i>Epm2aip1</i>	EPH2A (Aforin) interacting protein 1	
1423947_a	0.005399	-1.62	1.05	NM_019718//XM_0065272	<i>Arl3</i>	ADP-ribosylation factor-like 3	0008152 // metabolic process // inferred from electronic annotation
1450513_a	0.001252	-1.62	-1.24	NM_001081316//NM_0065	<i>Dxel</i>	dermatan sulfate epimerase-like	
1429377_a	0.000861	-1.62	-1.37	NM_001290655//NM_0299	<i>Mdb5l</i>	methyl-CpG binding domain protein 5	
1429096_a	0.004418	-1.62	-1.36	NM_001005784//NM_0010	<i>Inadi</i>	inad-like (Drosophila)	
1438871_a	0.002476	-1.62	-1.56	NM_028264	<i>Tmem55a</i>	transmembrane protein 55A	
1441123_a	0.005185	-1.62	-1.64	NM_001083114//NM_0012	<i>Pphl1n</i>	periphilin 1	
1419100_a	0.000061	-1.62	1.30	NM_026613	<i>Ccdc34</i>	coiled-coil domain containing 34	
1428237_a	0.000139	-1.62	-1.55	NM_145962	<i>Pank3</i>	panthothenate kinase 3	
1426235_a	0.004133	-1.63	-1.02	NM_021292//XM_0065040	<i>Evc</i>	Ellis van Creveld gene syndrome	
1420545_a	0.009494	-1.63	1.20	NM_001077354//XM_0065	<i>C73730</i>	expressed sequence C73730	
1431786_x	0.003611	-1.63	-1.42	NM_008960//NM_177096	<i>Pten</i>	phosphatase and tensin homolog	0001525 // angiogenesis // inferred from mutant phenotype//0001933 // negative regulation of protein phosphorylation // not recorded//0002902 // regulation of B cell apoptotic process // not recorded//0007616 // long-term memory // not recorded//0010738 // regulation of protein kinase A signaling // not recorded//0016567 // protein ubiquitination // not recorded
1428767_a	0.000272	-1.63	-1.35	NM_001025309//NM_1448	<i>Pja2</i>	pja2, RING-H2 motif containing	
1446565_a	0.000408	-1.63	-1.79	NM_00108090	<i>Nedd4</i>	neuronal precursor cell expressed, developmentally down-regulated 4	
1422123_x	0.000201	-1.63	1.13	NR_028574//NR_028573	<i>Shhg8//Snora24</i>	small nuclear RNA host gene 8//small nuclear RNA, H/ACA box 24	
1428495_a	0.001410	-1.63	-1.35	NM_172871	<i>Kth9</i>	kelch-like 9	
1425715_a	0.003403	-1.63	-1.00	NM_146162//XM_0065302	<i>Tmem119</i>	transmembrane protein 119	
1438953_a	0.002212	-1.63	-1.16	NM_013701//NM_145079	<i>Ugt1a1//Ugt1a10//Ugt1a2</i>	UDP glucuronosyltransferase 1 family, polypeptide A1//UDP	
1423252_a	0.006276	-1.63	1.09	NM_001159529//NM_0091	<i>Cox7a2l</i>	cytochrome c oxidase subunit VIIa polypeptide 2-like	
1445948_a	0.008738	-1.63	-1.77	NM_019550//XM_0065017	<i>Ptpb2</i>	polyphosphatase tract binding protein 2	
1454006_a	0.001179	-1.63	-1.31	NM_024288//XM_0065065	<i>Rrm45a</i>	required for meiotic nuclear division 5 homolog A (S. cerevisiae)	
1420991_a	0.002505	-1.63	1.17	NM_01290274//NM_1533	<i>Amat</i>	angiotensin	0001570 // vasculogenesis // inferred from mutant phenotype//0001701 // in utero embryonic development // inferred from mutant phenotype//0001702 // gastrulation with mouth
1421391_a	0.002863	-1.63	1.16	NR_028573//NR_028574	<i>Shhg8//Snora24</i>	small nuclear RNA host gene 8//small nuclear RNA, H/ACA box 24	
1445841_a	0.005400	-1.63	-1.77	NM_008209//XM_0065291	<i>Mr1</i>	major histocompatibility complex, class I-related	
1449451_a	0.000189	-1.63	-1.22	NM_001033275//XM_0065	<i>Gxylt1</i>	glucosylase xylosyltransferase 1	
1460282_a	0.000135	-1.63	-1.33	NM_001163239//NM_0011	<i>Nqo2</i>	NAD(P)H dehydrogenase, quinone 2	
1424908_a	0.007046	-1.63	1.02	NM_001103177//NM_0011	<i>Abilml</i>	actin-binding LIM protein 1	
1437360_a	0.000837	-1.63	-1.53	NM_025476	<i>Rmdn1</i>	regulator of microtubule dynamics 1	
1450718_a	0.009800	-1.63	-1.25	NM_080575	<i>Acsl1</i>	acyl-CoA synthetase short-chain family member 1	
1434372_a	0.005642	-1.64	-1.12	NM_198298//XM_0065345	<i>Helz</i>	helix with zinc finger domain	
1432120_a	0.008314	-1.64	-1.42	NM_172664//XM_0064991	<i>Tik1</i>	tousled-like kinase 1	
1434108_a	0.006230	-1.64	-1.12	NM_001039388//NM_0010	<i>Nsmf</i>	NMDA receptor synaptotagmin signaling and neuronal migration factor	0006376 // mRNA splice site selection // inferred from direct assay//0006376 // mRNA splice site selection // inferred from mutant phenotype//0006397 // mRNA processing // inferred from mutant phenotype
1452357_a	0.009197	-1.64	-1.29	NM_011273	<i>Xpr1</i>	xenotropic and polytropic retrovirus receptor 1	
1452013_a	0.003488	-1.64	-1.28	NM_008548//XM_0065125	<i>Man1a</i>	mannosidase 1, alpha	
1433857_a	0.000369	-1.64	-1.44	NM_009302	<i>Swap70</i>	SWA-70 protein	
1425890_a	0.000220	-1.64	-1.01	NM_019861	<i>Csf1</i>	cathespase 1	
1446018_a	0.001225	-1.64	-1.77	NM_146033//XM_0065110	<i>Snmp6</i>	SUMO1/sentin specific peptidase 6	
1434592_a	0.006743	-1.64	-1.46	NM_139200//XM_0064980	<i>Cytp</i>	cytochrome I interacting protein	
1426519_a	0.004733	-1.64	-1.02	NM_025598//XM_0065007	<i>Pdpf3</i>	pancreatic progenitor cell differentiation and proliferation factor homolog	
1426948_a	0.002056	-1.64	-1.04	NM_008716	<i>Notch3</i>	notch 3	
1422454_a	0.000021	-1.64	1.12	NM_010143//XM_0065217	<i>Ephb3</i>	Eph receptor B3	0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 // regulation of transcription, DNA-templated // not recorded//0007219 // Notch signaling pathway
1450165_a	0.000058	-1.64	-1.23	NM_001198570//NM_0011	<i>Abi2</i>	Abi-interactor 2	
1447738_x	0.004999	-1.64	-1.83	NM_025997//XM_0014788	<i>Fam103a1//Gm4199</i>	family with sequence similarity 103, member A1//predicted gene 4199	
1434822_a	0.000492	-1.65	-1.47	NM_177151//XM_0065201	<i>Vps13b</i>	vacuolar protein sorting 13B (yeast)	
1430488_a	0.002130	-1.65	-1.40	NM_009461//XM_0064991	<i>Ubr1</i>	ubiquitin protein ligase E3 component n-recogin 1	
1427074_a	0.004085	-1.65	-1.05	NM_001168491//NM_0011	<i>Pcdc4</i>	programmed cell death 4	
1452639_a	0.000465	-1.65	-1.30	NM_172731//XM_0065060	<i>Fgd5</i>	FYVE, RhoGEF and PH domain containing 5	
1429114_a	0.002353	-1.65	-1.36	NM_144812//NM_177124	<i>Tnrc6b</i>	triple helix repeat containing 6b	
1460227_a	0.000181	-1.65	-1.33	NM_173026	<i>Zbtb11</i>	zinc finger and BTB domain containing 11	

Table S7

Gene ID	p (Corr)	FC-RSV 1 d	FC-RSV 5 d	RefSeq Transcript ID	Gene Symbol	Gene Title	Gene Ontology Biological Process
1429454_a	0.006613	-1.65	-1.38	NM_133697// <i>XM_0065040</i>	<i>Smin14</i>	small integral membrane protein 14	0006337 // nucleosome disassembly // not recorded//0006355 // regulation of transcription, DNA-templated // inferred from electronic annotation//00045944 // positive regulation of
1432915_a	0.000675	-1.65	-1.43	NM_175251	<i>Arid2</i>	AT rich interactive domain 2 (ARID, RFX-like)	0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 // regulation of transcription, DNA-templated // inferred from electronic annotation
1432790_a	0.002732	-1.66	-1.43	NM_001081750	<i>Zfp664</i>	zinc finger protein 664	0006208 // pyrimidine nucleobase catabolic process // inferred from electronic annotation//0007399 // nervous system development // inferred from direct assay//0008152 // metabolic
1448618_a	0.005014	-1.66	-1.18	NM_001136086// <i>NM_0012</i>	<i>Dpys13</i>	dihydropyrimidinase-like 3	0008152 // metabolic process // inferred from electronic annotation//0004699 // fatty-acyl-CoA biosynthetic process // inferred from electronic annotation
1458121_a	0.008200	-1.66	-2.35	NM_010022// <i>XM_0065009</i>	<i>Dbt</i>	dihydroipomamide branched chain transacylase E2	0000122 // negative regulation of transcription from RNA polymerase II promoter // not recorded//0002062 // chondrocyte differentiation // inferred from mutant phenotype//0006260 //
1449909_a	0.008424	-1.66	-1.22	NM_00113209// <i>NM_0011</i>	<i>Nfib</i>	nuclear factor I/8	0006184 // GTP catalytic process // not recorded//0007165 // signal transduction // inferred from electronic annotation//0007264 // small GTPase mediated signal transduction // inferred
1423871_a	0.009300	-1.66	1.06	NM_029519	<i>Rap2a</i>	RAS related protein 2a	0003431 // growth plate cartilage chondrocyte development // inferred from mutant phenotype//00030198 // extracellular matrix organization // inferred from mutant phenotype
1442886_a	0.007064	-1.67	1.10	NM_025685// <i>XM_0065380</i>	<i>Col27a1</i>	collagen, type XXVII, alpha 1	000508 // proteolysis // not recorded//0006511 // ubiquitin-dependent protein catabolic process // inferred from electronic annotation//0016579 // protein deubiquitination // not
1440994_a	0.001205	-1.67	-1.20	NM_145628// <i>XM_0065276</i>	<i>Usp11</i>	ubiquitin specific peptidase 11	000508 // transmembrane transport // inferred from electronic annotation
1435106_a	0.000680	-1.67	-1.13	NM_029875// <i>KR_380382</i>	<i>Slc35e3</i>	solute carrier family 35, member E3	0006915 // apoptotic process // inferred from electronic annotation//0008152 // metabolic process // inferred from electronic annotation//0016055 // Wnt signaling pathway // inferred
1456648_a	0.004072	-1.67	-1.08	NM_009688// <i>XM_0065414</i>	<i>Xiap</i>	X-linked inhibitor of apoptosis	0007165 // signal transduction // not recorded//0022414 // reproductive process // inferred from mutant phenotype//0001532 // actin cytoskeleton reorganization // not
1420465_s	0.007846	-1.67	1.20	NM_054041// <i>XM_0065065</i>	<i>Antxr1</i>	anthrax toxin receptor 1	0000122 // negative regulation of transcription from RNA polymerase II promoter // not recorded//0001701 // in utero embryonic development // inferred from mutant phenotype//0001889
1446598_a	0.005128	-1.67	-1.79	NM_010258// <i>XM_0065256</i>	<i>Gata6</i>	GATA binding protein 6	0001657 // ureteric bud development // inferred from expression pattern//0008284 // positive regulation of cell proliferation // not recorded//0042517 // positive regulation of tyrosine
1426752_a	0.000931	-1.68	-1.03	NM_018827// <i>XM_0065095</i>	<i>Cr1f1</i>	cytokine receptor-like factor 1	0003009 // skeletal muscle contraction // not recorded//0006200 // ATP catabolic process // not recorded//0007519 //
1435087_a	0.000237	-1.68	-1.13	NM_001271538// <i>NM_0012</i>	<i>Myh14</i>	myosin, heavy polypeptide 14	0000122 // negative regulation of transcription from RNA polymerase II promoter // inferred from electronic annotation//0001654 // eye development // inferred from mutant
1434155_a	0.004108	-1.68	-1.12	NM_010439// <i>XM_0039453</i>	<i>Gm21596//Gm6115//Hmgbl1</i>	predicted gene, 21596//predicted gene 6115//high mobility group box	0007155 // cell adhesion // inferred from electronic annotation//0007160 // cell-matrix adhesion // inferred from mutant phenotype//0007160 // cell-matrix adhesion // not
1440686_a	0.009876	-1.68	-1.63	NM_146054// <i>XM_0065188</i>	<i>Fermt2</i>	fermitin family homolog 2 (Drosophila)	0003383 // apical constriction // inferred from genetic interaction//0032970 // regulation of actin filament-based process // inferred from genetic interaction//0034613 // cellular protein
1441233_a	0.009301	-1.68	-1.64	NM_028127// <i>XM_0065159</i>	<i>Frmtd6</i>	FERM domain containing 6	0006171 // cAMP biosynthetic process // inferred from mutant phenotype//0006171 // cAMP biosynthetic process // not recorded//0006171 // cAMP biosynthetic process // traceable
1424221_a	0.004132	-1.68	1.05	NM_001037723// <i>NM_0010</i>	<i>Adcy7</i>	adenylate cyclase 7	0016567 // protein ubiquitination // inferred from electronic annotation
1451068_s	0.007026	-1.68	-1.26	NM_029965// <i>XM_0065092</i>	<i>Rnf170</i>	ring finger protein 170	0016567 // protein ubiquitination // inferred from direct assay
1451584_a	0.007307	-1.68	-1.28	NM_025785// <i>XM_0065088</i>	<i>Fbxo25</i>	F-box protein 25	0006334 // nucleosome assembly // inferred from electronic annotation
1417894_a	0.005506	-1.68	1.51	NM_138742	<i>Nap13</i>	nucleosome assembly protein 1-like 3	0000187 // activation of MAPK activity // not recorded//0006661 // phosphatidylinositol biosynthetic process // not recorded//0008104 // protein localization // not recorded//0008284 //
1426900_a	0.007058	-1.68	-1.04	NM_145394	<i>Slc44a3</i>	solute carrier family 44, member 3	0001310 // phosphorylation // inferred from electronic annotation
1432820_a	0.000238	-1.68	-1.11	NM_133655	<i>CD81</i>	CD81 antigen	0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 // regulation of transcription, DNA-templated // inferred from electronic annotation//0006397 //
1427875_a	0.000680	-1.68	-1.06	G720477C19RIK		RIKEN cDNA G720477C19 gene	0008152 // metabolic process // inferred from electronic annotation
1433985_a	0.004550	-1.68	-1.44	NM_028410// <i>XM_0065082</i>	<i>Prkin</i>	protein-kinase, interferon-inducible double stranded RNA dependent	0008152 // metabolic process // inferred from electronic annotation
1456893_a	0.002265	-1.68	-2.11	NM_001079694// <i>NM_0010</i>	<i>Srpf5</i>	serine/arginine-rich splicing factor 5	0008152 // metabolic process // inferred from electronic annotation//0007144 // drug metabolic process // not recorded//0042373 // vitamin K metabolic process // not recorded//00055114
1440298_a	0.002796	-1.69	-1.61	NM_001033441	<i>Alg10b</i>	asparagine-linked glycosylation 10B (alpha-1,2-glucosyltransferase)	0002090 // regulation of receptor internalization // inferred from direct assay//0002092 // positive regulation of receptor internalization // inferred from direct assay//0006605 // protein
1436559_a	0.003251	-1.69	-1.15	NM_007620	<i>Cbr1</i>	carbonyl reductase 1	0004644 // cellular protein modification process // inferred from electronic annotation//0006479 // protein methylation // inferred from electronic annotation//0003259 // methylation //
1444693_a	0.005121	-1.69	-1.74	NM_025292	<i>Synj2bp</i>	synaptotagmin 2 binding protein	0002525 // acute inflammatory response to non-antigenic stimulus // not recorded//0006508 // proteolysis // inferred from reviewed computational
1444649_a	0.000201	-1.69	-1.73	NM_183028// <i>XM_0064955</i>	<i>Pcmtd1</i>	protein-L-isospartate (D-aspartate) O-methyltransferase domain	0006417 // regulation of translation // inferred from electronic annotation//0007015 // actin filament organization // inferred from mutant phenotype//0016477 // cell migration // inferred
1460283_a	0.00101	-1.69	-1.33	NM_009811	<i>Casp6</i>	caspace 6	0006200 // ATP catabolic process // not recorded//0006810 // transport // inferred from electronic annotation//0006811 // ion transport // inferred from electronic annotation//0006812 //
131717_a	0.001241	-1.69	-1.42	NM_010879// <i>XM_0064957</i>	<i>Nck2</i>	non-catalytic region of tyrosine kinase adaptor protein 2	0008594 // photoreceptor cell morphogenesis // not recorded//0003030 // cell projection organization // inferred from electronic annotation//0042073 // intracellular transport // inferred by
1432192_a	0.004415	-1.69	-1.42	NM_001253831// <i>NM_0012</i>	<i>Atp2c1</i>	ATPase, Ca++-sequestering	0001525 // angiogenesis // inferred from electronic annotation//0001541 // ovarian follicle development // inferred from mutant phenotype//0001579 // vasculogenesis // inferred from
1436246_a	0.004999	-1.69	-1.50	NM_153600// <i>XM_0065061</i>	<i>Ttc26</i>	tetratricopeptide repeat domain 26	0006355 // regulation of transcription, DNA-templated // inferred from direct assay//0007275 // multicellular organismal development // inferred from electronic annotation//0007283 //
1440430_a	0.004286	-1.69	-1.62	NM_010612	<i>Kdr</i>	kinase insert domain protein receptor	0006071 // glycerol metabolic process // inferred from electronic annotation//0006629 // lipid metabolic process // inferred from electronic annotation//0007186 // G-protein coupled
1455286_a	0.000772	-1.69	-1.32	NM_011818// <i>XM_0065060</i>	<i>Gmcl1</i>	germ cell-less homolog 1 (Drosophila)	0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 // regulation of transcription, DNA-templated // inferred from electronic annotation//0016568 //
1427050_a	0.002054	-1.70	-1.04	NM_019580	<i>Gde1</i>	glycerophosphodiester phosphodiesterase 1	0008284 // positive regulation of cell proliferation // inferred from mutant phenotype//0016477 // cell migration // inferred from mutant phenotype//0035556 // intracellular signal
1434433_x	0.002874	-1.70	-1.12	NM_080793	<i>Setd7</i>	SET domain containing [lysine methyltransferase] 7	0006935 // chemotaxis // inferred from electronic annotation
1429723_a	0.008788	-1.70	-1.09	NM_001083587// <i>XM_0065</i>	<i>Tns3</i>	tensin 3	0042325 // regulation of phosphorylation // inferred from electronic annotation//0043086 // negative regulation of catalytic activity // inferred from electronic annotation
1448188_a	0.001313	-1.70	-1.17	NM_153582	<i>Cmtm4</i>	CKLF-like MARVEL transmembrane domain containing 4	0006094 // acetyl-CoA metabolic process // not recorded//0006085 // acetyl-CoA biosynthetic process // traceable author statement//0006101 // citrate metabolic process // not
1426028_a	0.003780	-1.70	-1.01	NM_025731	<i>Ppp1r14a</i>	protein phosphatase 1, regulatory (inhibitor) subunit 14A	0008152 // metabolic process // inferred from electronic annotation//0016311 // dephosphorylation // inferred from electronic annotation
1449227_a	0.002426	-1.70	-1.70	NM_001141933// <i>NM_0214</i>	<i>Mkain4</i>	Na+/K+-transporting ATPase interacting 4	0000002 // mitochondrial genome maintenance // not recorded//0007605 // sensory perception of sound // inferred from mutant phenotype//0032836 // glomerular basement membrane
1450430_a	0.002564	-1.70	-1.24	NM_001199299// <i>NM_1340</i>	<i>Acly</i>	ATP citrate lyase	0034454 // microtubule anchoring at centrosome // inferred from mutant phenotype//0090222 // centrosome-templated microtubule nucleation // inferred from mutant phenotype
1439630_x	0.000026	-1.70	-1.58	NM_001290991// <i>NM_0012</i>	<i>Ctspd12</i>	CTD (carboxy-terminal domain), RNA polymerase II, polypeptide A) small	0008152 // metabolic process // inferred from electronic annotation//00018345 // protein palmitoylation // not recorded
1438688_a	0.000023	-1.70	-1.56	NM_001294323// <i>NM_0012</i>	<i>Mpv17</i>	Mpv17 mitochondrial inner membrane protein	0006355 // regulation of transcription, DNA-templated // inferred from electronic annotation
1433667_a	0.000021	-1.70	-1.43	NM_001081453// <i>NM_0012</i>	<i>Nin</i>	ninein	0000042 // protein targeting to Golgi // not recorded//0006605 // protein targeting // not recorded//0006622 // protein targeting to lysosome // not recorded//0006629 // lipid metabolic
1425062_a	0.001953	-1.70	-1.29	NM_146073// <i>XM_0065232</i>	<i>Zdhxc14</i>	zinc finger, DHHC domain containing 14	0007275 // multicellular organismal development // inferred from electronic annotation//0021510 // spinal cord development // inferred from electronic annotation
1424782_a	0.004883	-1.70	1.03	NM_001082485// <i>NM_0011</i>	<i>Zfp266</i>	zinc finger protein 266	0008360 // regulation of cell shape // inferred from electronic annotation
1449962_a	0.001733	-1.71	-1.23	NM_011436	<i>Sor1</i>	soritin-related receptor, LDLR class A repeats-containing	005085 // transmembrane transport // inferred from electronic annotation
1420609_a	0.008360	-1.71	1.20	NM_001163608// <i>NM_0281</i>	<i>Plxnc1</i>	plexin domain containing 1	0006044 // N-acetylglucosamine metabolic process // not recorded//0006612 // protein targeting to membrane // not recorded//0007568 // aging // inferred from electronic
1426661_a	0.005333	-1.71	-1.03	NM_026514// <i>XM_0065242</i>	<i>Cdc42ep3</i>	CDCA2 effector protein (Rho GTPase binding) 3	0006629 // lipid metabolic process // inferred from electronic annotation//0006631 // fatty acid metabolic process // inferred from electronic annotation//0006928 // cellular component
1450783_a	0.000017	-1.71	-1.25	NM_027872// <i>XM_0065048</i>	<i>Slc46a3</i>	SLC46A3 (lys-Asp-Glu-Leu) endoplasmic reticulum protein retention receptor 3	0001525 // angiogenesis // inferred from direct assay//0006469 // negative regulation of protein kinase activity // not recorded//0007010 // cytoskeleton organization // not
1433986_a	0.007989	-1.71	-1.44	NM_023799// <i>XM_0065274</i>	<i>Mgeo5</i>	meningioma expressed antigen 5 (hyaluronidase)	0001558 // regulation of cell growth // inferred from electronic annotation//0006508 // proteolysis // inferred from direct assay//0005012 // negative regulation of transforming growth
1439689_a	0.003823	-1.71	-1.59	NM_007440// <i>KR_388333//</i>	<i>Alox12</i>	arachidonate 12-lipoxygenase	0006260 // DNA replication // inferred by curator//0006261 // DNA-dependent DNA replication // inferred from sequence or structural similarity//0006281 // DNA repair // traceable author
1418394_a	0.004686	-1.71	1.39	NM_009382	<i>Thy1</i>	thymus cell antigen 1, theta	0006508 // proteolysis // inferred from direct assay//0007229 // integrin-mediated signaling pathway // inferred from electronic annotation//0009967 // positive regulation of signal
1427426_a	0.009685	-1.71	-1.05	NM_019564	<i>Htra1</i>	Htra serine peptidase 1	0000038 // very long-chain fatty acid metabolic process // inferred from mutant phenotype//0001649 // osteoblast differentiation // not recorded//0006629 // lipid metabolic process //
1451891_a	0.000762	-1.72	-1.28	NM_015810// <i>NR_027785//</i>	<i>Polg2</i>	polymerase (DNA directed), gamma 2, accessory subunit	0007283 // spermatogenesis // inferred from mutant phenotype//0003030 // cell projection organization // inferred from electronic annotation//0042384 // cilium assembly // inferred from
1443400_a	0.003682	-1.72	-1.70	NM_001164785// <i>NM_0011</i>	<i>Adams20</i>	a disintegrin-like and metallopeptidase (reprolysin type) with	0045329 // carnitine biosynthetic process // inferred from direct assay//0045329 // carnitine biosynthetic process // not recorded//0051354 // negative regulation of oxidoreductase activity
1449326_a	0.000023	-1.72	-1.21	NM_177794// <i>XM_0065137</i>	<i>Tmem26</i>	transmembrane protein 26	0001654 // eye development // inferred from sequence or structural similarity//0006184 // GTP catabolic process // inferred from electronic annotation//0006810 // transport // inferred
1452170_a	0.006170	-1.72	-1.29	NM_008292	<i>Hsd17b4</i>	hydroxysteroid (17-beta) dehydrogenase 4	0006468 // protein phosphorylation // not recorded//0006939 // smooth muscle contraction // inferred from mutant phenotype//0007015 // actin filament organization // not
1447937_a	0.006613	-1.72	-1.85	NM_001271533// <i>NM_0257</i>	<i>Spaq16</i>	sperm associated antigen 16	0000082 // G1/S transition of mitotic cell cycle // inferred from mutant phenotype//0001975 // response to amphetamine // inferred from electronic annotation//0006470 // protein
1446048_a	0.008742	-1.72	-1.78	NM_138758// <i>XM_0065358</i>	<i>Tmhe</i>	trimethyllysine hydroxylase, epsilon	0007420 // brain development // inferred from electronic annotation//0016310 // phosphorylation // inferred from electronic annotation//0030644 // cellular chloride ion homeostasis // not
1438350_a	0.006471	-1.72	-1.55	NM_138590// <i>NM_177027//</i>	<i>Zcchc7</i>	zinc finger, CCHC domain containing 7	0006621 // protein retention in ER lumen // inferred from electronic annotation//0006810 // transport // inferred from electronic annotation//0015031 // protein transport // inferred from
1458113_a	0.003048	-1.72	-2.34	NM_001278447// <i>NM_1810</i>	<i>Rab18</i>	RAB18, member RAS oncogene family	0006810 // transport // inferred from electronic annotation//0006812 // cation transport // inferred from direct assay//0006824 // cobalt ion transport // inferred from direct
1451097_a	0.009585	-1.72	-1.26	NM_139300// <i>XM_0065217</i>	<i>Myik</i>	myosin, light polypeptide kinase	0007343 // egg activation // not recorded//0010466 // negative regulation of peptidase activity // inferred from genetic interaction//0010951 // negative regulation of endopeptidase activity
1425624_a	0.009230	-1.72	-1.00	NM_001005341	<i>Ypel2</i>	yippee-like 2 (Drosophila)	0006461 // protein complex assembly // inferred from electronic annotation
1435241_a	0.005938	-1.72	-1.48	NM_001293622// <i>NM_0089</i>	<i>Ppp3ca</i>	protein phosphatase 3, catalytic subunit, alpha isoform	0000002 // mitochondrial genome maintenance // inferred from mutant phenotype//0000122 // negative regulation of transcription from RNA polymerase II promoter // not
1423570_a	0.001915	-1.72	1.07	NM_021273	<i>Ckb</i>	creatine kinase, brain	0006468 // eye development // inferred from sequence or structural similarity//0006184 // GTP catabolic process // inferred from electronic annotation//0006810 // transport // inferred
1427346_a	0.002360	-1.72	-1.05	NM_134090// <i>XM_0065202</i>	<i>Kdelr3</i>	KDEL (Lys-Asp-Glu-Leu) endoplasmic reticulum protein retention receptor 3	0000082 // G1/S transition of mitotic cell cycle // inferred from mutant phenotype//0001975 // response to amphetamine // inferred from electronic annotation//0006470 // protein
1430081_a	0.002506	-1.72	-1.39	NM_175002// <i>XM_0065328</i>	<i>Mmgf2</i>	membrane magnesium transporter 2	0007420 // brain development // inferred from electronic annotation//0016310 // phosphorylation // inferred from electronic annotation//0030644 // cellular chloride ion homeostasis // not
1422495_a	0.003009	-1.72	1.12	NM_172788// <i>XM_0065136</i>	<i>Sh3f3</i>	SH3 domain containing ring finger 3	0006621 // protein retention in ER lumen // inferred from electronic annotation//0006810 // transport // inferred from electronic annotation//0015031 // protein transport // inferred from
1446693_a	0.009715	-1.72	-1.79	NM_009817// <i>XM_0065170</i>	<i>Cost</i>	calpastatin	0006810 // transport // inferred from electronic annotation//0006812 // cation transport // inferred from direct assay//0006824 // cobalt ion transport // inferred from direct
1439647_a	0.006469	-1.73	-1.58	NM_181040	<i>Atpaf1</i>	ATP synthase mitochondrial F1 complex assembly factor 1	0007343 // egg activation // not recorded//0010466 // negative regulation of peptidase activity // inferred from genetic interaction//0010951 // negative regulation of endopeptidase activity
1455521_a	0.005031	-1.73	-2.00	NM_001033713// <i>NM_0012</i>	<i>Myoc</i>	myocyte enhancer factor 2A	0006461 // protein complex assembly // inferred from electronic annotation
1448845_a	0.006230	-1.73	-1.19	NM_001293633// <i>NM_0012</i>	<i>Nek1</i>	NIMA (never in mitosis gene a)-related expressed kinase 1	0000002 // mitochondrial genome maintenance // inferred from mutant phenotype//0000122 // negative regulation of transcription from RNA polymerase II promoter // not
1439811_a	0.004010	-1.73	-1.60	NM_178661// <i>XM_0065058</i>	<i>Creb2</i>	cAMP responsive element binding protein 3-like 2	0006468 // eye development // inferred from sequence or structural similarity//0006184 // GTP catabolic process // inferred from electronic annotation//0006810 // transport // inferred
1423072_a	0.008991	-1.73	-1.10	NM_025613	<i>Ed1</i>	EP300 interacting inhibitor of differentiation 1	0002062 // chondrocyte differentiation // inferred from mutant phenotype//0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 // regulation of
1442812_a	0.005290	-1.73	-1.69	NM_001081357// <i>NM_0012</i>	<i>Map4k3</i>	mitogen-activated protein kinase kinase kinase 3	0000122 // negative regulation of transcription from RNA polymerase II promoter // not recorded//0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 //
1423136_a	0.001225	-1.73	1.09	NM_008567	<i>Mcm6</i>	minichromosome maintenance deficient 6 (MIS5 homolog, S. pombe) (S.	000165 // MAPK cascade // not recorded//0000185 // activation of MAPKPK activity // not recorded//0006468 // protein phosphorylation // not recorded//0006950 // response to stress //
1429826_a	0.002495	-1.73	-1.39	NM_029613// <i>XM_0064975</i>	<i>Msrb2</i>	methionine sulfoxide reductase B2	0006260 // DNA replication // inferred from electronic annotation//0006268 // DNA unwinding involved in DNA replication // inferred from physical interaction//0006270 // DNA replication
1445132_a	0.002985	-1.73	-1.75	NM_010480// <i>XM_0065154</i>	<i>Hsp90aa1</i>	heat shock protein 90, alpha (cytosolic), class A member 1	0006979 // response to oxidative stress // inferred from electronic annotation//0030041 // actin filament polymerization // inferred from direct assay//0030091 // protein repair // inferred
1424921_a	0.000008						

Table S7

Gene ID	p (Corr)	FC-RSV 1 d	FC-RSV 5 d	RefSeq Transcript ID	Gene Symbol	Gene Title	Gene Ontology Biological Process
1427921_s	0.004711	-1.74	-1.06	NM_175271	<i>Lpar4</i>	lysophosphatidic acid receptor 4	0007165 // signal transduction // inferred from electronic annotation//0007186 // G-protein coupled receptor signaling pathway // inferred from electronic annotation
1444214_s	0.007352	-1.74	-1.72	NM_080855//XM_0065306	<i>Zcchc14</i>	zinc finger, CCHC domain containing 14	0007154 // cell communication // inferred from electronic annotation
1444600_a	0.005360	-1.74	-1.73	NM_053117//XM_0065265	<i>Pard6g</i>	par-6 family cell polarity regulator gamma	0007049 // cell cycle // inferred from electronic annotation//0051301 // cell division // inferred from electronic annotation
1434352_a	0.008272	-1.74	-1.45	NM_145381//XM_0064954	<i>Lactb2</i>	lactamase, beta 2	0008152 // metabolic process // inferred from electronic annotation
1428167_a	0.002013	-1.74	-1.34	NM_001168304//NM_0012	<i>Cdk19</i>	cyclin-dependent kinase 19	0006468 // protein phosphorylation // inferred from electronic annotation//0007049 // cell cycle // inferred from electronic annotation//0008152 // metabolic process // inferred from
1438527_a	0.004748	-1.75	-1.16	NM_010515	<i>Igf2r</i>	insulin-like growth factor 2 receptor	0001889 // liver development // not recorded//0006810 // transport // inferred from electronic annotation//0007186 // G-protein coupled receptor signaling pathway // not
1428707_a	0.009064	-1.75	-1.08	NM_001194921//NM_0011	<i>Cldn18</i>	claudin 18	0016338 // calcium-independent cell adhesion // inferred from sequence or structural similarity
1428779_a	0.005866	-1.75	-1.35	NM_009655	<i>Amd1</i>	S-adenosylmethionine decarboxylase 1	0001701 // in utero embryonic development // inferred from mutant phenotype//0006557 // S-adenosylmethionine biosynthetic process // inferred from electronic
1445790_a	0.005794	-1.75	-1.77	NM_001123037//NM_0011	<i>Etf4a2</i>	eukaryotic translation initiation factor 4A2	0006200 // ATP catabolic process // inferred from electronic annotation//0006412 // translation // inferred from electronic annotation//0006413 // translational initiation // inferred from
1434783_a	0.004054	-1.75	1.02	NM_00109288//NM_1750	<i>Ahrpaa44</i>	Rho GTPase activating protein 44	0007165 // signal transduction // inferred from electronic annotation//0043547 // positive regulation of GTPase activity // inferred from electronic annotation
1435160_a	0.005707	-1.75	-1.13	NM_029558	<i>Fom101b</i>	family with sequence similarity 101, member B	0001837 // epithelial to mesenchymal transition // inferred from genetic interaction//0030036 // actin cytoskeleton organization // inferred from genetic interaction//0030036 // actin
1443941_a	0.002583	-1.75	-1.72	NM_001077712//NM_0012	<i>Stag2</i>	stromal antigen 2	0007049 // cell cycle // inferred from electronic annotation//0007059 // chromosome segregation // inferred from electronic annotation//0007063 // sister chromatid cohesion // not
1434819_a	0.000044	-1.75	-1.47	NM_00128545//NM_0102	<i>Gfra1</i>	glial cell line derived neurotrophic factor family receptor alpha 1	0007169 // transmembrane receptor protein tyrosine kinase signaling pathway // traceable author statement//0007399 // nervous system development // inferred from mutant
1435897_a	0.004063	-1.75	-1.50	NM_011981	<i>Zfp260</i>	zinc finger protein 260	0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 // regulation of transcription, DNA-templated // not recorded//0007275 // multicellular organismal
1433963_a	0.007888	-1.75	-1.12	NM_183195	<i>Marveld1</i>	MARVEL (membrane-associating) domain containing 1	0007049 // cell cycle // inferred from electronic annotation
1439716_a	0.000782	-1.75	-1.59	NM_001171010//NM_0011	<i>Slc14a1</i>	solute carrier family 14 (urea transporter), member 1	0006810 // transport // inferred from electronic annotation//0006833 // water transport // inferred from direct assay//0006833 // water transport // inferred from genetic
1456563_a	0.000036	-1.75	-2.07	NM_028136	<i>Dhx36</i>	DEAH (Pse-Glu-Ala-His) box polypeptide 36	0001503 // ossification // inferred from mutant phenotype//0006200 // ATP catabolic process // not recorded//0006351 // transcription, DNA-templated // inferred from electronic
1449421_a	0.003307	-1.75	-1.22	NM_009012	<i>Rad50</i>	RAD50 homolog (S. cerevisiae)	0000019 // regulation of mitotic recombination // not recorded//0000737 // DNA catabolic process, endonucleolytic // not recorded//0006281 // DNA repair // not recorded//0006302 //
1424996_a	0.000224	-1.75	1.02	NM_001294279//NM_1782	<i>Zfp827</i>	zinc finger protein 827	0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 // regulation of transcription, DNA-templated // inferred from electronic annotation
1423153_x	0.005121	-1.75	1.09	NM_008086	<i>Gas1</i>	growth arrest specific 1	002053 // positive regulation of mesenchymal cell proliferation // inferred from mutant phenotype//0007049 // cell cycle // inferred from electronic annotation//0007050 // cell cycle arrest
1435444_a	0.007740	-1.75	-1.13	NM_008514//XM_0065056	<i>Lrp6</i>	low density lipoprotein receptor-related protein 6	0001702 // gastrulation with mouth forming second // inferred from genetic interaction//0001756 // somitogenesis // inferred from genetic interaction//0001843 // neural tube closure //
1436738_a	0.007972	-1.75	-1.52	NM_018818//XM_0065283	<i>Chm</i>	chondriomera	0001568 // blood vessel development // inferred from mutant phenotype//0006612 // protein targeting to membrane // not recorded//0006886 // intracellular protein transport // inferred
1429272_a	0.003836	-1.75	-1.37	NM_010330	<i>Emb</i>	embigin	0007155 // cell adhesion // not recorded//0035879 // plasma membrane lactate transport // not recorded
1418273_a	0.000473	-1.75	1.41	NM_008521//XM_0065323	<i>Ltc4s</i>	leukotriene C4 synthase	0006691 // leukotriene metabolic process // inferred from direct assay//0006691 // leukotriene metabolic process // not recorded//00019370 // leukotriene biosynthetic process // not
1436357_a	0.006469	-1.75	-1.14	NM_001166635//NM_0265	<i>Mid1p1</i>	Mid1 intracellular protein 1 (gastrulation specific G12-like [zebrafish])	0006629 // lipid metabolic process // inferred from electronic annotation//0007026 // negative regulation of microtubule depolymerization // inferred from genetic interaction//0045723 //
1432144_a	0.000469	-1.76	-1.10	NM_007974	<i>F2r1</i>	coagulation factor II (thrombin) receptor-like 1	0002286 // T cell activation involved in immune response // inferred from direct assay//0002376 // immune system process // inferred from electronic annotation//0002690 // positive
1419721_a	0.001335	-1.76	1.24	NM_176973//XM_0065062	<i>Podk2c</i>	podocalyxin-like 2	0007155 // cell adhesion // inferred from electronic annotation//0050901 // leukocyte tethering or rolling // not recorded
1422457_s	0.009516	-1.76	1.12	NM_007671//XM_0065026	<i>Cdkn2c</i>	cyclin-dependent kinase inhibitor 2C (p18, inhibits CDK4)	0000079 // regulation of cyclin-dependent protein serine/threonine kinase activity // not recorded//0000082 // G1/S transition of mitotic cell cycle // not recorded//0007049 // cell cycle //
1454826_a	0.008123	-1.76	-1.96	NM_001003719//NM_0011	<i>Ralgapa1</i>	Ral GTPase activating protein, alpha subunit 1	0006355 // regulation of transcription, DNA-templated // inferred from direct assay//0003283 // positive regulation of Ran GTPase activity // not recorded//0032859 // activation of Ral
1439465_x	0.000490	-1.76	-1.17	NM_001024917//NM_0065	<i>N4bp2</i>	NEDD4 binding protein 2	0016310 // phosphorylation // not recorded//0009305 // nucleic acid phosphodiester bond hydrolysis // not recorded
1452823_x	0.001914	-1.76	-1.30	NM_026038	<i>L3hpydh</i>	L-3-hydroxyproline dehydratase [trans-]	0008152 // metabolic process // inferred from direct assay//0008152 // metabolic process // not recorded
1418692_d	0.005691	-1.76	1.35	NM_001033166//NM_0010	2700094K13RIK	RIKEN cDNA 2700094K13 gene	0045454 // cell redox homeostasis // inferred from electronic annotation
1438259_a	0.003141	-1.76	-1.55	NM_013635//NM_198710	<i>Sypl</i>	synaptophysin-like protein	0006810 // transport // inferred from electronic annotation
1458367_a	0.000610	-1.76	-2.39	NM_018769//XM_0065064	<i>Dfna5</i>	deafness, autosomal dominant 5 (human)	0006915 // apoptotic process // inferred from electronic annotation//0007605 // sensory perception of sound // not recorded//0008285 // negative regulation of cell proliferation // not
1442640_a	0.001415	-1.76	-1.68	NM_029879//XM_0065177	<i>Rgs7bp</i>	regulator of G-protein signalling 7 binding protein	0007186 // G-protein coupled receptor signaling pathway // inferred from direct assay//0009968 // negative regulation of signal transduction // inferred from electronic annotation
1459908_a	0.006462	-1.77	-1.33	NM_018158//XM_0065028	<i>Pik3r3</i>	phosphatidylinositol 3 kinase, regulatory subunit, polypeptide 3 (p55)	0008286 // insulin receptor signaling pathway // inferred from direct assay//0016310 // phosphorylation // inferred from electronic annotation//0043551 // regulation of phosphatidylinositol
1449984_a	0.000537	-1.77	-1.23	NM_009367//XM_0064971	<i>Tgfb2</i>	transforming growth factor, beta 2	0009092 // cell morphogenesis // not recorded//0001501 // skeletal system development // inferred from mutant phenotype//0001502 // cartilage condensation // inferred from genetic
1437044_a	0.003109	-1.77	-1.15	NM_001085549//XM_0065	<i>Trabd2b</i>	Trab domain containing 2B	0006508 // proteolysis // not recorded//0008152 // metabolic process // not recorded//0016055 // Wnt signaling pathway // inferred from electronic annotation//0018158 // protein
1436633_a	0.000436	-1.77	-1.52	NM_001081163//XM_0065	<i>Chsy1</i>	chondroitin sulfate synthase 1	0020663 // chondrocyte development // inferred from mutant phenotype//0009954 // proximal/distal pattern formation // inferred from mutant phenotype//0030206 // chondroitin sulfate
1448842_a	0.001953	-1.77	-1.19	NM_026735	<i>Mob1b</i>	MOB kinase activator 18B	0016310 // phosphorylation // inferred from electronic annotation//0035329 // tyrosine phosphorylation // not recorded//0042327 // positive regulation of phosphorylation // not recorded//0043085
1428075_a	0.008393	-1.77	-1.07	NM_007976	<i>F5</i>	coagulation factor V	0006508 // proteolysis // not recorded//0007155 // cell adhesion // inferred from electronic annotation//0007596 // blood coagulation // inferred from direct assay//0007596 // blood
1439310_a	0.005495	-1.77	-1.57	NM_028007//XM_0065313	<i>Hg1</i>	integrin alpha FG-GAP repeat containing 1	0006508 // proteolysis // not recorded//0006590 // thyroid hormone generation // not recorded//0008152 // metabolic process // inferred from electronic annotation//0042246 // tissue
1436362_x	0.006500	-1.77	-1.14	NM_018755//NM_176073	<i>Cnq</i>	carboxypeptidase Q	0007165 // signal transduction // inferred from electronic annotation
1430786_a	0.004038	-1.77	-1.41	NM_027760	<i>Rossf8</i>	Ras association (RalGDS/AF-6) domain family (N-terminal) member 8	0008277 // regulation of G-protein coupled receptor protein signaling pathway // inferred from genetic interaction//0051260 // protein homooligomerization // inferred from electronic
1442434_a	0.001963	-1.77	-1.67	NM_177151//NR_039592	<i>Kctd12//Mir5130</i>	potassium channel tetramerisation domain containing 12//microRNA 5130	0001503 // ossification // inferred from electronic annotation//0003416 // endochondral bone growth // inferred from mutant phenotype//0006468 // protein phosphorylation // inferred
1428407_s	0.000218	-1.77	-1.34	NM_022563//XM_0064966	<i>Ddr2</i>	discoidin domain receptor family, member 2	0006810 // transport // inferred from electronic annotation//0006869 // lipid transport // inferred from electronic annotation
1435282_a	0.000228	-1.78	-1.48	NM_133774//XM_0065256	<i>Stard4</i>	STAR-related lipid transfer (START) domain containing 4	0001122 // negative regulation of transcription from RNA polymerase II promoter // inferred from genetic interaction//0006351 // transcription, DNA-templated // inferred from electronic
1447060_a	0.009309	-1.78	-1.81	NM_001009935//NM_0237	<i>Txnip</i>	thioredoxin interacting protein	0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 // regulation of transcription, DNA-templated // inferred from electronic annotation//0008284 //
1428656_a	0.009885	-1.78	-1.35	NM_001177751//NM_0093	<i>Tsc2d1</i>	TSC22 domain family, member 1	0006054 // N-acetyneuraminic acid metabolic process // not recorded//0006486 // protein glycosylation // inferred from mutant phenotype//0018279 // protein N-linked glycosylation via
1449085_a	0.003570	-1.78	-1.20	NM_001252505//NM_0012	<i>St6gal1</i>	beta galactoside alpha 2,6 sialyltransferase 1	0010038 // response to metal ion // inferred from electronic annotation
1426642_a	0.001581	-1.78	-1.03	NM_030021//XM_0064984	<i>Cutl1</i>	cut4/divalent cation tolerance homolog-like	0000245 // spliceosomal complex assembly // inferred from direct assay//0000245 // spliceosomal complex assembly // not recorded//0001525 // angiogenesis // inferred from direct
1433823_x	0.009810	-1.78	-1.44	NM_009274//XM_0065356	<i>Srpk2</i>	serine/arginine-rich protein specific kinase 2	0000077 // DNA damage checkpoint // inferred from mutant phenotype//0007077 // DNA damage checkpoint // not recorded//0006281 // DNA repair // inferred from direct
1429791_a	0.002775	-1.78	-1.39	NM_019864//XM_0065111	<i>Atr</i>	ataxia telangiectasia and Rad3 related	0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 // regulation of transcription, DNA-templated // inferred from electronic annotation//0016568 //
1441217_a	0.009324	-1.78	-1.64	NM_001081383//XM_0065	<i>Kmt2c</i>	lysine (K)-specific methyltransferase 2C	0007018 // microtubule-based movement // inferred from electronic annotation//0007049 // cell cycle // inferred from electronic annotation//0007052 // mitotic spindle organization //
1447933_a	0.008773	-1.78	-1.84	NM_001145779//NM_0084	<i>Kif2a</i>	kinesin family member 2A	0001666 // response to hypoxia // inferred from direct assay//0001666 // response to hypoxia // not recorded//0006810 // transport // inferred from electronic annotation//0006811 // ion
1441131_a	0.007868	-1.79	-1.64	NM_010585//XM_0065056	<i>Itrp1</i>	inositol 1,4,5-trisphosphate receptor 1	0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 // regulation of transcription, DNA-templated // not recorded
1444541_a	0.002013	-1.79	-1.73	NM_001111107//NM_0012	<i>Zfp322a</i>	zinc finger protein 322A	0000122 // negative regulation of transcription from RNA polymerase II promoter // not recorded//0001558 // regulation of cell growth // not recorded//0006351 // transcription, DNA-
1433266_a	0.000815	-1.79	-1.43	NM_011274//XM_0065396	<i>Un1</i>	URI1, prefoldin-like chaperone	0006166 // purine ribonucleoside salvage // inferred from direct assay//0006167 // AMP biosynthetic process // inferred from direct assay//0006175 // dATP biosynthetic process // inferred
1449196_a	0.001190	-1.79	-1.21	NM_001243041//NM_1340	<i>Adk</i>	adenosine kinase	0003030 // cell projection organization // inferred from electronic annotation//0042384 // cilium assembly // not recorded
1428405_a	0.000385	-1.79	-1.08	NM_028672//XM_0065148	<i>Fom161a</i>	family with sequence similarity 161, member A	0000122 // negative regulation of transcription from RNA polymerase II promoter // inferred from electronic annotation//0001654 // eye development // inferred from mutant
1419255_a	0.006276	-1.79	1.29	NM_977361	<i>LOC665506//Tcbr-1//Trtb1</i>	T-cell receptor beta-2 chain C region-like//T cell receptor beta, joining	0007612 // learning // inferred from mutant phenotype//0007626 // locomotory behavior // inferred from mutant phenotype
1442105_a	0.001403	-1.79	-1.66	NM_010439//XM_0039453	<i>Gm21596//Gm6115//Hmgbl1</i>	predicted gene, 21596//predicted gene 6115//high mobility group box	0000165 // MAPK cascade // inferred from direct assay//0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 // regulation of transcription, DNA-
1447937_a	0.006613	-1.79	-1.85	NM_022023//XM_0065193	<i>Gnfb</i>	gla maturation factor, beta	0006470 // protein dephosphorylation // inferred from electronic annotation//0016311 // dephosphorylation // inferred from electronic annotation//0035335 // peptidyl-tyrosine
1424762_a	0.005015	-1.80	1.03	NM_001098789//XM_0065	<i>Ndufa4l2</i>	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 4-like 2	0001501 // skeletal system development // inferred from mutant phenotype//0001501 // skeletal system development // not recorded//0001503 // ossification // inferred from electronic
1460278_a	0.000184	-1.80	-1.33	NM_008702	<i>Nlk</i>	nemo like kinase	0007723 // telomere maintenance // inferred from electronic annotation//0006974 // cellular response to DNA damage stimulus // inferred from electronic annotation//0007049 // cell cycle
1433571_a	0.001916	-1.80	-1.43	NM_026279//NR_033793	<i>Bend5</i>	BER domain containing 5	0006954 // inflammatory response // inferred from direct assay//0032496 // response to lipopolysaccharide // inferred from direct assay//0070935 // 3'-UTR-mediated mRNA stabilization //
1460334_a	0.002623	-1.80	-1.33	NM_008978//XM_0065187	<i>Ptpn20</i>	protein tyrosine phosphatase, non-receptor type 20	0006289 // nucleotide-excision repair // inferred from electronic annotation//0004361 // proteasome-mediated ubiquitin-dependent protein catabolic process // inferred from electronic
1418343_a	0.008555	-1.80	1.40	NM_007742	<i>Col1a1</i>	collagen, type I, alpha 1	0000122 // negative regulation of transcription from RNA polymerase II promoter // inferred from mutant phenotype//0001525 // angiogenesis // inferred from genetic interaction//0001657
1430596_s	0.001947	-1.80	-1.40	NM_175238//XM_0064981	<i>Rf1</i>	Rap1 interacting factor 1 homolog (yeast)	0008152 // metabolic process // inferred from sequence or structural similarity//0007187 // peptidyl-glutamic acid carboxylation // not recorded
1454804_a	0.001149	-1.80	-1.32	NM_029872	<i>Hmnpa0</i>	heterogeneous nuclear ribonucleoprotein A0	0007049 // cell cycle // inferred from electronic annotation//0007067 // mitotic nuclear division // inferred from electronic annotation//0051225 // spindle assembly // not
1451422_a	0.001347	-1.81	-1.27	NM_018798	<i>Ubqln2</i>	ubiquilin 2	0001974 // blood vessel remodeling // inferred from electronic annotation//0007519 // skeletal muscle tissue development // inferred from mutant phenotype//0030158 // extracellular
1448163_a	0.005416	-1.81	-1.17	NM_010207//NM_201601	<i>Fgfr2</i>	fibroblast growth factor receptor 2	0006311 // ubiquitin-dependent protein catabolic process // not recorded//0010771 // negative regulation of cell morphogenesis involved in differentiation // inferred from direct
1453141_a	0.008191	-1.81	-1.90	NM_019802//XM_0065064	<i>Ggxc</i>	gamma-glutamyl carboxylase	0006304 // DNA modification // not recorded//0006749 // glutathione metabolic process // inferred from direct assay//0006749 // glutathione metabolic process // inferred from mutant
1433570_s	0.006748	-1.81	-1.11	NM_146089//XM_0065264	<i>Hous1</i>	HAUS augmin-like complex, subunit 1	0000122 // negative regulation of transcription from RNA polymerase II promoter // inferred from direct assay//0000122 // negative regulation of transcription from RNA polymerase II promoter
1417109_s	0.002360	-1.81	1.79	NM_007925//XM_0065043	<i>Eln</i>	elastin	0006508 // proteolysis // inferred from electronic annotation//0006509 // membrane protein ectodomain proteolysis // not recorded//0042985 // negative regulation of amyloid precursor
1432478_a	0.003314	-1.81	1.09	NM_008447//XM_0065239	<i>Hg3</i>	tetratricopeptide repeat domain 3	0007165 // signal transduction // inferred from electronic annotation//0007399 // nervous system development // inferred from electronic annotation//0008045 // motor neuron axon
1423070_a	0.000755	-1.81	1.09	NM_008185//XM_0065132	<i>Gt1t1</i>	glutathione S-transferase, theta 1	0046491 // L-methylmalonyl-CoA metabolic process // not recorded
1453299_a	0.000184	-1.81	-1.31	NM_007554//XM_0065184	<i>Bmp4</i>	bone morphogenetic protein 4	0008285 // negative regulation of cell proliferation // not recorded//0019511 // peptidyl-proline hydroxylation // inferred from electronic annotation//0055114 // oxidation-reduction process
1425737_a	0.004478	-1.81	-1.01	NM_019517//XM_0065230	<i>Bace2</i>	beta-site APP-cleaving enzyme 2	0007050 // cell cycle arrest // inferred from electronic annotation//0051896 // regulation of protein kinase B signaling // inferred from direct assay//1901031 // regulation of response to
1457944_a	0.001589	-1.81	-2.25	NM_001113246//NM_0011	<i>Chn1</i>	chimerin 1	0008203 // cholesterol metabolic process // not recorded//0036378 // calcitriol biosynthetic process from calcitriol // not recorded//0055114 // oxidation-reduction process // not recorded
1430610_a	0.000755	-1.82	-1.10	NM_028626//XM_0065412	<i>Mcee</i>	methylmalonyl CoA epimerase	0006874 // cellular calcium ion homeostasis // traceable author statement//0007155 // cell adhesion // inferred from electronic annotation//0007156 // homophilic cell adhesion // inferred
1450570_a	0.004034	-1.82	-1.24	NM_013534//XM_0065055	<i>Leprel2</i>	leprecan-like 2	0002790 // peptide cation // inferred from mutant phenotype//0006200 // ATP catabolic process // not recorded//0006497 // protein lipolysis // inferred from mutant
1436612_a	0.000550	-1.82	-1.52	NM_001025572//XM_0065	<i>Ankrd12</i>	ankyrin repeat domain 12	0006198 // cAMP catabolic process // inferred from electronic annotation//0007165 // signal transduction // inferred from electronic annotation//0008152 // metabolic process // --
1436317_a	0.000882	-1.82	-1.51	NM_001013370//NM_00			

Table S7

Gene ID	p (Corr)	FC-RSV 1 d	FC-RSV 5 d	RefSeq Transcript ID	Gene Symbol	Gene Title	Gene Ontology Biological Process	
1450489_a	0.005014	-1.83	-1.24	NM_001081437//NM_0079	<i>Fbln2</i>	fibulin 2	0010811 // positive regulation of cell-substrate adhesion // inferred from direct assay	
1426556_a	0.002896	-1.83	-1.03	NM_019413//XM_0065229	<i>Robo1</i>	roundabout homolog 1 (Drosophila)	0020042 // cell migration involved in sprouting angiogenesis // not recorded//0006919 // activation of cysteine-type endopeptidase activity involved in apoptotic process // not	
1434285_a	0.002704	-1.83	-1.45	NM_181541//XM_0065070	<i>Coprin2</i>	capsin family member 2	0017148 // negative regulation of translation // inferred from electronic annotation//0030154 // cell differentiation // inferred from electronic annotation//0030308 // negative regulation of	
1438243_a	0.005121	-1.83	-1.16	NM_153534//XM_0065171	<i>Adcy2</i>	adenylyl cyclase 2	0006171 // cAMP biosynthetic process // not recorded//0006171 // cAMP biosynthetic process // traceable author statement//0007188 // adenylate cyclase-modulating G-protein coupled	
1418963_a	0.000447	-1.83	1.31	NM_183046//XM_0065270	<i>Kif20b</i>	kinesin family member 20B	0001843 // neural tube closure // inferred from mutant phenotype//0006200 // ATP catabolic process // not recorded//0007018 // microtubule-based movement // inferred from electronic	
1420711_a	0.007067	-1.83	1.19	NM_007743	<i>Col1a2</i>	collagen, type I, alpha 2	0001501 // skeletal system development // not recorded//0001568 // blood vessel development // not recorded//0007179 // transforming growth factor beta receptor signaling pathway //	
1443284_a	0.002738	-1.83	-1.70	NM_008173//XM_0065256	<i>Nrc1</i>	nuclear receptor subfamily 3, group C, member 1	0006111 // regulation of gluconeogenesis // inferred from mutant phenotype//0006338 // chromatin remodeling // not recorded//0006351 // transcription, DNA-templated // inferred from	
1443327_a	0.007632	-1.83	-1.70	NM_001107048//NM_0011	<i>Luc7l2</i>	Luc7-like 2 (S. cerevisiae)	0006376 // mRNA splice site selection // inferred from electronic annotation	
1455574_a	0.001133	-1.83	-2.01	NM_001164099//NM_0011	<i>Adg3</i>	adducin 3 (gamma)	0042493 // response to drug // not recorded	
1435291_a	0.006940	-1.83	-1.48	NM_023877//XM_0065113	<i>Csp70</i>	centrosomal protein 70	0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 // regulation of transcription, DNA-templated // inferred from electronic annotation//0006357 //	
1428436_a	0.009051	-1.83	-1.35	NM_175494	<i>Zfp367</i>	zinc finger protein 367	0001568 // blood vessel development // inferred from mutant phenotype//0003007 // heart morphogenesis // inferred from genetic interaction//0007155 // cell adhesion // not	
1421912_a	0.003371	-1.83	1.14	NM_015734//XM_0064976	<i>Col5a1</i>	collagen, type V, alpha 1	0006810 // transport // inferred from electronic annotation//0007049 // cell cycle // inferred from electronic annotation//0007067 // mitotic nuclear division // inferred from electronic	
1428457_a	0.005589	-1.84	-1.35	NM_025975//XM_0065276	<i>Dynl13</i>	dynein light chain Tctex-type 3	0007049 // cell cycle // inferred from electronic annotation//0008283 // cell proliferation // not recorded	
1431879_a	0.002126	-1.84	-1.42	NM_145220//XM_0065135	<i>Appl2</i>	adaptor protein, phosphotyrosine interaction, PH domain and leucine	0006351 // transcription, DNA-templated // inferred from electronic annotation//0016477 // cell migration // not recorded	
1431192_a	0.009639	-1.84	-1.41	NM_172049	<i>Tmem18</i>	transmembrane protein 18	0008152 // metabolic process // ---//0008152 // metabolic process // inferred from electronic annotation	
1424712_a	0.007395	-1.84	1.03	NM_025421//XM_0065161	<i>Acp1</i>	acylphosphatase 1, erythrocyte (common) type	0043966 // histone H3 acetylation // not recorded	
1440682_a	0.005375	-1.84	-1.63	NM_154442//XM_0065156	<i>Mbp1</i>	MAP3K12 binding inhibitory protein 1	0006068 // ethanol catabolic process // inferred from electronic annotation//0008152 // metabolic process // inferred from electronic annotation//0043066 // negative regulation of	
1428733_a	0.000751	-1.84	-1.35	NM_009566	<i>Aldh2</i>	aldehyde dehydrogenase 2, mitochondrial	0007049 // cell cycle // inferred from electronic annotation//0007067 // mitotic nuclear division // inferred from electronic annotation//0051301 // cell division // inferred from electronic	
1436677_a	0.005386	-1.84	-1.15	NM_001162941//NM_0011	<i>Mapre2</i>	microtubule-associated protein, Rb/EP family, member 2	0006605 // protein targeting // inferred from direct assay//0008286 // insulin receptor signaling pathway // inferred from direct assay//0015758 // glucose transport // inferred from direct	
1452989_a	0.005329	-1.84	-1.89	NM_146008	<i>Tcp112</i>	t-complex 11 (mouse) like 2	0001932 // regulation of protein phosphorylation // inferred from direct assay//0006260 // DNA replication // inferred from electronic annotation//0006275 // regulation of DNA replication	
1451611_a	0.004253	-1.84	-1.28	NM_011505//XM_0065327	<i>Stxbp4</i>	syntaxin binding protein 4	0043462 // regulation of ATPase activity // inferred from mutant phenotype//0045672 // positive regulation of osteoclast differentiation // inferred from mutant phenotype//0045780 //	
1434798_a	0.004225	-1.84	-1.47	NM_176841//XM_0065144	<i>Ccdc88a</i>	coiled coil domain containing 88A	0001122 // negative regulation of transcription from RNA polymerase II promoter // inferred from direct assay//0006351 // transcription, DNA-templated // inferred from electronic	
1428394_a	0.003855	-1.84	-1.08	NM_181401	<i>Tmem64</i>	transmembrane protein 64	0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 // regulation of transcription, DNA-templated // not recorded	
1432614_a	0.005311	-1.84	-1.43	NM_001008542//NM_0010	<i>Mxi1</i>	Max interacting protein 1	0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 // regulation of transcription, DNA-templated // inferred from electronic annotation//0007275 //	
1437085_a	0.007229	-1.84	-1.53	NM_001001880//NM_0010	<i>Mp11</i>	myelin protein zero-like 1	000413 // protein peptidyl-prolyl isomerization // not recorded//0006457 // protein folding // inferred from direct assay//0018208 // peptidyl-proline modification // not	
1440933_a	0.005944	-1.84	-1.63	NM_00104469//NM_0010	<i>Zfp2</i>	zinc finger protein 2	0006810 // transport // inferred from electronic annotation//0006811 // ion transport // inferred from electronic annotation//0006829 // zinc ion transport // inferred from electronic	
1433766_a	0.004128	-1.85	-1.44	NM_00125386//NM_0012	<i>Tcf12</i>	transcription factor 12	0032313 // regulation of Rab GTPase activity // not recorded//0032851 // positive regulation of Rab GTPase activity // inferred from electronic annotation//0032851 // positive regulation of	
1431893_a	0.002360	-1.85	-1.10	NM_012056	<i>Fkbp9</i>	FK506 binding protein 9	0001568 // blood vessel development // inferred from mutant phenotype//0001701 // in utero embryonic development // inferred from mutant phenotype//0001756 // somitogenesis //	
1446547_a	0.004076	-1.85	-1.78	NM_172653//XM_0064959	<i>Sic39o1</i>	solute carrier family 39 (zinc transporter), member 10	0007165 // signal transduction // inferred from electronic annotation//0007186 // G-protein coupled receptor signaling pathway // inferred from electronic annotation	
1448479_a	0.000856	-1.85	-1.18	NM_001134465//NM_0012	<i>Denn6da</i>	DENN/MADD domain containing 6A	0006464 // cellular protein modification process // not recorded//0007605 // sensory perception of sound // inferred from mutant phenotype//0016567 // protein ubiquitination // inferred	
1540405_a	0.002008	-1.85	-1.31	NM_144860//XM_0065258	<i>Mib1</i>	mindbomb homolog 1 (Drosophila)	0005975 // carbohydrate metabolic process // inferred from electronic annotation//0006044 // N-acetylglucosamine metabolic process // not recorded//0006790 // sulfur compound	
1423768_a	0.009534	-1.85	1.06	NM_025331	<i>Gng11</i>	guanine nucleotide binding protein (G protein), gamma 11	0006468 // protein phosphorylation // inferred from direct assay//0006468 // protein phosphorylation // not recorded//0006810 // transport // inferred from electronic	
1446088_a	0.000469	-1.85	-1.78	NM_001081034//XM_0065	<i>Fbxo11</i>	F-box protein 11	000413 // protein peptidyl-prolyl isomerization // not recorded//0006457 // protein folding // inferred from electronic annotation//0018208 // peptidyl-proline modification // not	
1437133_a	0.002746	-1.85	-1.15	NM_021715	<i>Chst7</i>	carbohydrate (N-acetylglucosamine) sulfotransferase 7	0016567 // protein ubiquitination // inferred from electronic annotation	
1452766_a	0.006259	-1.85	-1.88	NM_001164325//NM_0214	<i>Trpm7</i>	transient receptor potential cation channel, subfamily M, member 7	0001937 // negative regulation of endothelial cell proliferation // not recorded//0006470 // protein dephosphorylation // not recorded//0007155 // cell adhesion // inferred from electronic	
1451171_a	0.003176	-1.85	-1.26	NM_010222//XM_0064987	<i>Fkbp7</i>	FK506 binding protein 7	0001662 // behavioral fear response // inferred from mutant phenotype//0006508 // proteolysis // not recorded//0006511 // ubiquitin-dependent protein catabolic process // inferred from	
1437396_a	0.004580	-1.86	-1.15	NM_146193//XM_0065413	<i>Btdb1</i>	BTB (POZ) domain containing 1	0001560 // regulation of cell growth by extracellular stimulus // inferred from mutant phenotype//0007018 // microtubule-based movement // inferred from direct assay//0009968 //	
1419568_a	0.005416	-1.86	1.25	D12Ert123e		DNA segment, Chr 12, ERATO Doi 123, expressed	0032868 // response to insulin // inferred from genetic interaction//0042593 // glucose homeostasis // inferred from genetic interaction//0051896 // regulation of protein kinase B signaling	
1429053_a	0.009263	-1.86	-1.36	NM_008984//XM_0065238	<i>Ptprm</i>	protein tyrosine phosphatase, receptor type, M	0006898 // receptor-mediated endocytosis // inferred from direct assay//0007155 // cell adhesion // inferred from electronic annotation//0007157 // heterophilic cell-cell adhesion //	
1430117_a	0.000734	-1.86	-1.09	NM_177561//XM_0065042	<i>Usp46</i>	ubiquitin specific peptidase 46	0006810 // transport // inferred from electronic annotation//0015886 // heme transport // not recorded//0055085 // transmembrane transport // inferred from electronic annotation	
1425480_a	0.000827	-1.86	-1.00	NM_001097621//XM_0065	<i>Kf26a</i>	kinesin family member 26A	0016567 // protein ubiquitination // inferred from direct assay//0016567 // protein ubiquitination // traceable author statement//0030217 // T cell differentiation // traceable author	
1427175_a	0.005459	-1.86	-1.05	NM_030261	<i>Scn3</i>	scsrtin 3	0001243 // negative regulation of intrinsic apoptotic signaling pathway // inferred from mutant phenotype	
1426126_a	0.006007	-1.86	-1.01	NM_153790//XM_0065220	<i>Scarf2</i>	scavenger receptor class F, member 2	0001605 // MAPK cascade // not recorded//0000186 // activation of MAPK activity // not recorded//0006468 // protein phosphorylation // not recorded//0016310 // phosphorylation //	
1424242_a	0.002604	-1.86	1.05	NM_145447//XM_0065157	<i>Mfcd7c</i>	major facilitator superfamily domain containing 7C	0046485 // ether lipid metabolic process // not recorded	
1434574_a	0.001176	-1.86	-1.46	NM_001081403//XM_0065	<i>Klh14</i>	kelch-like 14	0001122 // negative regulation of transcription from RNA polymerase II promoter // not recorded//0006351 // transcription, DNA-templated // inferred from electronic annotation//0006352 //	
1451746_a	0.009605	-1.86	-1.28	NM_001276292//NM_1773	<i>Wwp1</i>	WW domain containing E3 ubiquitin protein ligase 1	0006112 // energy reserve metabolic process // inferred from direct assay//0006112 // energy reserve metabolic process // inferred from sequence or structural similarity//0006810 //	
1452016_a	0.009085	-1.86	-1.28	NM_001039511//NM_0010	<i>Ivms1abp</i>	influenza virus NS1A binding protein	0006184 // GTP catabolic process // inferred from electronic annotation//0006412 // translation // inferred from electronic annotation//0045727 // positive regulation of translation //	
1433624_a	0.001265	-1.86	-1.43	NM_011946	<i>Map3k2</i>	mitogen-activated protein kinase kinase kinase 2	0043066 // negative regulation of apoptotic process // inferred from mutant phenotype//0045600 // positive regulation of fat cell differentiation // inferred from direct assay//0045600 //	
1435641_a	0.003103	-1.86	-1.49	NM_023440	<i>Tmem86b</i>	transmembrane protein 86B	0006486 // protein glycosylation // inferred from electronic annotation//0036065 // fucosylation // inferred from electronic annotation	
1455970_a	0.000370	-1.86	-2.04	NM_001001176//NM_0011	<i>Taf9b</i>	TAF9B RNA polymerase II, TATA box binding protein (TBP)-associated factor	0006810 // transport // inferred from electronic annotation//0006811 // ion transport // inferred from electronic annotation//0006812 // cation transport // inferred from electronic	
1415190_a	0.000638	-1.86	16.21	NM_001045550//NM_0011	<i>Gm2083//Mup1//Mup10//</i>	major urinary protein LOC100048885//major urinary protein 1//major	0030032 // lamellipodium assembly // inferred from mutant phenotype//0032321 // positive regulation of Rho GTPase activity // inferred from electronic annotation//0035023 // regulation	
1439189_a	0.002352	-1.87	-1.57	NM_172711//NM_182768	<i>Gul1</i>	GU1 GTPase homolog (S. cerevisiae)	0006355 // regulation of transcription, DNA-templated // inferred from electronic annotation	
1449990_a	0.002683	-1.87	-1.23	NM_001081341//NM_1755	<i>Scaper</i>	S-phase cyclin A-associated protein in the ER	0006401 // RNA catabolic process // not recorded	
1434484_a	0.002755	-1.87	-1.12	NM_001177945//NM_0011	<i>Aamd</i>	adipogenesis associated Mth938 domain containing	0015074 // DNA integration // inferred from electronic annotation	
1436651_a	0.000415	-1.87	-1.52	NM_028428	<i>Fut11</i>	fucosyltransferase 11	0001944 // vasculature development // not recorded//0006355 // regulation of transcription, DNA-templated // not recorded//0006357 // regulation of transcription from RNA polymerase II	
1460268_a	0.008695	-1.87	-1.33	NM_172780//XM_0065279	<i>Sic906</i>	solute carrier family 9 (sodium/hydrogen exchanger), member 6	0001525 // angiogenesis // inferred from direct assay//0001666 // response to hypoxia // inferred from electronic annotation//0001942 // hair follicle development // inferred from mutant	
1425719_a	0.000021	-1.87	-1.01	NM_001081380//XM_0065283	<i>Arhgef5</i>	Rac/Cdc42 guanine nucleotide exchange factor (GEF) 5	0007049 // cell cycle // inferred from electronic annotation//0007067 // mitotic nuclear division // inferred from electronic annotation//0007346 // regulation of mitotic cell cycle // not	
1434054_a	0.000570	-1.87	-1.12	NM_028651//XM_0065195	<i>Tmtc4</i>	transmembrane and tetratricopeptide repeat containing 4	0006397 // mRNA processing // inferred from electronic annotation//0007275 // multicellular organismal development // inferred from electronic annotation//000380 // RNA splicing //	
1426328_a	0.000620	-1.88	-1.02	NM_001198048//NM_1769	<i>Zfp942//Zfp944</i>	zinc finger protein 942//zinc finger protein 944	0007417 // central nervous system development // inferred from electronic annotation//0007568 // aging // inferred from electronic annotation//0008285 // negative regulation of cell	
1425193_a	0.000917	-1.88	1.01	NM_028616	<i>Rnash22c</i>	ribonuclease H2, subunit C	0006355 // regulation of transcription, DNA-templated // inferred from electronic annotation	
1429145_a	0.006908	-1.88	-1.36	NM_001163557//NM_0089	<i>Pofbtp2</i>	PTPRF interacting protein, binding protein 2 (liprin beta 2)	0006229 // lipid metabolic process // inferred from electronic annotation//0008611 // ether lipid biosynthetic process // not recorded//0010025 // wax biosynthetic process // inferred from	
1439051_a	0.006508	-1.88	-1.16	NM_008057	<i>Fzd7</i>	frizzled homolog 7 (Drosophila)	0001782 // B cell homeostasis // inferred from mutant phenotype//0002636 // positive regulation of germinal center formation // inferred from mutant phenotype//0006955 // immune	
1449951_a	0.007460	-1.88	-1.23	NM_008808//XM_0065046	<i>Pdgfra</i>	platelet-derived growth factor, alpha	0007165 // signal transduction // inferred from electronic annotation	
1448328_a	0.001772	-1.88	-1.17	NM_001267622//NM_0244	<i>Ttc28</i>	tetratricopeptide repeat domain 28	0001122 // negative regulation of transcription from RNA polymerase II promoter // inferred from direct assay//0006351 // transcription, DNA-templated // inferred from electronic	
1427460_a	0.009245	-1.88	-1.05	NM_134163//XM_0065414	<i>Mbn13</i>	muscleblind-like 3 (Drosophila)	0007275 // multicellular organismal development // inferred from electronic annotation//0007283 // spermatogenesis // inferred from electronic annotation//00030154 // cell differentiation	
1451006_a	0.000283	-1.88	-1.25	NM_011594	<i>Tim2</i>	tissue inhibitor of metalloproteinase 2	0012937 // coenzyme A biosynthetic process // inferred from direct assay//0015937 // coenzyme A biosynthetic process // inferred from mutant phenotype//0015937 // coenzyme A	
1429549_a	0.001520	-1.88	-1.38	NM_181278	<i>B230219D22rik</i>	RIKEN cDNA B230219D22 gene	0006108 // malate metabolic process // not recorded//0006108 // malate metabolic process // inferred from sequence or structural similarity//0009725 // response to hormone // not	
1432164_a	0.003351	-1.88	-1.10	NM_009052	<i>Bex1</i>	brain expressed gene 1	0023133 // regulation of Rab GTPase activity // inferred from electronic annotation//0032851 // positive regulation of Rab GTPase activity // not recorded//0032880 // regulation of protein	
1435603_a	0.003011	-1.88	-1.49	NM_001285831//NM_0261	<i>For1</i>	fatty acyl CoA reductase 1	0006200 // ATP catabolic process // not recorded//0006635 // fatty acid beta-oxidation // not recorded//0006810 // transport // inferred from electronic annotation//0007031 //	
1437979_a	0.005101	-1.88	-1.54	NM_025669//XM_0065381	<i>Pnir</i>	PNN interacting serine/arginine-rich	0001122 // negative regulation of transcription from RNA polymerase II promoter // not recorded//0001702 // gastrulation with mouth forming second // inferred from mutant	
1433864_a	0.009682	-1.88	-1.44	NM_033622//XM_0065087	<i>Tnfrsf13b</i>	tumor necrosis factor (ligand) superfamily, member 13b		
1430300_a	0.001133	-1.89	-1.39	NM_001166064//XM_0065	<i>Syde2</i>	syndap defective 1, Rho GTPase, homolog 2 (C. elegans)		
1432037_a	0.003886	-1.89	-1.42	NM_001083967//NM_0136	<i>Tcf4</i>	transcription factor 4		
1428636_a	0.002485	-1.89	-1.35	NM_025943//XM_0065193	<i>Dap1</i>	DAX interacting protein 1		
1425405_a	0.000451	-1.89	1.00	NM_001114339//NM_0237	<i>Pank1</i>	panthothenate kinase 1		
1430978_a	0.005139	-1.89	-1.57	NM_001108933//NM_0086	<i>Me1</i>	malic enzyme 1, NAD(P)-dependent, cytosolic		
1450224_a	0.007374	-1.89	-1.24	NM_001038623//NM_0138	<i>Rabgap11</i>	RAB GTPase activating protein 1-like		
1421644_a	0.000021	-1.89	1.15	NM_001177881//NM_0011	<i>Mfap31</i>	microfibrillar-associated protein 3-like		
1427984_a	0.007554	-1.89	-1.06	NM_172619//NR_037707//	<i>Adamts10</i>	a disintegrin-like and metalloproteinase (reprolysin type) with		
1437773_a	0.002995	-1.89	-1.16	NM_009712	<i>Arsb</i>	arylsulfatase B		
1435950_a	0.001606	-1.89	-1.58	NM_001193303//NM_0261	<i>Lims1</i>	LIM and senescent cell antigen-like domains 1		
1454820_a	0.002663	-1.90	-1.32	NM_009924//XM_0065385	<i>Cnr2</i>	cannabinoid receptor 2 (macrophage)		
1444110_a	0.003836	-1.90	-1.72	NM_011908//XM_0065048	<i>Ubi3</i>	ubiquitin-like 3		
1437103_a	0.000614	-1.90	-1.15	NM_021345//XM_0065113	<i>Ptplad1</i>	protein tyrosine phosphatase-like A domain containing 1		
1460174_a	0.003203	-1.90	-1.33	NM_176837//XM_0065128	<i>Arhgap18</i>	Rho GTPase activating protein 18		
1457966_a	0.001170	-1.90	-1.25	NM_028757//XM_0064975	<i>Nebi</i>	nebulin		
1452065_a	0.000114	-1.90	-1.29	NM_008991//XM_0065011	<i>Abcd3</i>	ATP-binding cassette, sub-family D (ALD), member 3		
1439048_a	0.008298	-1.90	-1.57	NM_001190466//NM_0215	<i>Dact1</i>	dapper homolog 1, antagonist of beta-catenin (xenopus)		

Table S7

Gene ID	p (Corr)	FC-RSV 1 d	FC-RSV 5 d	RefSeq Transcript ID	Gene Symbol	Gene Title	Gene Ontology Biological Process
1447937_a	0.006613	-1.90	-1.85	NM_133854	<i>Snapi</i>	SNAP-associated protein	0006886 // intracellular protein transport // inferred from electronic annotation // 0006887 // exocytosis // inferred from electronic annotation // 0007268 // synaptic transmission // inferred
1436760_a	0.004213	-1.91	-1.15	NM_183116// <i>XM_0065129</i>	<i>Sk18b1</i>	solute carrier family 18, subfamily B, member 1	0006810 // transport // inferred from electronic annotation // 0005085 // transmembrane transport // inferred from electronic annotation
1438531_a	0.000094	-1.91	-1.56	NM_009409	<i>Top2b</i>	topoisomerase (DNA) II beta	0000712 // resolution of meiotic recombination intermediates // not recorded // 0000819 // sister chromatid segregation // not recorded // 0001764 // neuron migration // inferred from
1449913_a	0.004740	-1.91	-1.23	NM_138956// <i>XM_0065133</i>	<i>Ross3j</i>	Ras association (RalGDS/AF-6) domain family member 3	0007165 // signal transduction // inferred from electronic annotation
1436003_a	0.001429	-1.91	-1.50	NM_001177319// <i>NM_0011</i>	<i>Tjpi</i>	tissue factor pathway inhibitor	0007596 // blood coagulation // inferred from electronic annotation // 0007599 // hemostasis // inferred from electronic annotation // 0010466 // negative regulation of peptidase activity //
1444524_a	0.004253	-1.91	-1.73	NM_019551// <i>XM_0065167</i>	<i>Tdp2</i>	lysyl-DNA phosphodiesterase 2	0006281 // DNA repair // inferred from electronic annotation // 0006302 // double-strand break repair // not recorded // 0006974 // cellular response to DNA damage stimulus // inferred from
1427346_a	0.001260	-1.91	-1.05	NM_016704// <i>XM_0065199</i>	<i>C6</i>	component component 6	0001701 // in utero embryonic development // inferred from genetic interaction // 0001970 // positive regulation of activation of membrane attack complex // inferred from mutant
1435208_a	0.001466	-1.91	-1.48	NM_029436// <i>XM_0065226</i>	<i>Khlh24</i>	ketch-like 24	
1456777_a	0.003779	-1.92	-2.09	NM_00103272// <i>NM_0012</i>	<i>Sybu</i>	synaptoblin (syntaxin-interacting)	0061178 // regulation of insulin secretion involved in cellular response to glucose stimulus // not recorded
1449308_a	0.000370	-1.92	-1.21	NM_001007220// <i>NM_0010</i>	<i>Adam22</i>	a disintegrin and metalloproteinase domain 22	0006508 // proteolysis // inferred from electronic annotation // 0007229 // integrin-mediated signaling pathway // inferred from electronic annotation // 0008344 // adult locomotory behavior
1448116_a	0.002623	-1.92	-1.17	NM_001195268// <i>NM_0157</i>	<i>Dos</i>	downstream of Sltk1	
1434387_a	0.001403	-1.92	-1.45	NM_021356// <i>XM_0065306</i>	<i>Gab1</i>	growth factor receptor bound protein 2-associated protein 1	0000187 // activation of MAPK activity // inferred from direct assay // 0006979 // response to oxidative stress // inferred from direct assay // 0007165 // signal transduction // inferred from
1438081_a	0.004415	-1.92	-1.54	NM_001290576// <i>NM_0167</i>	<i>Pbx3</i>	pre B cell leukemia homeobox 3	0002087 // regulation of respiratory gaseous exchange by neurological system process // inferred from mutant phenotype // 0006351 // transcription, DNA-templated // inferred from
1433184_a	0.004422	-1.92	-1.43	NM_027225// <i>NM_177025</i>	<i>Cobll1</i>	CobL-like 1	
1424391_a	0.005961	-1.92	1.04	NM_178738// <i>XM_0065111</i>	<i>Prss35</i>	protease, serine 35	0006508 // proteolysis // inferred from electronic annotation // 0008152 // metabolic process // inferred from electronic annotation
1426750_a	0.004805	-1.92	-1.03	NM_009670// <i>NM_146005</i>	<i>Ank3</i>	ankyrin 3, epithelial	0000281 // mitotic cytokinesis // not recorded // 0007009 // plasma membrane organization // not recorded // 0007165 // signal transduction // inferred from electronic annotation // 0007409
1434182_a	0.003933	-1.92	-1.45	NM_001199113// <i>NM_0011</i>	<i>Sk29a1</i>	solute carrier family 29 (nucleoside transporters), member 1	0006810 // transport // inferred from electronic annotation // 0007595 // lactation // inferred from electronic annotation // 0015858 // nucleoside transport // inferred from direct
1448429_a	0.000165	-1.92	-1.18	NM_024236	<i>Qdpr</i>	quinoid dihydropteridine reductase	0001889 // liver development // inferred from electronic annotation // 0006559 // L-phenylalanine catabolic process // inferred from electronic annotation // 0006729 // tetrahydrobiopterin
1424139_a	0.004759	-1.92	1.05	NM_026046// <i>XM_0065403</i>	<i>Zfp329</i>	zinc finger protein 329	0006351 // transcription, DNA-templated // inferred from electronic annotation // 0006355 // regulation of transcription, DNA-templated // inferred from electronic annotation
1457646_a	0.005374	-1.92	-2.22	NM_201515// <i>XM_0065160</i>	<i>Map4k5</i>	mitogen-activated protein kinase kinase kinase 5	000165 // MAPK cascade // not recorded // 0000185 // activation of MAPKK activity // not recorded // 0006468 // protein phosphorylation // not recorded // 0006950 // response to stress //
1429090_a	0.005651	-1.92	-1.09	NM_029938	<i>H2afp</i>	H2A histone family, member V	0006334 // nucleosome assembly // inferred from electronic annotation
1427597_a	0.007339	-1.93	-1.06		<i>Tcrg//Tcrg-C2//Tcrg-</i>	Mus musculus 2 day neonate thymus thymic cells cDNA, RIKEN full-length	
1437493_a	0.001902	-1.93	-1.54	NM_133821	<i>Phlpp1</i>	PH domain and leucine rich repeat protein phosphatase 1	0006470 // protein dephosphorylation // not recorded // 0006915 // apoptotic process // inferred from electronic annotation // 0008152 // metabolic process // inferred from electronic
1452604_a	0.008650	-1.93	-1.30	NM_018826	<i>Irx5</i>	Iroquois related homeobox 5 (Drosophila)	0002027 // regulation of heart rate // inferred from mutant phenotype // 0006351 // transcription, DNA-templated // inferred from electronic annotation // 0006355 // regulation of
1453364_a	0.007169	-1.93	-1.32	NM_001199414// <i>NM_1445</i>	<i>Zmynd11</i> // <i>AK215297</i>	zinc finger, MYND domain containing 11//Mus musculus cDNA,	0006351 // transcription, DNA-templated // inferred from electronic annotation // 0006355 // regulation of transcription, DNA-templated // inferred from electronic annotation // 0001658 //
1451395_a	0.004897	-1.93	-1.27	NM_008737// <i>XM_0065307</i>	<i>Nrp1</i>	neuropilin 1	0001576 // angiogenesis // inferred from mutant phenotype // 0001569 // patterning of blood vessels // inferred from mutant phenotype // 0001764 // neuron migration // inferred from
1426708_a	0.007908	-1.93	-1.03	NM_007642	<i>Cd28</i>	CD28 antigen	0002863 // positive regulation of inflammatory response to antigenic stimulus // inferred from mutant phenotype // 0006955 // immune response // inferred from electronic
1424322_a	0.005561	-1.93	-1.67	NM_172772// <i>XM_0065111</i>	<i>Fam63b</i>	family with sequence similarity 63, member B	
1428373_a	0.009350	-1.93	-1.34	NM_009427	<i>Tob1</i>	transducer of ErbB-2.1	
1445473_a	0.008248	-1.94	-1.76	XM_001474060	<i>Gm2590</i>	predicted gene 2590	0007184 // SMAD protein import into nucleus // inferred from direct assay // 0008285 // negative regulation of cell proliferation // not recorded // 0017148 // negative regulation of translation
1452289_a	0.004578	-1.94	-1.29	NM_019989	<i>Sh3bgrl</i>	SH3-binding domain glutamic acid-rich protein like	0006605 // protein targeting // inferred from direct assay
1429189_a	0.001305	-1.94	-1.36	NM_008867// <i>XM_0064989</i>	<i>Pla2r1</i>	phospholipase A2 receptor 1	0001816 // cytokine production // not recorded // 0006897 // endocytosis // inferred from electronic annotation // 0006898 // receptor-mediated endocytosis // inferred from direct
1449555_a	0.000050	-1.94	-1.22	NM_022018// <i>XM_0065297</i>	<i>Fam129a</i>	family with sequence similarity 129, member A	0001933 // negative regulation of protein phosphorylation // inferred from mutant phenotype // 0001934 // positive regulation of protein phosphorylation // inferred from mutant
1437867_a	0.005086	-1.94	-1.16	NM_001080746// <i>NM_0010</i>	<i>Gtj2</i>	general transcription factor II	0006351 // transcription, DNA-templated // inferred from electronic annotation // 0006355 // regulation of transcription, DNA-templated // inferred from electronic annotation // 0009790 //
1425218_a	0.003632	-1.94	1.01	NM_175329// <i>XM_0065129</i>	<i>Chchd10</i>	coiled-coil-helix-coiled-coil-helix domain containing 10	0006119 // oxidative phosphorylation // not recorded // 0006754 // ATP biosynthetic process // not recorded // 00200984 // negative regulation of ATP citrate synthase activity // not recorded
1450840_a	0.006785	-1.94	-1.25	NM_001282071// <i>NM_1477</i>	<i>Sftbp</i>	surfactant associated protein B	0006629 // lipid metabolic process // inferred from electronic annotation // 0006665 // sphingolipid metabolic process // inferred from electronic annotation // 0007585 // respiratory gaseous
1422677_a	0.007169	-1.94	1.11	NM_001141474// <i>XM_0065</i>	<i>Fam189a2</i>	family with sequence similarity 189, member A2	
1437200_a	0.009301	-1.95	-1.53	NM_010453	<i>Hoxa5</i>	homeobox A5	0001501 // skeletal system development // inferred from mutant phenotype // 0002009 // morphogenesis of an epithelium // inferred from mutant phenotype // 0003016 // respiratory system
1450734_a	0.003103	-1.95	-1.25	NM_026512// <i>XM_0065167</i>	<i>Bphl</i>	biphenyl hydrolase-like (serine hydrolase, breast epithelial mucin-	0006508 // proteolysis // inferred from electronic annotation // 0008152 // metabolic process // inferred from electronic annotation
1450816_a	0.004548	-1.95	-1.25	NM_009261// <i>NM_176932</i>	<i>Strbp</i>	spermatid perinuclear RNA binding protein	0006928 // cellular component movement // inferred from mutant phenotype // 0007275 // multicellular organismal development // inferred from electronic annotation // 0007283 //
1428029_a	0.000101	-1.95	-1.07	NM_001110271// <i>NM_0011</i>	<i>Ahn14a</i>	ahmatol domain containing 14A	0008152 // metabolic process // inferred from electronic annotation
1434931_a	0.000426	-1.95	-1.13	NM_026860	<i>Ghrk3</i>	gastrokine 3	0050680 // negative regulation of epithelial cell proliferation // inferred from direct assay
1433812_a	0.006320	-1.95	-1.44	NM_008517// <i>XM_0065132</i>	<i>Lc4d</i>	leukotriene A4 hydrolase	0006508 // proteolysis // not recorded // 0006691 // leukotriene metabolic process // not recorded // 0019370 // leukotriene biosynthetic process // not recorded // 0043171 // peptide
1429795_a	0.002673	-1.95	-1.39	NM_212457	<i>Bex4</i>	brain expressed gene 4	
1455116_a	0.006301	-1.95	-1.98	NM_175312	<i>B630005N14Rik</i>	RIKEN cDNA B630005N14 gene	0031167 // rRNA methylation // inferred from electronic annotation // 0032259 // methylation // inferred from electronic annotation
1452339_a	0.009730	-1.96	-1.29	NM_001081413// <i>NM_0214</i>	<i>Unc13b</i>	unc-13 homolog B (C. elegans)	0006887 // exocytosis // inferred from electronic annotation // 0007165 // signal transduction // traceable author statement // 0007268 // synaptic transmission // inferred from mutant
1452693_a	0.007802	-1.96	-1.87	NM_010513// <i>XM_0065406</i>	<i>Igf1r</i>	insulin-like growth factor 1 receptor	0006468 // protein phosphorylation // inferred from direct assay // 0006955 // immune response // not recorded // 0007169 // transmembrane receptor protein tyrosine kinase signaling
1426220_a	0.002289	-1.96	-1.01	NM_153403// <i>XM_0065030</i>	<i>Ago1</i>	argonaute RISC catalytic subunit 1	0009956 // nuclear-transcribed mRNA catabolic process // not recorded // 0006351 // transcription, DNA-templated // inferred from electronic annotation // 0006355 // regulation of
1451361_a	0.001818	-1.96	-1.27	NM_001293757// <i>NM_0012</i>	<i>Dctn6</i>	dystinctin 6	0007005 // microtubule organization // not traceable author statement // 0007052 // mitotic spindle organization // inferred from direct assay // 0008610 // lipid biosynthetic process // non-
1449013_a	0.005184	-1.96	-1.20	NM_001162494// <i>NM_0080</i>	<i>Fzd6//Gm26704</i>	frizzled homolog 6 (Drosophila) //predicted gene, 26704	0001525 // angiogenesis // not recorded // 0001736 // establishment of planar polarity // inferred from genetic interaction // 0001843 // neural tube closure // inferred from genetic
1434539_a	0.008856	-1.96	-1.46	NM_001166303// <i>NM_0011</i>	<i>Sotb1</i>	special AT-rich sequence binding protein 1	0000122 // negative regulation of transcription from RNA polymerase II promoter // inferred from direct assay // 0000122 // negative regulation of transcription from RNA polymerase II
1418809_a	0.000852	-1.96	1.33	NM_001252627// <i>NM_0012</i>	<i>Cdh16</i>	cadherin 16	0007155 // cell adhesion // inferred from electronic annotation // 0007156 // homophilic cell adhesion // inferred from electronic annotation // 0016339 // calcium-dependent cell-cell adhesion
1429167_a	0.002506	-1.96	-1.36	NM_026674// <i>NM_177583</i>	<i>Aph1b//Aph1c</i>	anterior pharynx defective 1b homolog (C. elegans) //anterior pharynx	0001656 // metanephros development // inferred from mutant phenotype // 0006508 // proteolysis // inferred from genetic interaction // 0007219 // notch signaling pathway // inferred from
1427009_a	0.004225	-1.97	-1.04	NM_025429// <i>XM_0065167</i>	<i>Serpinb1a</i>	serine (or cysteine) peptidase inhibitor, clade B, member 1a	0010466 // negative regulation of peptidase activity // inferred from electronic annotation // 0010951 // negative regulation of endopeptidase activity // not recorded // 0030162 // regulation
1434456_a	0.003699	-1.97	-1.46	NM_019706// <i>NM_207623</i>	<i>Rnf138</i>	ring finger protein 138	0016055 // Wnt signaling pathway // inferred from electronic annotation // 0016567 // protein ubiquitination // inferred from electronic annotation
1455868_a	0.001128	-1.97	-1.32	NM_001253857// <i>NM_0273</i>	<i>Tet1</i>	tet methylcytosine dioxygenase 1	0001826 // inner cell mass cell differentiation // inferred from mutant phenotype // 0006351 // transcription, DNA-templated // inferred from electronic annotation // 0006355 // regulation of
1434517_a	0.004525	-1.97	-1.13	NM_009955// <i>XM_0065185</i>	<i>Dpys12</i>	dihydropyrimidinase-like 2	0001975 // response to amphetamine // inferred from electronic annotation // 0006208 // pyrimidine nucleobase catabolic process // inferred from electronic annotation // 0006897 //
1438434_a	0.006562	-1.97	-1.56	NM_172643// <i>XM_0065294</i>	<i>Zbtb41</i>	zinc finger and BTB domain containing 41 homolog	0006351 // transcription, DNA-templated // inferred from electronic annotation // 0006355 // regulation of transcription, DNA-templated // inferred from electronic annotation
1441895_x	0.002249	-1.97	-1.65	NM_001037937// <i>NM_1454</i>	<i>Deptor</i>	DEP domain containing MTOR-interacting protein	0006469 // negative regulation of protein kinase activity // not recorded // 0032007 // negative regulation of TOR signaling // not recorded // 0035556 // intracellular signal transduction //
1456393_a	0.001495	-1.97	-1.33	NM_010180// <i>XM_0065304</i>	<i>Fbin1</i>	fibulin 1	0007566 // embryo implantation // inferred from electronic annotation // 0010552 // positive regulation of peptidase activity // inferred from direct assay // 0030198 // extracellular matrix
1450764_a	0.000456	-1.97	-1.25	NM_001178058// <i>NM_0011</i>	<i>Tnfrd3</i>	thioredoxin reductase 3	0006749 // glutathione metabolic process // inferred from direct assay // 0006810 // transport // inferred from electronic annotation // 0007275 // multicellular organismal development //
1431066_a	0.005535	-1.98	-1.41	NM_001290308// <i>NM_0077</i>	<i>Col12a1</i>	collagen, type XII, alpha 1	0007155 // cell adhesion // inferred from electronic annotation
1427875_a	0.006080	-1.98	-1.06	NM_001111314// <i>NM_0198</i>	<i>Ngef</i>	neuronal guanine nucleotide exchange factor	0007275 // multicellular organismal development // inferred from electronic annotation // 0007399 // nervous system development // inferred from electronic annotation // 0009097 // cellular
1440922_a	0.004290	-1.98	-1.63	NM_001253708// <i>NM_0012</i>	<i>Mbn1</i>	muscleblind-like 1 (Drosophila)	0000380 // alternative mRNA splicing, via spliceosome // inferred from mutant phenotype // 0000380 // alternative mRNA splicing, via spliceosome // not recorded // 0003381 // regulation of
1416697_a	0.000435	-1.98	2.21	NM_030143	<i>Ddit4l</i>	DNA damage-inducible transcript 4-like	0009968 // negative regulation of signal transduction // inferred from electronic annotation
1437486_a	0.007989	-1.98	-1.53	NM_172458	<i>Zfp871</i>	zinc finger protein 871	0006355 // regulation of transcription, DNA-templated // inferred from electronic annotation
1439771_x	0.000473	-1.98	-1.17	NM_001122952// <i>NM_0011</i>	<i>Nfia</i>	nuclear factor I/A	0006260 // DNA replication // inferred from electronic annotation // 0006351 // transcription, DNA-templated // inferred from electronic annotation // 0006355 // regulation of transcription,
1416429_a	0.001456	-1.98	2.97	NM_001177625// <i>NM_0011</i>	<i>Ect2</i>	ect2 oncogene	0009092 // cell morphogenesis // inferred from direct assay // 0000910 // cytokinesis // not recorded // 0006810 // transport // inferred from electronic annotation // 0007049 // cell cycle //
1436756_x	0.001689	-1.98	-1.15	NM_001114311// <i>NM_0012</i>	<i>Stox2</i>	storkhead box 2	0001893 // maternal placenta development // inferred from electronic annotation // 0001893 // maternal placenta development // inferred from sequence or structural similarity // 0009790 //
1438719_a	0.007792	-1.98	-1.56	NM_001113416// <i>NM_1455</i>	<i>Epb4.1f5</i>	erythrocyte protein band 4.1-like 5	0000904 // cell morphogenesis involved in differentiation // inferred from mutant phenotype // 0001701 // in utero embryonic development // inferred from mutant phenotype // 0001756 //
1437003_a	0.006113	-1.98	-1.53	NM_001197321// <i>NM_0011</i>	<i>Foxp1</i>	forkhead box P1	0000122 // negative regulation of transcription from RNA polymerase II promoter // inferred from direct assay // 0000122 // negative regulation of transcription from RNA polymerase II
1439980_a	0.005800	-1.98	-1.60	NM_00117479// <i>XM_0065220</i>	<i>Zfp148</i>	zinc finger protein 148	0000122 // negative regulation of transcription from RNA polymerase II promoter // not recorded // 0006351 // transcription, DNA-templated // inferred from electronic annotation // 0006355 //
1451219_a	0.002847	-1.98	-1.26	NM_029007	<i>Fam84a</i>	family with sequence similarity 84, member A	
1446417_a	0.008142	-1.98	-1.78	NM_001290500// <i>NM_0012</i>	<i>Ttc14</i>	tetratricopeptide repeat domain 14	
1441214_x	0.000791	-1.99	-1.64	NM_008989// <i>XM_0065257</i>	<i>Pgipr//hgp</i>	purine rich element binding protein A//IgA inducing protein	0006268 // DNA unwinding involved in DNA replication // not recorded // 0006270 // DNA replication initiation // traceable author statement // 0006351 // transcription, DNA-templated //
1443866_a	0.005407	-1.99	-1.71	NM_008139	<i>Gnag</i>	guanine nucleotide binding protein, alpha q polypeptide	0001501 // skeletal system development // inferred from mutant phenotype // 0001508 // action potential // inferred from mutant phenotype // 0006384 // GTP catabolic process // not
1423140_a	0.000921	-1.99	1.13	NM_019641	<i>Stmn1</i>	stathmin 1	0007019 // microtubule depolymerization // not recorded // 0007052 // mitotic spindle organization // not recorded // 0007275 // multicellular organismal development // inferred from
1422659_a	0.007426	-2.00	1.11	NM_001277305// <i>NM_1756</i>	<i>Adams2</i>	a disintegrin-like and metalloproteinase (repolyrin type) with	0006508 // proteolysis // inferred from direct assay // 0007283 // spermatogenesis // inferred from mutant phenotype // 0016485 // protein processing // inferred from mutant
1442646_a	0.006019	-2.00	-1.68	NM_001077202// <i>NM_0012</i>	<i>Hs612</i>	heparan sulfate 6-O-sulfotransferase 2	0015015 // heparan sulfate proteoglycan biosynthetic process, enzymatic modification // inferred from direct assay
1455263_a	0.005684	-2.00	-1.99	NM_007734	<i>Col4a3</i>	collagen, type IV, alpha 3	0006919 // activation of cysteine-type endopeptidase activity involved in apoptotic process // not recorded // 0007155 // cell adhesion // inferred from electronic annotation // 0007166 // cell
1439906_a	0.005983	-2.00	-1.60	NM_001077398// <i>NM_0012</i>	<i>Ldb2</i>	LIM domain binding 2	0001942 // hair follicle development // inferred from genetic interaction // 0010669 // epithelial structure maintenance // inferred from genetic interaction // 00035019 // somatic stem cell
1453788_a	0.007879	-2.00	-1.31	NM_019405	<i>Cetn2</i>	centrin 2	0006200 // ATP catabolic process // inferred from electronic annotation // 0006281 // DNA repair // inferred from electronic annotation // 0006289 // nucleotide-excision repair // not
1456328_a	0.003010	-2.01	-2.05	NM_016805// <i>XR_373612</i>	<i>A1503316//Hnmpu</i>	expressed sequence A1503316//heterogeneous nuclear ribonucleoprotein	0001649 // osteoblast differentiation // not recorded // 0006397 // mRNA processing // inferred from electronic annotation // 0008380 // RNA splicing // inferred from electronic
1447059_a	0.000019	-2.01	-1.81	NM_001038999// <i>NM_0012</i>	<i>Atp8a1</i>	ATPase, aminophospholipid transporter (APLT), class I, type 8A, member 1	0006810 // transport // inferred from electronic annotation

Table S7

Gene ID	p (Corr)	FC-RSV 1 d	FC-RSV 5 d	RefSeq Transcript ID	Gene Symbol	Gene Title	Gene Ontology Biological Process
1437819_s	0.004033	-2.02	-1.54	NM_009502//XM_0065189	Vcl	vinculin	0002009 // morphogenesis of an epithelium // not recorded//0007155 // cell adhesion // inferred from direct assay//0030032 // lamellipodium assembly // inferred from direct
1440156_s	0.002712	-2.02	-1.61	NM_007866//XM_0065277	Dmd	dystrophin, muscular dystrophy	0001954 // positive regulation of cell-matrix adhesion // inferred from mutant phenotype//0002027 // regulation of heart rate // inferred from mutant phenotype//0002027 // regulation of
1430126_a	0.007847	-2.02	-1.39	NM_008306//XM_0065256	Ndst1	N-acetylglucosyl-6-sulfatase (heparan glucosaminyl) 1	0000165 // MAPK cascade // inferred from mutant phenotype//0000271 // polysaccharide biosynthetic process // inferred from mutant phenotype//0006476 // protein deacetylation //
1433626_a	0.006899	-2.02	-1.61	NM_007555	Bmp5	bone morphogenetic protein 5	0001501 // skeletal system development // inferred from mutant phenotype//0001503 // ossification // inferred from electronic annotation//0003323 // type B pancreatic cell development
1416482_a	0.000163	-2.02	2.56	NM_007630	Ccnb2	cyclin B2	0000079 // regulation of cyclin-dependent protein serine/threonine kinase activity // inferred from electronic annotation//0001701 // in utero embryonic development // inferred from
1443719_x	0.003570	-2.02	-1.71	NM_01025377//NM_1538	Arhgap15	Rho GTPase activating protein 15	0007165 // signal transduction // inferred from electronic annotation//0008360 // regulation of cell shape // not recorded//0032855 // positive regulation of Rac GTPase activity // not
1449321_x	0.005192	-2.02	-1.21	NM_020510	Fzd2	frizzled homolog 2 (Drosophila)	0001944 // vasculature development // not recorded//0003149 // membranous septum morphogenesis // inferred from genetic interaction//0003150 // muscular septum morphogenesis //
1435151_a	0.000598	-2.02	-1.13	NM_009180//XR_388384	Sf6galnac2	ST6 (alpha-N-acetyl-neuraminyl-2,3-beta-galactosyl-1,3)-N-	0006486 // protein glycosylation // inferred from electronic annotation//0007503 // sialylation // inferred from electronic annotation
1421044_a	0.001367	-2.02	1.17	NM_025806//XM_0065064	Pbd1	phospholipase B domain containing 1	0006529 // lipid metabolic process // inferred from electronic annotation//0016042 // lipid catabolic process // inferred from electronic annotation
1428154_s	0.003741	-2.02	-1.34	NM_028882//XM_0065035	Sema3d	sema domain, immunoglobulin domain (lg), short basic domain, secreted,	0007275 // multicellular organismal development // inferred from electronic annotation//0007399 // nervous system development // inferred from electronic annotation//0030154 // cell
1428330_a	0.009635	-2.03	-1.08	NM_011056//XM_0065176	Pde4d	phosphodiesterase 4D, cAMP specific	0002027 // regulation of heart rate // inferred from mutant phenotype//0006198 // cAMP catabolic process // inferred from direct assay//0006198 // cAMP catabolic process // inferred from
1436729_a	0.005980	-2.03	-1.52	NM_001286158//NM_0273	MLT3	myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog,	0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 // regulation of transcription, DNA-templated // inferred from electronic annotation//0007379 //
1460243_a	0.009835	-2.03	-1.33	NM_001163567	Fam102b	family with sequence similarity 102, member B	
1451793_a	0.000878	-2.03	-1.28	NM_001038642//NM_0118	Ets1	E26 avian leukemia oncogene 1, 5' domain	0001666 // response to hypoxia // inferred from electronic annotation//0002376 // immune system process // inferred from electronic annotation//0006351 // transcription, DNA-templated
1431522_a	0.001952	-2.03	-1.42	NM_007472	Aqp1	aquaporin 1	0003094 // glomerular filtration // inferred from mutant phenotype//0003097 // renal water transport // not recorded//0006182 // cGMP biosynthetic process // not recorded//0006810 //
1441181_a	0.006036	-2.03	-1.64	NM_145823//XM_0065342	Pitpnc1	phosphatidylinositol transfer protein, cytoplasmic 1	0006810 // transport // inferred from electronic annotation//0006869 // lipid transport // inferred from electronic annotation//0007165 // signal transduction // inferred from sequence or
1451243_a	0.000216	-2.03	-1.27	NM_138756//XM_0065108	Slc25a36	solute carrier family 25, member 36	0006810 // transport // inferred from electronic annotation//0003235 // response to estradiol // not recorded//005085 // transmembrane transport // inferred from electronic annotation
1420851_a	0.004337	-2.04	1.18	NM_001252453//NM_0012	Ptptr	protein tyrosine phosphatase, receptor type, 5	0006470 // protein dephosphorylation // inferred from electronic annotation//0007155 // cell adhesion // inferred from electronic annotation//0016311 // dephosphorylation // inferred
1419925_s	0.007948	-2.04	-1.34	NM_172854	Olfml2a	olfactomedin-like 2A	0030198 // extracellular matrix organization // inferred from direct assay
1420532_a	0.009245	-2.04	1.20	NM_019759	Dpt	dermatopontin	0007155 // cell adhesion // inferred from electronic annotation//0008285 // negative regulation of cell proliferation // inferred from direct assay//0030199 // collagen fibril organization //
1453218_a	0.000008	-2.04	-1.90	NM_008249//XM_0064966	Tfb2m	transcription factor B2, mitochondrial	0000154 // rRNA modification // inferred from electronic annotation//0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 // regulation of transcription, /
1450168_a	0.001135	-2.04	-1.23	NM_001284392//NM_0012	42617	septin 4	0007049 // cell cycle // inferred from electronic annotation//0007286 // spermatid development // inferred from mutant phenotype//0007420 // brain development // inferred from mutant
1453285_a	0.007621	-2.04	-1.92	NM_026271	Fibin	fin bud initiation factor homolog (zebrafish)	
1434018_a	0.003323	-2.04	-1.44	NM_00130188//NM_0011	Spce	sarcoglycan, epsilon	
1454897_a	0.002619	-2.04	-1.32	NM_177909	Slc9a9	solute carrier family 9 (sodium/hydrogen exchanger), member 9	0006810 // transport // inferred from electronic annotation//0006811 // ion transport // inferred from electronic annotation//0006812 // cation transport // inferred from electronic
1455067_a	0.008548	-2.05	-1.97	NM_146224//XM_0065111	Zfp280d	zinc finger protein 280D	0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 // regulation of transcription, DNA-templated // inferred from electronic annotation
1452081_a	0.001110	-2.05	-1.29	NM_133218//XM_0065300	Zfp704	zinc finger protein 704	
1439820_a	0.009301	-2.05	-1.60	NR_028380//NR_028381	Ftx	Ftx transcript, Xist regulator (non-protein coding)	0006325 // chromatin organization // inferred from mutant phenotype//0010468 // regulation of gene expression // inferred from mutant phenotype//0040030 // regulation of DNA
1442988_a	0.000058	-2.05	-1.69	NM_018761//XM_0065380	Ctnnol1	catenin (cadherin associated protein), alpha-like 1	0007155 // cell adhesion // inferred from electronic annotation//0007266 // Rho protein signal transduction // not recorded
1427658_a	0.005961	-2.05	-1.06	NM_008482//XM_0065149	Lamb1	laminin B1	0007155 // cell adhesion // inferred from electronic annotation//0007162 // negative regulation of cell adhesion // inferred from direct assay//0007566 // embryo implantation // inferred
1443122_a	0.003704	-2.06	-1.69	NM_001130163//NM_0011	Oxr1	oxidation resistance 1	0007628 // adult wading behavior // inferred from mutant phenotype//0001699 // cell wall macromolecule catabolic process // inferred from electronic annotation//0004352 // negative
1439586_a	0.000920	-2.06	-1.58	NM_134065//XM_0065165	Epd-r1	ependymin related protein 1 (zebrafish)	0007160 // cell-matrix adhesion // inferred from electronic annotation
1452198_a	0.003584	-2.06	-1.29	NM_001165997//NM_0011	Spopl	specple-type P02 protein-like	0016567 // protein ubiquitination // inferred from electronic annotation//0031397 // negative regulation of protein ubiquitination // not recorded//0004316 // proteasome-mediated
1420798_s	0.007879	-2.07	1.19	NM_011107//XM_0065301	Pla2g1b	phospholipase A2, group IIb, pancreas	0002227 // innate immune response in mucosa // not recorded//0006629 // lipid metabolic process // inferred from electronic annotation//0006633 // fatty acid biosynthetic process // not
1430736_a	0.003444	-2.07	-1.41	NR_015601	Fam120aos	family with sequence similarity 120, opposite strand	
1450344_a	0.006771	-2.07	-1.24	NM_134054	Sptssa	serine palmitoyltransferase, small subunit A	0006629 // lipid metabolic process // inferred from electronic annotation//0006665 // sphingolipid metabolic process // inferred from electronic annotation
1451574_a	0.004072	-2.08	-1.28	NM_001033342//XM_0065	Cdc42bpg	CDC42 binding protein kinase gamma (DMPK-like)	0006468 // protein phosphorylation // not recorded//0016310 // phosphorylation // inferred from electronic annotation//0031532 // actin cytoskeleton reorganization // inferred from
1457753_a	0.000126	-2.08	-2.23	NM_015822//XM_0065192	Fbx13	F-box and leucine-rich repeat protein 3	0016567 // protein ubiquitination // inferred from direct assay//0031146 // SCF-dependent proteasomal ubiquitin-dependent protein catabolic process // inferred from direct assay//0031146
1430048_a	0.002292	-2.08	-1.39	NM_001160345//NR_02770	Svip	small VCP/p97-interacting protein	
1438570_a	0.001088	-2.08	-1.56	NM_027626//NM_030263	Ps3d	pleckstrin and Sec7 domain containing 3	0030182 // neuron differentiation // not recorded//0032011 // ARF protein signal transduction // inferred by curator//0032012 // regulation of ARF protein signal transduction // inferred
1443220_a	0.009481	-2.08	-1.07	NM_016783	Pgrmc1	progesterone receptor membrane component 1	0007411 // axon guidance // inferred from electronic annotation
1449625_a	0.009770	-2.08	-1.22	NM_02035917//NM_0296	Dpkl1	death associated protein kinase 1	0006417 // regulation of translation // inferred from electronic annotation//0006468 // protein phosphorylation // not recorded//0006468 // protein phosphorylation // inferred from direct
1456288_a	0.000464	-2.08	-1.05	NM_011851	Ntse	5' nucleotidase, ecto	0006164 // purine nucleotide biosynthetic process // not recorded//0006195 // AMP catabolic process // inferred from mutant phenotype//0006196 // AMP catabolic process // not
1452971_a	0.009278	-2.08	-1.89	NM_133810//XM_0064963	Slk17b	serine/threonine kinase 17b (apoptosis-inducing)	0006468 // protein phosphorylation // not recorded//0006915 // apoptotic process // not recorded//0012501 // programmed cell death // not recorded//0016310 // phosphorylation //
1448871_a	0.008831	-2.08	-1.19	NM_001164791//NM_0230	Zak	sterile alpha motif and leucine zipper containing kinase AZK	0000075 // cell cycle checkpoint // not recorded//0000077 // DNA damage checkpoint // not recorded//0000165 // MAPK cascade // inferred from direct assay//0000186 // activation of
1431609_a	0.002713	-2.08	-1.10	NM_177351	Hykk	hydroxylase kinase 1	0016310 // phosphorylation // inferred from electronic annotation
1416636_a	0.005254	-2.09	2.31	NM_009696//XM_0065394	Apoe	apolipoprotein E	0001937 // negative regulation of endothelial cell proliferation // not recorded//0002021 // response to dietary excess // inferred from mutant phenotype//0006629 // lipid metabolic
1428448_a	0.007971	-2.09	-1.08	NM_008609	Mmp15	matrix metalloproteinase 15	0006508 // proteolysis // inferred from sequence or structural similarity//0032355 // response to estradiol // inferred from electronic annotation
1418965_a	0.006740	-2.09	1.31	NM_146007//XM_0065131	Col6a2	collagen, type VI, alpha 2	0007155 // cell adhesion // inferred from electronic annotation//0009749 // response to glucose // inferred from electronic annotation//0070208 // protein heterotrimerization // not
1447937_a	0.006613	-2.09	-1.86	NM_198105//XM_0065287	Fam120c	family with sequence similarity 120, member C	
1427059_a	0.003550	-2.10	-1.05	NM_008625	Mrc1	mannose receptor, C type 1	0006897 // endocytosis // inferred from electronic annotation//0006898 // receptor-mediated endocytosis // not recorded//0007165 // signal transduction // inferred from direct assay
1453255_a	0.006947	-2.10	-1.92	NM_013881//XM_0065335	Ulk2	unc-51 like kinase 2	0000045 // autophagic vacuole assembly // --//0006468 // protein phosphorylation // inferred from direct assay//0006914 // autophagy // inferred from electronic annotation//0007165 //
1439993_a	0.009303	-2.10	-1.60	NM_001038990//NM_0010	Id5	iduronate 2-sulfatase	0008152 // metabolic process // inferred from electronic annotation
1419824_a	0.009239	-2.10	-1.34	NM_001013833//NM_0111	Prgk1	protein kinase, cGMP-dependent, type I	0001764 // neuron migration // inferred from mutant phenotype//0006468 // protein phosphorylation // inferred from direct assay//0006468 // protein phosphorylation // not
1446212_a	0.002270	-2.10	-1.78	NM_145452//XR_382439	Rasa1	RAS p21 protein activator 1	0001570 // vasculogenesis // inferred from sequence or structural similarity//0001570 // vasculogenesis // inferred from mutant phenotype//0001593 // negative regulation of cell-matrix
1429012_a	0.000344	-2.10	-1.36	NM_001098222//NM_1981	Bhlhb9	basic helix-loop-helix domain containing, class B9	0007611 // learning or memory // inferred from direct assay//0043524 // negative regulation of neuron apoptotic process // inferred from direct assay//0050769 // positive regulation of
1442101_a	0.002449	-2.10	-1.66	NM_001003971//NM_0010	Senp7	SUMO1/sentrin specific peptidase 7	0006508 // proteolysis // inferred from electronic annotation
1424382_a	0.002292	-2.10	1.04	NM_008011//XM_0065170	Fgfr4	fibroblast growth factor receptor 4	0001759 // organ induction // inferred from mutant phenotype//0006468 // protein phosphorylation // inferred from electronic annotation//0008284 // positive regulation of cell
1433937_a	0.003575	-2.11	-1.44	NM_021310	Jmy	junction-mediating and regulatory protein	0006281 // DNA repair // inferred from electronic annotation//0006357 // regulation of transcription from RNA polymerase II promoter // inferred from direct assay//0006974 // cellular
1425821_a	0.001174	-2.11	-1.01	NM_001271599//NM_0199	Sor11	soritin 1	0001503 // ossification // inferred from electronic annotation//0006810 // transport // inferred from electronic annotation//0006895 // Golgi to endosome transport // not
1430343_a	0.002257	-2.11	-1.40	NM_001004359//NM_0010	Gprasp1	G protein-coupled receptor associated sorting protein 1	0008233 // endosome to lysosome transport // not recorded//1990172 // G-protein coupled receptor catabolic process // not recorded
1443354_a	0.008840	-2.11	-1.70	NM_007635	Cnsg2	cyclin G2	0007049 // cell cycle // inferred from electronic annotation//0007067 // mitotic nuclear division // inferred from electronic annotation//0051301 // cell division // inferred from electronic
1426442_a	0.009725	-2.11	-1.02	NM_178394//XM_0065041	Jokmp1	janus kinase and microtubule interacting protein 1	0006810 // transport // inferred from electronic annotation//0015031 // protein transport // inferred from electronic annotation//0005089 // cognition // not recorded
1425398_a	0.002771	-2.11	1.00	NM_001110843//NM_0011	Cnca2a1	calcium channel, voltage-dependent, alpha2/delta subunit 1	0006810 // transport // inferred from electronic annotation//0006811 // ion transport // inferred from electronic annotation//0006816 // calcium ion transport // not recorded//0034765 //
1457145_a	0.004083	-2.11	-2.16	NM_001081251//NM_0258	Pbrm1	polybromo 1	0001890 // placenta development // inferred from mutant phenotype//0001974 // blood vessel remodeling // traceable author statement//0003007 // heart morphogenesis // traceable
1449901_a	0.006031	-2.11	-1.22	NM_009701	Aqp5	aquaporin 5	0006810 // transport // inferred from electronic annotation//0006833 // water transport // inferred from mutant phenotype//0006833 // water transport // not recorded//0006833 //
1446001_a	0.007668	-2.12	-1.77	NM_172513//XM_0064958	Fam126b	family with sequence similarity 126, member B	
1457034_a	0.005751	-2.12	-2.13	NM_0111699	Lin7c	lin-7 homolog C (C. elegans)	0002011 // morphogenesis of an epithelial sheet // not recorded//0006810 // transport // inferred from electronic annotation//0006887 // exocytosis // inferred from electronic
1456603_a	0.009714	-2.12	-1.33	NM_001168679//NM_0011	Tspan8	tetraspanin 8	0030195 // negative regulation of blood coagulation // not recorded
1428887_a	0.006425	-2.12	-1.36	NM_053128	Pcdhb3	protocadherin beta 3	0007155 // cell adhesion // inferred from electronic annotation//0007156 // homophilic cell adhesion // inferred from electronic annotation
1429330_a	0.002420	-2.12	-1.37	NM_031999//NR_003568//	Gpr137b//Gpr137b-ps	G protein-coupled receptor 137B//G protein-coupled receptor 137B,	
1439191_a	0.005719	-2.13	-1.16	NM_018588//XM_0065201	Cmb1	carboxymethylglutathione lyase-like (Pseudomonas)	0008152 // metabolic process // inferred from electronic annotation
1425632_a	0.001373	-2.13	-1.00	NM_011395	Slc22a3	solute carrier family 22 (organic cation transporter), member 3	0006810 // transport // inferred from electronic annotation//0006811 // ion transport // inferred from electronic annotation//0015695 // organic cation transport // inferred from direct
1425473_a	0.004107	-2.13	1.00	NM_031392	Wdr6	WD repeat domain 6	0007049 // cell cycle // inferred from electronic annotation//0007050 // cell cycle arrest // not recorded//0008285 // negative regulation of cell proliferation // not recorded//0010507 //
1437643_a	0.004433	-2.13	-1.54	NM_025626//XM_0064975	Fam107b	family with sequence similarity 107, member B	0007605 // sensory perception of sound // inferred from mutant phenotype
1433141_a	0.005535	-2.14	-1.43	NM_026641//XM_0065019	Irb0	intraflagellar transport 80	0001649 // osteoblast differentiation // inferred from genetic interaction//0001649 // osteoblast differentiation // inferred from mutant phenotype//0002062 // chondrocyte differentiation
1454141_a	0.007928	-2.14	-1.94	NM_178920	Mal2	mal, T cell differentiation protein 2	
1450297_a	0.001533	-2.14	-1.24	NM_001033281//XM_0065	Prdm6	PR domain containing 6	0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 // regulation of transcription, DNA-templated // inferred from electronic annotation//0016568 //
1452346_a	0.006155	-2.14	-1.29	NM_007731//XM_0065131	Col13a1	collagen, type XIII, alpha 1	0001503 // ossification // inferred from electronic annotation//0001763 // morphogenesis of a branching structure // inferred from expression pattern//0001958 // endochondral ossification
1424636_a	0.002930	-2.15	1.03	NM_009181//XM_0065407	Slc8a2	ST8 alpha-N-acetyl-neuraminidase alpha-2,8-sialyltransferase 2	0001574 // ganglioside biosynthetic process // not recorded//0006486 // protein glycosylation // not recorded//0006491 // N-glycan processing // not recorded//0009311 // oligosaccharide
1424775_a	0.000374	-2.15	1.03	NM_027491	Rrag2	Ras-related GTP binding D	
1452738_a	0.000581	-2.15	-1.87	NM_026582//NR_037590//	Wls	wntless homolog (Drosophila)	0001707 // mesoderm formation // inferred from mutant phenotype//0007275 // multicellular organismal development // inferred from electronic annotation//0009948 //
1435770_a	0.009604	-2.15	-1.49	NM_030018//XM_0065231	Tmem50b	transmembrane protein 50B	
1435985_a	0.008144	-2.15	-1.50	NM_001081006//NM_0011	Et14	enhancer trap locus 4	0007275 // multicellular organismal development // inferred from electronic annotation//0048706 // embryonic skeletal system development // inferred from mutant phenotype
1439734_a	0.005761	-2.15	-1.59	NM_001291069//NM_1751	Golim4	golgi integral membrane protein 4	0006810 // transport // inferred from electronic annotation
1442019_a	0.000775	-2.15	-1.66	NM_181444//XM_0065060	Gprc5a	G protein-coupled receptor, family C, group 5, member A	0007165 // signal transduction // inferred from electronic annotation//0007186 // G-protein coupled receptor signaling pathway // inferred from electronic annotation
1447123_a	0.000687	-2.15	-1.82	NM_001005510	Syne2	spectrin repeat containing, nuclear envelope 2	0006998 // nuclear envelope organization // inferred from mutant phenotype//0007097 // nuclear migration // not recorded//0007163 // establishment or maintenance of cell polarity //
1428843_a	0.000085	-2.16	-1.08	NM_008862//XM_0065300	Pkia	protein kinase inhibitor, alpha	0000122 // negative regulation of transcription from RNA polymerase II promoter // inferred from direct assay//0006469 // negative regulation of protein kinase activity // inferred from direct

Table S7

Gene ID	p (Corr)	FC-RSV 1 d	FC-RSV 5 d	RefSeq Transcript ID	Gene Symbol	Gene Title	Gene Ontology Biological Process
1438712_a	0.004592	-2.16	-1.16	NM_007549	<i>Blk</i>	B lymphoid kinase	0006468 // protein phosphorylation // inferred from electronic annotation//00016310 // phosphorylation // inferred from electronic annotation//00018108 // peptidyl-tyrosine phosphorylation
1448987_a	0.000732	-2.16	-1.20	NM_028763	<i>Cbx6</i>	chromobox 6	0001022 // negative regulation of transcription from RNA polymerase II promoter // not recorded//0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355
1460335_a	0.009347	-2.16	-1.33	NM_001145947//NM_0117	<i>Bace1</i>	beta-site APP cleaving enzyme 1	0006508 // proteolysis // inferred from direct assay//0006508 // proteolysis // not recorded//00050435 // beta-amyloid metabolic process // not recorded
1433477_a	0.002918	-2.16	-1.11	NM_008584	<i>Meox2</i>	mesenchyme homeobox 2	0001525 // angiogenesis // inferred from mutant phenotype//0001757 // somite specification // inferred from genetic interaction//0006355 // regulation of transcription, DNA-templated //
1453495_a	0.003048	-2.16	-1.93	NM_001130184//NM_0011	<i>Jade1</i>	jade family PHD finger 1	0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 // regulation of transcription, DNA-templated // inferred from electronic annotation//0006366 //
1429792_a	0.008117	-2.17	-1.39	NM_183186//NM_0065162	<i>Foxn3</i>	forkhead box N3	0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 // regulation of transcription, DNA-templated // inferred from electronic annotation//0007049 //
1439606_a	0.009725	-2.17	-1.58	NM_001163493//NM_1462	<i>Stard13</i>	STAR-related lipid transfer (START) domain containing 13	0007049 // cell cycle // inferred from electronic annotation//0007165 // signal transduction // inferred from electronic annotation//00043547 // positive regulation of GTPase activity //
1438046_a	0.003838	-2.17	-1.54	NM_172516//NM_0065293	<i>Dstyk</i>	dual serine/threonine and tyrosine protein kinase	0006468 // protein phosphorylation // inferred from electronic annotation//00016310 // phosphorylation // inferred from electronic annotation//00018108 // peptidyl-tyrosine phosphorylation
1428553_a	0.006724	-2.17	-1.35	NM_173746	<i>Maao</i>	monoamine oxidase A	0005584 // catecholamine metabolic process // inferred from electronic annotation//00042135 // neurotransmitter catabolic process // inferred from electronic annotation//00042420 //
1434876_a	0.001662	-2.17	-1.47	NM_009511//NM_0065158	<i>Vipr2</i>	vasointestinal peptide receptor 2	0007165 // signal transduction // inferred from electronic annotation//0007168 // cell surface receptor signaling pathway // inferred from electronic annotation//0007186 // G-protein
1449581_a	0.000786	-2.17	-1.22	NM_144942//NM_0065209	<i>Cadca</i>	cysteine sulfonic acid decarboxylase	0008152 // metabolic process // inferred from electronic annotation//00019452 // L-cysteine catabolic process to taurine // traceable author statement//00019530 // taurine metabolic process
1454666_a	0.005458	-2.17	-1.96	NM_010295//NM_0065108	<i>Gclc</i>	glutamate-cysteine ligase, catalytic subunit	0006534 // cysteine metabolic process // not recorded//0006536 // glutamate metabolic process // not recorded//0006749 // glutathione metabolic process // inferred from mutant
1454648_a	0.007868	-2.18	-1.31	NM_028130//NM_0065046	<i>Zfp157</i>	zinc finger protein 157	0006355 // regulation of transcription, DNA-templated // inferred from electronic annotation//0010453 // regulation of cell fate commitment // inferred from mutant phenotype//00048286 //
1452283_a	0.003976	-2.18	-1.29	NM_177730	<i>Impad1</i>	inositol monophosphatase domain containing 1	0001501 // skeletal system development // inferred from mutant phenotype//0001958 // endochondral ossification // inferred from mutant phenotype//0002063 // chondrocyte
1452754_a	0.003985	-2.18	-1.30	NM_009655//NM_0065217	<i>Alcam</i>	activated leukocyte cell adhesion molecule	0007155 // cell adhesion // inferred from electronic annotation//0007411 // axon guidance // inferred from mutant phenotype//0008045 // motor neuron axon guidance // inferred from
1444350_a	0.009994	-2.18	-1.73	NM_001195338//NM_0011	<i>Bbp1</i>	BBsome interacting protein 1	0042384 // cilium assembly // not recorded//00042755 // eating behavior // inferred from mutant phenotype//0009750 // receptor localization to nonmotile primary cilium // inferred from
1416488_a	0.006844	-2.19	2.53	NM_001146031//NM_1769	<i>Nrcam</i>	neuron-glia-CAM-related cell adhesion molecule	0001525 // angiogenesis // inferred from electronic annotation//0007155 // cell adhesion // inferred from electronic annotation//0007411 // axon guidance // inferred from direct
1429121_a	0.008658	-2.19	-1.36	NM_001040395//NM_0010	<i>Nadk2</i>	NAD kinase 2, mitochondrial	0006741 // NADP biosynthetic process // inferred from electronic annotation//0008152 // metabolic process // inferred from electronic annotation//00016310 // phosphorylation // not
1458916_a	0.005213	-2.20	-2.50	NM_172591	<i>Fcho2</i>	FCH domain only 2	0006897 // endocytosis // inferred from electronic annotation//0010324 // membrane invagination // inferred from direct assay//0048268 // clathrin coat assembly // not
1451161_a	0.001018	-2.20	-1.26	NM_001111026//NM_0011	<i>Runx1t1</i>	runt-related transcription factor 1; translocated to, 1 (cyclin D-related)	0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 // regulation of transcription, DNA-templated // inferred from direct assay//0010977 // negative
1442141_a	0.002179	-2.20	-1.66	NM_182808//NM_0065062	<i>Fam19a1</i>	family with sequence similarity 19, member A1	
1434277_a	0.000796	-2.20	-1.45	NM_145599//NM_0065308	<i>Tmem184c</i>	transmembrane protein 184C	
1448455_a	0.000331	-2.20	-1.18	NM_030203	<i>Tspyl4</i>	TSPY-like 4	0006334 // nucleosome assembly // inferred from electronic annotation
1433327_a	0.000173	-2.21	-1.43	NM_001163336//NM_0011	<i>Atp2a3</i>	ATPase, Ca++ transporting, ubiquitous	0006200 // ATP catabolic process // not recorded//0006810 // transport // inferred from electronic annotation//0006811 // ion transport // inferred from electronic annotation//0006812 //
1440245_a	0.001365	-2.21	-1.61	NM_172803//NM_0065150	<i>Dock4</i>	dedicator of cytokinesis 4	0007264 // small GTPase mediated signal transduction // inferred from electronic annotation//0032855 // positive regulation of Rac GTPase activity // not recorded//0043547 // positive
1430073_a	0.003762	-2.21	-1.39	NM_029555	<i>Gskt1</i>	glutathione S-transferase kappa 1	0006749 // glutathione metabolic process // inferred from direct assay//00055114 // oxidation-reduction process // inferred from direct assay//00055114 // oxidation-reduction process // not
1448318_a	0.005433	-2.22	-1.17	NM_172467	<i>Zc3hov1</i>	zinc finger CCH-type, antiviral 1-like	
1434828_a	0.005127	-2.22	-1.47	NM_172872//NM_0065030	<i>Kank4</i>	KN motif and ankyrin repeat domains 4	0001497 // negative regulation of stress fiber assembly // not recorded
1450550_a	0.005864	-2.22	-1.24	NM_138745	<i>Mthfd1</i>	methylene tetrahydrofolate dehydrogenase (NADP+ dependent),	0001005 // histidine biosynthetic process // inferred from electronic annotation//0006164 // purine nucleotide biosynthetic process // inferred from electronic annotation//0006730 // one-
1426215_a	0.000823	-2.22	-1.01	NM_008722//NM_0065200	<i>Ctnnd2</i>	catenin (cadherin associated protein), delta 2	0001763 // morphogenesis of a branching structure // inferred from direct assay//0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 // regulation of
1456512_a	0.000399	-2.22	-2.06	NM_030595//NM_0065015	<i>Nbea</i>	neurobeachin	0006605 // protein targeting // inferred from sequence or structural similarity//0006892 // post-Golgi vesicle-mediated transport // not-traceable author statement//0008104 // protein
1450611_a	0.004225	-2.22	-1.24	NM_008817	<i>Peg3</i>	paternally expressed 3	0001701 // in utero embryonic development // inferred from mutant phenotype//0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 // regulation of
1449453_a	0.002171	-2.23	-1.22	NM_007963//NM_021442	<i>Mecom</i>	MD51 and EV11 complex locus	0001701 // in utero embryonic development // inferred from mutant phenotype//0001780 // neutrophil homeostasis // inferred from mutant phenotype//0006351 // transcription, DNA-
1428522_a	0.007471	-2.23	-1.35	NM_031999//NR_003568//	<i>Gpr137b</i>	G protein-coupled receptor 137b//G protein-coupled receptor 137b,	
1431126_a	0.000775	-2.23	-1.41	NM_001206367//NM_0012	<i>Gsn</i>	gelsolin	0006915 // apoptotic process // not recorded//0007568 // aging // inferred from electronic annotation//0008154 // actin polymerization or depolymerization // not recorded//0014003 //
1439573_a	0.000591	-2.23	-1.58	NM_025359	<i>Tspan13</i>	tetraspanin 13	
1422044_a	0.005836	-2.23	1.13	NM_013755//NM_0065354	<i>Gyg</i>	glycogenin	0005978 // glycogen biosynthetic process // not recorded//0008152 // metabolic process // inferred from electronic annotation
1451354_a	0.002754	-2.23	-1.27	NM_172463//NM_0065293	<i>Sned1</i>	sushi, nidogen and EGF-like domains 1	0007160 // cell-matrix adhesion // inferred from electronic annotation
1434583_a	0.002945	-2.23	-1.46	NM_145398//NM_0065050	<i>Casd1</i>	CAS1 domain containing 1	
1450920_a	0.008817	-2.24	-1.25	NM_001170866//NM_0011	<i>Ncal</i>	neuronal delta	0003073 // regulation of systemic arterial blood pressure // inferred from mutant phenotype//0019722 // calcium-mediated signaling // inferred from mutant phenotype
1420560_a	0.006048	-2.24	1.03	NM_008182//NM_0065108	<i>Gsta2</i>	glutathione S-transferase, alpha 2 (Yc2)//predicted gene	0006749 // glutathione metabolic process // inferred from sequence or structural similarity//0008152 // metabolic process // inferred from electronic annotation//00035634 // inferred from
1424599_a	0.006602	-2.24	1.20	NM_001111274//NM_0011	<i>Igf1</i>	insulin-like growth factor 1	0001649 // osteoblast differentiation // inferred from expression pattern//0001775 // cell activation // not recorded//0001932 // regulation of protein phosphorylation // inferred from direct
1416827_a	0.008742	-2.24	2.08	NM_019506	<i>Gcm1</i>	carboxypeptidase X (NM14 family)	0006508 // proteolysis // inferred from direct assay//0007155 // cell adhesion // inferred from electronic annotation//0008155 // metabolic process // inferred from electronic annotation
1456986_a	0.005120	-2.24	-2.13	NM_001289769//NM_0012	<i>Rarb</i>	retinoic acid receptor, beta	0001022 // negative regulation of transcription from RNA polymerase II promoter // inferred from direct assay//0001657 // uterine bud development // inferred from mutant
1434781_a	0.004525	-2.24	-1.46	NM_001079844//NM_0118	<i>Gpc6</i>	glycophan 6	0016477 // cell migration // not recorded
1419401_a	0.001060	-2.24	1.27	NM_175501//NM_0065200	<i>Adams12</i>	a disintegrin-like and metalloproteinase (reprolysin type) with	0006508 // proteolysis // inferred from electronic annotation//0007160 // cell-matrix adhesion // not recorded//0016477 // cell migration // not recorded//00030167 // proteoglycan
1428613_a	0.000940	-2.25	-1.35	NM_001146180//NM_1448	<i>Mtss1</i>	metastasis suppressor 1	0001701 // in utero embryonic development // inferred from genetic interaction//0007015 // actin filament organization // inferred from direct assay//0007165 // signal transduction //
1433708_a	0.002420	-2.25	-1.11	NM_175446	<i>Zmat1</i>	zinc finger, matrix type 1	
1434511_a	0.001178	-2.25	-1.13	NM_011707	<i>Vtn</i>	vitronection	0006898 // receptor-mediated endocytosis // inferred from electronic annotation//0006955 // immune response // inferred from electronic annotation//0007155 // cell adhesion // inferred
1431918_a	0.006718	-2.26	-1.42	NM_011682//NM_0065127	<i>Utrn</i>	utrophin	0001954 // positive regulation of cell-matrix adhesion // not recorded//0007527 // adult somatic muscle development // traceable author statement//0007528 // neuromuscular junction
1436742_a	0.004127	-2.26	-1.52	NM_001114098//NM_1729	<i>Mtcl1</i>	microtubule crosslinking factor 1	0001578 // microtubule bundle formation // inferred from direct assay//0001506 // regulation of autophagy // inferred from electronic annotation//00045197 // establishment or
1431075_a	0.005121	-2.27	-1.10	NM_080595//NM_0065145	<i>Emid1</i>	EMI domain containing 1	0008152 // metabolic process // inferred from electronic annotation//0018345 // protein palmitoylation // not recorded
1454933_a	0.004715	-2.27	-1.97	NM_029492//NM_0065196	<i>Zdhc20</i>	zinc finger, DHHC domain containing 20	0046548 // retinal rod cell development // inferred from mutant phenotype//0006060 // post-embryonic retina morphogenesis in camera-type eye // inferred from mutant phenotype
1447177_a	0.003754	-2.27	-1.82	NM_001114879//NM_0289	<i>Fam208a</i>	family with sequence similarity 208, member A	0042771 // intrinsic apoptotic signaling pathway in response to DNA damage by p53 class mediator // inferred from mutant phenotype//0006548 // negative regulation of cell death // not
1429061_a	0.004662	-2.28	-1.08	NM_134142//NM_0065273	<i>Tmem109</i>	transmembrane protein 109	0006955 // immune response // inferred from electronic annotation//00021680 // cerebellar Purkinje cell layer development // inferred from expression pattern//0021681 // cerebellar
1452651_a	0.002997	-2.28	-1.30	NM_178649//NR_033123//	<i>4933409K07Rik//Gm10509//</i>	RIKEN cDNA 4933409K07 gene//predicted gene 10590//predicted gene,	0006468 // protein phosphorylation // inferred from electronic annotation//0006915 // apoptotic process // inferred from electronic annotation//0007165 // signal transduction // inferred
1453076_a	0.007269	-2.28	-1.31	NM_001122889//NM_0012	<i>Epha7</i>	Eph receptor A7	
1449139_a	0.001187	-2.29	-1.20	NM_028135	<i>Tmem163</i>	transmembrane protein 163	
1437510_x	0.007853	-2.29	-1.16	NM_172588	<i>Serinc5</i>	serine incorporator 5	0006629 // lipid metabolic process // inferred from electronic annotation//0006658 // phosphatidylserine metabolic process // not recorded//0008654 // phospholipid biosynthetic process //
1436425_a	0.002168	-2.29	-1.51	NM_007964//NM_0065347	<i>Evi5</i>	ecotropic viral integration site 5	0007049 // cell cycle // inferred from electronic annotation//0032313 // regulation of Rab GTPase activity // inferred from electronic annotation//0003285 // positive regulation of Rab
1453234_a	0.000169	-2.30	-1.91	NM_001038015//NM_0276	<i>Gnpda2</i>	glucosamine-6-phosphate deaminase 2	0005975 // carbohydrate metabolic process // inferred from electronic annotation//0006044 // N-acetylglucosamine metabolic process // inferred from electronic annotation
1438697_a	0.001133	-2.30	-1.56	NM_013835//NM_0065292	<i>Trove2</i>	TROVE domain family, member 2	0002520 // immune system development // inferred from mutant phenotype//0007224 // smoothened signaling pathway // inferred from mutant phenotype//0009411 // response to UV //
1422617_a	0.006230	-2.30	1.11	NM_008606//NM_0065133	<i>Mmp11</i>	matrix metalloproteinase 11	0006508 // proteolysis // inferred from direct assay//0007275 // multicellular organismal development // inferred from electronic annotation//0030198 // extracellular matrix organization //
1453609_x	0.001948	-2.30	-1.31	NM_181595//NM_0065050	<i>Ppp19a</i>	protein phosphatase 1, regulatory (inhibitor) subunit 9A	0007015 // actin filament organization // inferred from physical interaction//0007122 // calcium-mediated signaling // inferred from mutant phenotype//00031175 // neuron projection
1454956_a	0.000053	-2.30	-1.77	NM_172597//NM_0065195	<i>Txndc16</i>	thioredoxin domain containing 16	0045454 // cell redox homeostasis // inferred from electronic annotation
1440299_a	0.000998	-2.30	-1.61	NM_011416//NM_026003	<i>Smarca2</i>	SWI/SNF related, matrix associated, actin dependent regulator of	0006325 // chromatin organization // traceable author statement//0006334 // nucleosome assembly // traceable author statement//0006351 // transcription, DNA-templated // inferred
1429352_a	0.003890	-2.30	-1.09	NM_011125//NM_0064989	<i>Pltp</i>	phospholipid transfer protein	0006810 // transport // inferred from electronic annotation//0006869 // lipid transport // inferred from electronic annotation//0010189 // vitamin E biosynthetic process // inferred from
1445497_a	0.007550	-2.31	-1.76	NM_001033228	<i>Igtal1</i>	integrin alpha 1	0001187 // activation of MAPK activity // not recorded//0007155 // cell adhesion // inferred from mutant phenotype//0007229 // integrin-mediated signaling pathway // inferred from
1424455_a	0.006003	-2.31	1.04	NM_001293229//NM_1773	<i>Zfp799</i>	zinc finger protein 799	0006355 // regulation of transcription, DNA-templated // inferred from electronic annotation
1436841_a	0.004836	-2.31	-1.52	NM_177606//NM_0065239	<i>Plekhh2</i>	plekstrin homology domain containing, family H (with MyTH domain)	0030835 // negative regulation of actin filament depolymerization // inferred from direct assay
1449347_a	0.002168	-2.32	-1.22	NM_178778//NM_0064981	<i>Scal</i>	suppressor of cancer cell invasion	0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 // regulation of transcription, DNA-templated // inferred from electronic annotation//0009968 //
1451209_a	0.000918	-2.32	-1.26	NM_001145826//NM_1534	<i>Spec1l</i>	sperm antigen with calponin homology and coiled-coil domains 1-like	0007026 // negative regulation of microtubule depolymerization // inferred from direct assay//0007049 // cell cycle // inferred from electronic annotation//0007155 // cell adhesion // not
1439565_a	0.008220	-2.33	-1.58	NM_175518//NM_0065379	<i>Tmem245</i>	transmembrane protein 245	
1440919_a	0.001954	-2.33	-1.63	NM_010241//NM_0065306	<i>Aktip</i>	thymoma viral proto-oncogene 1 interacting protein	0001934 // positive regulation of protein phosphorylation // not recorded//0006810 // transport // inferred from electronic annotation//0006915 // apoptotic process // inferred from
1426416_a	0.004652	-2.34	-1.02	NM_001193074//NM_0065	<i>Adams13</i>	ADAMTS-like 3	0006508 // proteolysis // inferred from electronic annotation
1428805_a	0.005207	-2.34	-1.36	NM_001256224//NM_0095	<i>Wnt5a</i>	wingless-type MMTV integration site family, member 5A	0001187 // activation of MAPK activity // not recorded//0001667 // ameboid cell migration // inferred from mutant phenotype//0001736 // establishment of planar polarity // inferred from
1426797_a	0.002641	-2.34	-1.03	NM_009131	<i>Clec11a</i>	C-type lectin domain family 11, member 1	0002894 // positive regulation of cell proliferation // not recorded
1436080_a	0.001923	-2.34	-1.50	NM_001081642//NM_0012	<i>Xlr4a//Xlr4b//Xlr4c</i>	X-linked lymphocyte-regulated 4A//X-linked lymphocyte-regulated 4B//X-	0051965 // positive regulation of synapse assembly // inferred from mutant phenotype//0061003 // positive regulation of dendritic spine morphogenesis // inferred from mutant phenotype
1436207_a	0.009350	-2.34	-1.14	NM_00115455	<i>Tcf21</i>	transcription factor 21	0001022 // negative regulation of transcription from RNA polymerase II promoter // inferred from direct assay//0000122 // negative regulation of transcription from RNA polymerase II
1435452_a	0.005232	-2.34	-1.48	NM_011158//NM_0065150	<i>Prkar2b</i>	protein kinase, cAMP dependent regulatory, type II beta	0001932 // regulation of protein phosphorylation // inferred from electronic annotation//0006468 // protein phosphorylation // traceable author statement//0006631 // fatty acid metabolic
1453897_a	0.000714	-2.35	-1.93	NM_001290535//NM_1391	<i>Ogt</i>	O-linked N-acetylglucosamine (GlcNAc) transferase (UDP-N-	0006110 // regulation of glycolytic process // not recorded//0006486 // protein glycosylation // inferred from electronic annotation//0006493 // protein O-linked glycosylation // inferred
1453743_a	0.006204	-2.35	-1.49	NM_153127	<i>Mmrn2</i>	multimerin 2	0001525 // angiogenesis // inferred from electronic annotation//00030948 // negative regulation of vascular endothelial growth factor receptor signaling pathway // not recorded//00090051 //
1425002_a	0.004050	-2.35	1.02	NM_001039175//NM_0010	<i>Elovl1</i>	elongation of very long chain fatty acids (FEN1/Elo2, SUR4/Elo3, yeast)-like	0006629 // lipid metabolic process // inferred from electronic annotation//0006631 // fatty acid metabolic process // inferred from electronic annotation//0006633 // fatty acid biosynthetic
1442336_a	0.001998	-2.36	-1.67	NM_022881	<i>Rgs18</i>	regulator of G-protein signaling 18	0007186 // G-protein coupled receptor signaling pathway // inferred from physical interaction//0008277 // regulation of G-protein coupled receptor protein signaling pathway // inferred from
1444498_a	0.009643	-2.36	-1.73	NM_001039546//NM_0086	<i>Myo6</i>	myosin VI	0006605 // protein targeting // inferred from physical interaction//0006810 // transport // inferred from electronic annotation//0006897 // endocytosis // inferred from mutant
1450115_a	0.006391	-2.36	-1.23	NM_009672//NM_0065107	<i>Anp32a</i>	anion (leucine-rich) nuclear phosphoprotein 32 family, member A	0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 // regulation of transcription, DNA-templated // inferred from electronic annotation
1448165_a	0.004579	-2.36	-1.17				

Table S7

Gene_ID	p (Corr)	FC-RSV 1 d	FC-RSV 5 d	RefSeq Transcript ID	Gene Symbol	Gene Title	Gene Ontology Biological Process
1440360_a	0.005949	-2.37	-1.61	NM_001253754//NM_0012	<i>Gpm6a</i>	glycoprotein m6a	0001764 // neuron migration // not recorded//0003407 // neural retina development // inferred from direct assay//0007399 // nervous system development // inferred from electronic
1439849_a	0.005672	-2.37	-1.60	NM_019933//X/M_0065292	<i>Ptpn4</i>	protein tyrosine phosphatase, non-receptor type 4	0006470 // protein dephosphorylation // inferred from electronic annotation//0001631 // dephosphorylation // inferred from electronic annotation//0005335 // peptidyl-tyrosine
1433490_s	0.005998	-2.37	-1.11	NM_172867//X/M_0065379	<i>Zfp462</i>	zinc finger protein 462	0006325 // chromatin organization // inferred from mutant phenotype//0007010 // cytoskeleton organization // inferred from electronic annotation//0043392 // negative regulation of DNA
1442416_a	0.008593	-2.37	-1.67	NM_001033453//NM_0010	<i>Pdp1</i>	pyruvate dehydrogenase phosphatase catalytic subunit 1	0006470 // protein dephosphorylation // not recorded//0003590 // peptidyl-threonine dephosphorylation // not recorded
1459531_a	0.006846	-2.37	-2.66	NM_000391337//NM_0012	<i>Scoc</i>	short coiled-coil protein	0016239 // positive regulation of macrotubophagy // not recorded
1435633_a	0.007232	-2.38	-1.49	NM_153578//X/M_0065408	<i>Nipa1</i>	non imprinted in Prader-Willi/Angelman syndrome 1 homolog (human)	0006810 // transport // inferred from electronic annotation//0006811 // ion transport // inferred from electronic annotation//0015693 // magnesium ion transport // inferred from direct
1443889_a	0.005098	-2.38	-1.72	NM_011921	<i>Aldha7</i>	aldehyde dehydrogenase family 1, subfamily A7	0006068 // ethanol catabolic process // inferred from electronic annotation//0008152 // metabolic process // inferred from electronic annotation//0008218 // bioluminescence // inferred
1426666_a	0.002292	-2.39	-1.03	NM_145376//X/M_0065171	<i>Lpcat1</i>	lysophosphatidylcholine acyltransferase 1	0006629 // lipid metabolic process // inferred from electronic annotation//0006644 // phospholipid metabolic process // inferred from electronic annotation//0008152 // metabolic process
1455991_a	0.004661	-2.39	-1.32	NM_212445//X/M_0065105	<i>Kdelc2</i>	KDEL (Lys-Asp-Glu-Leu) containing 2	0007009 // plasma membrane organization // inferred from mutant phenotype//0032287 // peripheral nervous system myelin maintenance // inferred from mutant phenotype//0032288 //
1458407_s	0.000852	-2.39	-2.40	NM_019579//X/M_0065160	<i>Mtp5p</i>	membrane protein, palmitoylated 5 (MAGUK p55 subfamily member 5)	0002376 // immune system process // inferred from electronic annotation//0006508 // proteolysis // not recorded//0006957 // complement activation, alternative pathway // inferred from
1448508_a	0.000404	-2.39	-1.18	NM_00129191//NM_0134	<i>Cld</i>	component factor D (adipsin)	0006511 // ubiquitin-dependent protein catabolic process // not recorded//0016055 // Wnt signaling pathway // inferred from electronic annotation//0016567 // protein ubiquitination // not
1435370_a	0.000500	-2.39	-1.13	NM_001080924//NM_0012	<i>Znf3</i>	zinc and ring finger 3	0006355 // regulation of transcription, DNA-templated // inferred from direct assay//0007155 // cell adhesion // inferred from electronic annotation//0007520 // myoblast fusion // inferred
1425199_a	0.006128	-2.39	1.01	NM_001042752//NM_0086	<i>Neol1</i>	neogenin	0007155 // cell adhesion // inferred from electronic annotation//0001637 // single organismal cell-cell adhesion // not recorded//0032760 // positive regulation of tumor necrosis factor
1421911_a	0.000614	-2.40	1.14	NM_013486//X/M_0065009	<i>Cd2</i>	CD2 antigen	0007155 // cell adhesion // inferred from electronic annotation//0001637 // single organismal cell-cell adhesion // not recorded//0032760 // positive regulation of tumor necrosis factor
1442777_a	0.005146	-2.40	-1.68	NM_022319//X/M_0065113	<i>Cstn2</i>	calsynin 2	0007155 // cell adhesion // inferred from electronic annotation//0001637 // single organismal cell-cell adhesion // not recorded//0032760 // positive regulation of tumor necrosis factor
1428626_a	0.003080	-2.42	-1.08	NM_145467//X/M_0065189	<i>Itgbl1</i>	integrin, beta-like 1	0007155 // cell adhesion // inferred from electronic annotation//0001637 // single organismal cell-cell adhesion // not recorded//0032760 // positive regulation of tumor necrosis factor
1457043_a	0.005088	-2.42	-2.14	NM_001159555//NM_0011	<i>Cd36</i>	CD36 antigen	0000122 // negative regulation of transcription from RNA polymerase II promoter // inferred from mutant phenotype//0001676 // long-chain fatty acid metabolic process // not
1437995_x	0.003462	-2.42	-1.16	NM_028279//X/M_0065106	<i>Naalad2</i>	N-acetylated alpha-linked acidic dipeptidase 2	0006508 // proteolysis // inferred from direct assay//0008152 // metabolic process // inferred from electronic annotation//00042135 // neurotransmitter catabolic process // inferred from
1459359_a	0.000583	-2.43	-2.58	NM_001081187	<i>Htra4</i>	HTRA serine peptidase 4	0001558 // regulation of cell growth // inferred from electronic annotation//0006508 // proteolysis // not recorded
1418015_a	0.003912	-2.43	1.47	NM_00111348//NM_0113	<i>Sema4f</i>	sema domain, immunoglobulin domain (IG), TM domain, and short	0007275 // multicellular organismal development // inferred from electronic annotation//0007399 // nervous system development // inferred from electronic annotation//0007411 // axon
1428838_a	0.003606	-2.44	-1.08	NM_001170537//NM_0252	<i>Me2c</i>	myocyte enhancer factor 2C	0000122 // negative regulation of transcription from RNA polymerase II promoter // inferred from genetic interaction//0000122 // negative regulation of transcription from RNA polymerase II
1428408_a	0.006989	-2.44	-1.34	NM_001194940//NM_0011	<i>Dlc1</i>	deleted in liver cancer 1	0001843 // neural tube closure // inferred from mutant phenotype//0003007 // heart morphogenesis // inferred from mutant phenotype//0006915 // apoptotic process // not
1435784_a	0.005244	-2.44	-1.49	NM_146234	<i>Mmg1</i>	membrane magnesium transporter 1	0006810 // transport // inferred from electronic annotation//0006812 // cation transport // inferred from direct assay//0006824 // cobalt ion transport // inferred from direct
1440247_a	0.005575	-2.44	-1.61	NM_009888	<i>Cfh</i>	complement component factor h	0002376 // immune system process // inferred from electronic annotation//0006957 // complement activation, alternative pathway // inferred from electronic annotation//0030449 //
1450825_a	0.009528	-2.45	-1.25	NM_010753	<i>Lxn</i>	lactoxin	0006954 // inflammatory response // inferred from electronic annotation//0001466 // negative regulation of peptidase activity // inferred from electronic annotation//0010951 // negative
1443322_a	0.006916	-2.45	-1.70	NM_001170745//NM_0011	<i>Magi2</i>	membrane associated guanylate kinase, WW and PDZ domain containing 2	0002092 // positive regulation of receptor internalization // not recorded//0007165 // signal transduction // inferred from physical interaction//0007399 // nervous system development //
1429297_a	0.000014	-2.45	-1.37	NM_001177503//X/M_0065	<i>Plekhd1</i>	pleckstrin homology domain containing, family D (with coiled-coil domains)	0000122 // negative regulation of transcription from RNA polymerase II promoter // inferred from direct assay//0000902 // cell morphogenesis // inferred from mutant phenotype//0001541
1430411_a	0.008115	-2.46	-1.40	NM_013464	<i>Ahr</i>	aryl-hydrocarbon receptor	0000122 // negative regulation of transcription from RNA polymerase II promoter // inferred from direct assay//0000902 // cell morphogenesis // inferred from mutant phenotype//0001541
1427945_a	0.002729	-2.46	-1.06	NM_001177794//NM_1982	<i>Sertad4</i>	SERTA domain containing 4	0010629 // negative regulation of gene expression // not recorded//0035356 // cellular triglyceride homeostasis // not recorded//0042347 // negative regulation of NF-kappaB import into
1418580_a	0.000407	-2.46	1.36	NM_001204134//NM_0308	<i>C1qtnf3</i>	C1q and tumor necrosis factor related protein 3	001574 // ganglioside biosynthetic process // not recorded//0006486 // protein glycosylation // not recorded//0006491 // N-glycan processing // not recorded//0003311 // oligosaccharide
1435324_x	0.001134	-2.47	-1.13	NM_001159745//NM_0091	<i>S8iso4</i>	S18 alpha-N-acetyl-neuraminide alpha-2,8-sialyltransferase 4	0016567 // protein ubiquitination // inferred from direct assay//0043523 // regulation of neuron apoptotic process // inferred from mutant phenotype//0043523 // regulation of neuron
1447589_a	0.006255	-2.47	-1.83	NM_001271725//NM_0012	<i>Trim2</i>	trifurcate motif-containing 2	0048678 // response to axon injury // inferred from direct assay
1422094_a	0.004579	-2.47	1.13	NM_001252563//NM_0135	<i>Matn4</i>	matrilin 4	0001525 // angiogenesis // inferred from direct assay//0001525 // angiogenesis // inferred from mutant phenotype//0006470 // protein dephosphorylation // inferred from electronic
1455213_a	0.002008	-2.47	-1.99	NM_029928//X/M_0065133	<i>Ptpbr</i>	protein tyrosine phosphatase, receptor type, B	1902600 // hydrogen ion transmembrane transport // inferred from electronic annotation
1439443_x	0.000459	-2.48	-1.16	NM_001289848//NM_0012	<i>Cox6b2</i>	cytochrome c oxidase subunit VIb polypeptide 2	0001541 // ovarian follicle development // not recorded//0001755 // neural crest cell migration // inferred from direct assay//0002763 // positive regulation of myeloid leukocyte
1456348_x	0.002796	-2.48	-2.05	NM_013598//X/M_0065133	<i>Kltl</i>	kit ligand	0000122 // negative regulation of transcription from RNA polymerase II promoter // inferred from genetic interaction//0006351 // transcription, DNA-templated // inferred from electronic
1460223_a	0.000262	-2.48	-1.33	NM_001199304//NM_0011	<i>Atxn1</i>	ataxin 1	0000132 // establishment of mitotic spindle orientation // inferred from mutant phenotype//0008277 // regulation of G-protein coupled receptor protein signaling pathway // inferred from
1449287_a	0.005032	-2.48	-1.21	NM_029522//X/M_0065022	<i>Gpsm2</i>	G-protein signalling modulator 2 (AGS3-like, C. elegans)	0000187 // activation of MAPK activity // not recorded//0006629 // lipid metabolic process // inferred from electronic annotation//0006175 // signal transduction // inferred from electronic
1434934_a	0.006099	-2.49	-1.47	NM_019588//X/M_0065273	<i>P1ce1</i>	phospholipase C, epsilon 1	0000302 // response to reactive oxygen species // not recorded//0001649 // osteoblast differentiation // not recorded//0001657 // ureteric bud development // not recorded//0001666 //
1451858_a	0.000187	-2.49	-1.28	NM_009804//X/M_0064986	<i>Cot</i>	catalase	0000122 // negative regulation of transcription from RNA polymerase II promoter // inferred from mutant phenotype//0006629 // lipid metabolic process // inferred from electronic annotation//0001666 //
1430404_a	0.009785	-2.49	-1.40	NM_001161420//NM_0137	<i>Vldlr</i>	very low density lipoprotein receptor	0001501 // skeletal system development // inferred from mutant phenotype//0007179 // transforming growth factor beta receptor signaling pathway // inferred from mutant
1421871_a	0.000868	-2.49	1.14	NM_008520//X/M_0065316	<i>Lbp3p</i>	latent transforming growth factor beta binding protein 3	0006464 // cellular protein modification process // inferred from electronic annotation//0006479 // protein methylation // inferred from electronic annotation//0032259 // methylation //
1425184_a	0.001994	-2.49	-1.36	NM_001080616//NM_0065	<i>Ptdsl1</i>	PZD domain containing 2 //uncharacterized LOC102642479	0032836 // glomerular basement membrane development // inferred from mutant phenotype//0032836 // glomerular basement membrane development // not recorded
1455250_a	0.004621	-2.50	-1.93	NM_00129121//NM_1535	<i>Pcmtd2</i>	protein-L-isoaspartate (D-aspartate) O-methyltransferase domain	0006145 // purine nucleobase catabolic process // not recorded//0006208 // pyrimidine nucleobase catabolic process // inferred from direct assay//0006208 // pyrimidine nucleobase
1453922_a	0.009140	-2.50	-1.94	NM_025811//X/M_0065272	<i>Nhlrc2</i>	NHL repeat containing 2	0006955 // immune response // inferred from electronic annotation//0002180 // cerebellar Purkinje cell layer development // inferred from expression pattern//0002181 // cerebellar
1440343_a	0.009018	-2.50	-1.61	NM_007735	<i>Col4a4</i>	collagen, type IV, alpha 4	0001525 // angiogenesis // inferred from electronic annotation//0001945 // lymph vessel development // inferred from mutant phenotype//0002042 // cell migration involved in sprouting
1429543_a	0.000778	-2.50	-1.38	NM_170778//X/M_0065024	<i>Dpyd</i>	dihydropyrimidine dehydrogenase	0030154 // cell differentiation // inferred from electronic annotation
1428278_a	0.001430	-2.50	-1.34	NM_178649//NR_033123//	<i>4933409K07RIK//Gm10590//</i>	RIKEN cDNA 4933409K07 gene//predicted gene 10590//predicted gene,	0006281 // DNA repair // inferred from electronic annotation//0006310 // DNA recombination // inferred from electronic annotation//0007049 // cell cycle // inferred from electronic
1446649_a	0.002834	-2.51	-1.79	NM_010111//X/M_0065086	<i>Efnb2</i>	ephrin B2	0001666 // response to hypoxia // inferred from electronic annotation//0005114 // oxidation-reduction process // inferred from electronic annotation
1446553_a	0.002896	-2.51	-1.78	NM_001160215//NM_1451	<i>Fcrla</i>	Fc receptor-like A	0007155 // cell adhesion // inferred from electronic annotation//0007155 // cell adhesion // traceable author statement//0007156 // homophilic cell adhesion // inferred from electronic
1448876_a	0.007370	-2.51	-1.19	NM_133786//X/M_0065020	<i>Smc4</i>	structural maintenance of chromosomes 4	0001525 // angiogenesis // inferred from sequence or structural similarity//0001637 // single organismal cell-cell adhesion // inferred from sequence or structural similarity//0003015 //
1429862_a	0.005254	-2.52	-1.39	NM_001142916//NM_0119	<i>Plod2</i>	procollagen lysine, 2-oxoglutarate 5-dioxygenase 2	0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 // regulation of transcription, DNA-templated // not recorded
1441361_a	0.007878	-2.52	-1.65	NM_001003671//NM_0010	<i>Pcdha10</i>	protocadherin alpha 10//protocadherin alpha 10//protocadherin alpha 10	0005977 // glycogen metabolic process // inferred from mutant phenotype//0007155 // cell adhesion // inferred from electronic annotation//0007156 // homophilic cell adhesion // inferred
1458212_a	0.009436	-2.52	-2.39	NM_001163522//NM_0168	<i>Emcn</i>	endomucin	0000122 // negative regulation of transcription from RNA polymerase II promoter // inferred from mutant phenotype//0001660 // fever generation // inferred from mutant phenotype//0007165 // signal transduction // inferred from electronic
1441328_a	0.006230	-2.54	-1.64	NM_013922//X/M_0065335	<i>Zfp354c</i>	zinc finger protein 354C	0007155 // cell adhesion // inferred from electronic annotation//0007155 // cell adhesion // traceable author statement//0007156 // homophilic cell adhesion // inferred from electronic
1451978_a	0.005185	-2.55	-1.28	NM_017378	<i>Pcdh12</i>	protocadherin 12	0001525 // angiogenesis // inferred from sequence or structural similarity//0001637 // single organismal cell-cell adhesion // inferred from sequence or structural similarity//0003015 //
1444749_a	0.000634	-2.55	-1.75	NM_001289464//NM_0012	<i>Sox17</i>	SRF (sex determining region Y)-box 17	0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 // regulation of transcription, DNA-templated // not recorded
1418144_a	0.009997	-2.55	1.44	NM_011196//X/M_0065011	<i>Ptger3</i>	prostaglandin E receptor 3 (subtype EP3)	0005977 // glycogen metabolic process // inferred from mutant phenotype//0007155 // cell adhesion // inferred from electronic annotation//0007156 // homophilic cell adhesion // inferred
1453739_a	0.009316	-2.55	-1.93	NM_001172160//NM_1783	<i>Fhlr3</i>	fibronectin leucine rich transmembrane protein 3	0001660 // fever generation // inferred from direct assay//0001660 // fever generation // inferred from mutant phenotype//0007165 // signal transduction // inferred from electronic
1436532_a	0.007928	-2.56	-1.51	NM_001289496//NM_0012	<i>Egflam</i>	EGF-like, fibronectin type III and laminin G domains	0007411 // axon guidance // not recorded//0005919 // negative chemotaxis // inferred from direct assay
1454668_a	0.001503	-2.57	-1.32	NM_001159543//NM_0100	<i>Dpp4</i>	dipeptidylpeptidase 4	001811 // positive regulation of cell-substrate adhesion // inferred from direct assay//0001900 // peptide cross-linking via chondroitin 4-sulfate glycosaminoglycan // inferred from direct
1424215_a	0.001262	-2.57	1.05	NM_008626//X/M_0065324	<i>Mrc2</i>	mannose receptor, C type 2	0001666 // response to hypoxia // not recorded//0007209 // regulation of T cell mediated immunity // not recorded//0006508 // proteolysis // not recorded//0007155 // cell adhesion //
1421734_a	0.007451	-2.57	1.14	NM_026950//X/M_0065040	<i>Ociad2</i>	OClA domain containing 2	0001649 // osteoblast differentiation // not recorded//0006897 // endocytosis // inferred from electronic annotation//0003074 // collagen catabolic process // not recorded
1421365_a	0.004286	-2.57	1.16	NM_173749	<i>Pamr1</i>	peptidase domain containing associated with muscle regeneration 1	0006508 // proteolysis // inferred from electronic annotation//0008152 // metabolic process // inferred from electronic annotation
1449170_a	0.003134	-2.57	-1.20	NM_001044720//NM_0115	<i>Abcc9</i>	ATP-binding cassette, sub-family C (CFTR/MRP), member 9	0006200 // ATP catabolic process // inferred from electronic annotation//0006810 // transport // inferred from electronic annotation//0006813 // potassium ion transport // inferred from
1438527_a	0.004748	-2.58	-1.16	NM_001162532	<i>Fam174b</i>	family with sequence similarity 174, member B	0007275 // multicellular organismal development // inferred from electronic annotation
1428017_a	0.002401	-2.58	-1.07	NM_133859	<i>Olfml3</i>	olfactomedin-like 3	0001706 // endoderm formation // not recorded//0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 // regulation of transcription, DNA-templated //
1456303_a	0.006614	-2.58	-2.05	NM_011446	<i>Sox7</i>	SRF (sex determining region Y)-box 7	0006508 // proteolysis // inferred from direct assay//0010952 // positive regulation of peptidase activity // not recorded
1448583_a	0.003604	-2.58	-1.18	NM_008788//X/M_0065045	<i>Pcolce</i>	procollagen C-endopeptidase enhancer protein	0006955 // immune response // inferred from electronic annotation//0006326 // cell chemotaxis // inferred from electronic annotation
1452680_a	0.006667	-2.58	-1.30	NR_033506//X/M_00653839	<i>Gm10600//Gm21075//Gm21</i>	predicted gene 10600//predicted gene, 21075//predicted gene,	0006915 // apoptotic process // inferred from electronic annotation//0007049 // cell cycle // inferred from electronic annotation//0007417 // central nervous system development // inferred
1453108_a	0.006068	-2.59	-1.90	NM_173378	<i>Trp53bp2</i>	transformation related protein 53 binding protein 2	0006810 // transport // inferred from electronic annotation//0006811 // ion transport // inferred from electronic annotation//0006812 // cation transport // inferred from electronic
1442184_a	0.007888	-2.59	-1.66	NM_177535//X/M_0065276	<i>633050SMOSRIK//SLC97</i>	633050SMOSRIK gene//solute carrier family 9 (sodium/hydrogen	0001965 // positive regulation of synapse assembly // inferred from mutant phenotype//0001003 // positive regulation of dendritic spine morphogenesis // inferred from mutant phenotype
1438491_x	0.002510	-2.60	-1.52	NM_001081643//NM_0012	<i>Xlra4//Xlra4b//Xlra4c</i>	X-linked lymphocyte-regulated 4A//X-linked lymphocyte-regulated 4B//X-	0007155 // cell adhesion // inferred from direct assay//0007155 // cell adhesion // not recorded//0008593 // regulation of Notch signaling pathway // inferred from mutant
1436656_a	0.003860	-2.60	-1.56	NM_001198765//NM_0011	<i>Postn</i>	periostin, osteoblast specific factor	0001222 // negative regulation of transcription from RNA polymerase II promoter // inferred from direct assay//0000122 // negative regulation of transcription from RNA polymerase II
1435725_x	0.009151	-2.60	-1.14	NM_009170//X/M_0065336	<i>Shn</i>	sonic hedgehog	0007155 // cell adhesion // inferred from electronic annotation
1455108_a	0.005466	-2.60	-2.16	NM_012050//X/M_0065169	<i>Omd</i>	osteonectin	0007420 // brain development // inferred from electronic annotation//0003036 // actin cytoskeleton organization // not recorded
1449514_a	0.002987	-2.60	-1.22	NM_080285//X/M_0065051	<i>Ctnbp2</i>	catenin binding protein 2	0002376 // immune system process // inferred from electronic annotation//0006958 // complement activation, classical pathway // inferred from electronic annotation//0030450 //
1455750_a	0.007789	-2.60	-2.02	NM_010016//X/M_0065291	<i>Cd55</i>	CD55 antigen	0008152 // metabolic process // inferred from electronic annotation//0009305 // nucleic acid phosphodiester bond hydrolysis // inferred from electronic annotation
1437288_a	0.002791	-2.61	-1.15	NM_008287//X/M_0065200	<i>Hrsp12</i>	heat-responsive protein 12	0006915 // apoptotic process // inferred from electronic annotation
1441962_a	0.002770	-2.61	-1.65	NM_026931	<i>1810011O10RIK</i>	RIKEN cDNA 1810011O10 gene	0006468 // protein phosphorylation // inferred from electronic annotation//0010611 // regulation of cardiac muscle hypertrophy // inferred from electronic annotation//00016310 //
1429017_a	0.003328	-2.61	-1.36	LOC75771		uncharacterized LOC75771	0001666 // response to hypoxia // inferred from mutant phenotype//0006801 // superoxide metabolic process // inferred from electronic annotation//0019430 // removal of superoxide
1446525_a	0.006240	-2.62	-1.78	NM_011435	<i>Sod3</i>	superoxide dismutase 3, extracellular	0001937 // negative regulation of endothelial cell proliferation // inferred from mutant phenotype//0001937 // negative regulation of endothelial cell proliferation // not recorded//0001938
1434881_s	0.001409	-2.62	-1.13	N			

Table S7

Gene ID	p (Corr)	FC-RSV 1 d	FC-RSV 5 d	RefSeq Transcript ID	Gene Symbol	Gene Title	Gene Ontology Biological Process
1455500_a	0.00023	-2.66	-2.00	NM_011074// <i>XM_0065035</i>	<i>Cdk14</i>	cyclin-dependent kinase 14	0000086 // G2/M transition of mitotic cell cycle // not recorded//0006468 // protein phosphorylation // inferred from sequence or structural similarity//0007049 // cell cycle // inferred from
1455545_a	0.004915	-2.66	-2.00	NM_138751	<i>Tmem47</i>	transmembrane protein 47	
1452586_a	0.002420	-2.67	-1.30	NM_001004363	<i>Nuak1</i>	NUAK family, SNF1-like kinase, 1	0006468 // protein phosphorylation // not recorded//0006974 // cellular response to DNA damage stimulus // inferred from electronic annotation//0007155 // cell adhesion // inferred from
1449952_s	0.004523	-2.67	-1.23	NM_001039485// <i>NM_1726</i>	<i>Piezo2</i>	piezo-type mechanosensitive ion channel component 2	0006810 // transport // inferred from electronic annotation//0006811 // ion transport // inferred from electronic annotation//0006812 // cation transport // inferred from direct
1434139_a	0.000605	-2.68	-1.45	NM_008957// <i>XM_0065171</i>	<i>Ptch1</i>	patched homolog 1	0000122 // negative regulation of transcription from RNA polymerase II promoter // not recorded//0001658 // branching involved in ureteric bud morphogenesis // inferred from mutant
1453056_a	0.008191	-2.69	-1.89	NM_001037221// <i>NM_0011</i>	<i>Samd4</i>	sterile alpha motif domain containing 4	0006417 // regulation of translation // inferred from electronic annotation//0017148 // negative regulation of translation // not recorded//0045727 // positive regulation of translation // not
1444831_a	0.009355	-2.70	-1.75	NM_001113283// <i>NM_1535</i>	<i>Fam214a</i>	family with sequence similarity 214, member A	
1437940_a	0.000734	-2.71	-1.54	NM_001159631// <i>NM_1336</i>	<i>Atp6v1c2</i>	ATPase, H+ transporting, lysosomal V1 subunit C2	0006200 // ATP catabolic process // inferred from direct assay//0006810 // transport // inferred from electronic annotation//0006811 // ion transport // inferred from electronic
1453292_a	0.004671	-2.72	-1.48	NM_001081756// <i>NM_1724</i>	<i>Nckap5</i>	NCK-associated protein 5	
1452351_a	0.009297	-2.72	-1.29	NM_001146299// <i>NM_1729</i>	<i>Sh3p2</i>	SH3 domain containing ring finger 2	0010923 // negative regulation of phosphatase activity // not recorded//0016567 // protein ubiquitination // inferred from electronic annotation
1458425_a	0.009871	-2.73	-1.49	NM_001286062// <i>NM_0096</i>	<i>Angpt1</i>	angiopoietin 1	0001525 // angiogenesis // inferred from direct assay//0001525 // angiogenesis // inferred from mutant phenotype//0001541 // ovarian follicle development // not recorded//0001569 //
1435153_a	0.008977	-2.73	-1.47	NM_001267796// <i>NM_0089</i>	<i>Igip1//Pura</i>	IGa-inducing protein//purine rich element binding protein A	0006268 // DNA unwinding involved in DNA replication // not recorded//0006270 // DNA replication initiation // traceable author statement//0006351 // transcription, DNA-templated //
1436962_a	0.000999	-2.74	-1.53	NM_026280// <i>XM_0065340</i>	<i>Mxra7</i>	matrix-remodelling associated 7	
1427947_a	0.002710	-2.74	-1.06	NM_031176// <i>XM_0065251</i>	<i>Tnxb</i>	tenascin XB	0006629 // lipid metabolic process // inferred from mutant phenotype//0006631 // fatty acid metabolic process // inferred from mutant phenotype//0006641 // triglyceride metabolic
1451486_a	0.009350	-2.74	-1.27	NM_011261// <i>XM_0065356</i>	<i>Reln</i>	reelin	0009094 // cell morphogenesis involved in differentiation // inferred from mutant phenotype//0001764 // neuron migration // inferred from genetic interaction//0001764 // neuron
1442649_a	0.001001	-2.75	-1.68	NM_001145830// <i>NM_0196</i>	<i>Pcb1</i>	phospholipase C, beta 1	0000086 // G2/M transition of mitotic cell cycle // inferred from direct assay//0000086 // G2/M transition of mitotic cell cycle // non-traceable author statement//0001556 // oocyte
1452739_a	0.009876	-2.75	-1.87	NM_010636// <i>XM_0065186</i>	<i>Klf12</i>	Kruppel-like factor 12	0000122 // negative regulation of transcription from RNA polymerase II promoter // inferred from direct assay//0000122 // negative regulation of transcription from RNA polymerase II
1451344_a	0.001819	-2.77	-1.27	NM_011828// <i>XM_0065014</i>	<i>Hs2st1</i>	heparan sulfate 2-O-sulfotransferase 1	0015014 // heparan sulfate proteoglycan biosynthetic process, polysaccharide chain biosynthetic process // inferred from mutant phenotype//0030202 // heparin metabolic process // inferred
1444406_a	0.002505	-2.77	-1.73	NM_001163154// <i>NM_0079</i>	<i>Etv1//Gm5454</i>	ets variant 1//predicted gene 5454	0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 // regulation of transcription, DNA-templated // traceable author statement//0006357 // regulation
1435917_a	0.004065	-2.78	-1.50	NM_001080707// <i>NM_0011</i>	<i>Gpr155</i>	G-protein-coupled receptor 155	0035556 // intracellular signal transduction // inferred from electronic annotation//0005089 // cognition // not recorded//0005085 // transmembrane transport // inferred from electronic
1438030_a	0.002056	-2.78	-1.54	NM_001286607// <i>NM_0532</i>	<i>Foxp2</i>	forkhead box P2	0000122 // negative regulation of transcription from RNA polymerase II promoter // inferred from direct assay//0002053 // positive regulation of mesenchymal cell proliferation // inferred
1430786_a	0.004038	-2.78	-1.41	NM_001198914// <i>NM_0108</i>	<i>Myb</i>	myeloblastosis oncogene	0000082 // G1/S transition of mitotic cell cycle // inferred from mutant phenotype//0000122 // negative regulation of transcription from RNA polymerase II promoter // not
1433328_a	0.002008	-2.78	-1.43	NM_001289645// <i>NM_0012</i>	<i>Pxylp1</i>	2-phosphoxylase phosphatase 1	0008152 // metabolic process // inferred from electronic annotation//0016311 // dephosphorylation // inferred from electronic annotation
1425386_a	0.007465	-2.79	-1.00	NM_008409	<i>Itm2a</i>	integral membrane protein 2A	
1451201_s	0.007129	-2.80	-1.26	NM_00129679// <i>NM_0293</i>	<i>Tmem14a</i>	transmembrane protein 14A	
1424148_a	0.002056	-2.80	-1.05	NM_008483// <i>XM_0065125</i>	<i>Lama2</i>	laminin, alpha 2	0007155 // cell adhesion // inferred from electronic annotation//0007411 // axon guidance // inferred from genetic interaction//0016192 // vesicle-mediated transport // inferred from
1449277_a	0.000545	-2.80	-1.21	NM_001168393// <i>NM_0168</i>	<i>Ramp1</i>	receptor (calcitonin) activity modifying protein 1	0001525 // angiogenesis // not recorded//0006810 // transport // inferred from electronic annotation//0006816 // calcium ion transport // not recorded//0006886 // intracellular protein
1448391_a	0.002561	-2.81	-1.18	NM_026481// <i>XM_0065313</i>	<i>Tppp3</i>	tubulin polymerization-promoting protein family member 3	0001578 // microtubule bundle formation // not recorded
1440890_a	0.000331	-2.82	-1.63	NM_172833// <i>XM_0065270</i>	<i>Scl6a12</i>	solute carrier family 16 (monocarboxylic acid transporters), member 12	0006810 // transport // inferred from electronic annotation//0005085 // transmembrane transport // inferred from electronic annotation
1439901_a	0.002420	-2.82	-1.60	NM_153803// <i>XM_0065102</i>	<i>Glib12</i>	galactosidase, beta 1-like 2	0005975 // carbohydrate metabolic process // inferred from electronic annotation//0008152 // metabolic process // inferred from electronic annotation
1460355_a	0.006003	-2.82	-1.33	NM_007934	<i>Enpep</i>	glutamyl aminopeptidase	0001525 // angiogenesis // inferred from mutant phenotype//0003081 // regulation of systemic arterial blood pressure by renin-angiotensin // not recorded//0006508 // proteolysis //
1440668_a	0.000304	-2.82	-1.62	NM_178711// <i>XM_0065111</i>	<i>Plscr4</i>	phospholipid scramblase 4	0071222 // cellular response to lipopolysaccharide // inferred from expression pattern
1449940_a	0.006740	-2.83	-1.23	NM_001145813// <i>NM_0101</i>	<i>Elf5</i>	EF4-like factor 5	0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 // regulation of transcription, DNA-templated // inferred from electronic annotation//0006357 //
1428331_a	0.001947	-2.83	-1.08	NM_001077361// <i>NM_0010</i>	<i>Fhl1</i>	four and a half LIM domains 1	0003254 // regulation of membrane depolarization // not recorded//0007275 // multicellular organismal development // inferred from electronic annotation//0010972 // negative regulation
1453480_a	0.009230	-2.83	-1.92	NM_001159354// <i>NM_1338</i>	<i>Magi3</i>	membrane associated guanylate kinase, WW and PDZ domain containing 3	0016310 // phosphorylation // inferred from electronic annotation//00043507 // positive regulation of JUN kinase activity // inferred from genetic interaction
1433091_a	0.008770	-2.83	-1.43	NM_001083810// <i>NM_0011</i>	<i>Prr51</i>	proline rich 5 like	0001933 // negative regulation of protein phosphorylation // not recorded//0001934 // positive regulation of protein phosphorylation // inferred from genetic interaction//0009968 //
1426299_a	0.002985	-2.84	-1.02	NM_001164491// <i>NM_1986</i>	<i>Abim3</i>	actin binding LIM protein family, member 3	0006351 // transcription, DNA-templated // inferred from electronic annotation//0007010 // cytoskeleton organization // inferred from electronic annotation//0003036 // actin cytoskeleton
1440096_a	0.002307	-2.84	-1.61	NM_007592	<i>Car8</i>	carbonic anhydrase 8	0006730 // one-carbon metabolic process // inferred from electronic annotation//0048015 // phosphatidylinositol-mediated signaling // inferred from direct assay
1422535_a	0.002053	-2.84	-1.12	NM_001099774	<i>Krtap17-1</i>	keratin associated protein 17-1	
1426968_a	0.008511	-2.84	-1.04	NM_018778	<i>Cldn8</i>	claudin 8	0016338 // calcium-independent cell-cell adhesion // inferred from sequence or structural similarity
1454652_a	0.009997	-2.84	-1.31	NM_00102563// <i>NM_0302</i>	<i>Pogrla//Prrt2</i>	PAXP1 associated glutamate rich protein 1A//proline-rich transmembrane	0009607 // response to biotic stimulus // inferred from electronic annotation//0005084 // neuromuscular process controlling posture // not recorded//0071557 // histone H3-K27
1455672_a	0.006203	-2.84	-2.01	NM_023053	<i>Twsg1</i>	twisted gastrulation homolog 1 (Drosophila)	0001503 // ossification // inferred from mutant phenotype//0001707 // mesoderm formation // inferred from genetic interaction//0007275 // multicellular organismal development //
1442340_a	0.001148	-2.85	-1.70	NM_008339	<i>Ct79b</i>	CD79B antigen	0002376 // immune system process // inferred from electronic annotation//0007166 // cell surface receptor signaling pathway // inferred from electronic annotation//0002853 // B cell
1444725_a	0.004028	-2.85	-1.75	NM_009506	<i>Vegf3</i>	vascular endothelial growth factor C	0001525 // angiogenesis // not recorded//0001954 // positive regulation of cell-matrix adhesion // inferred from direct assay//0002052 // positive regulation of neuroblast proliferation // not
1422617_a	0.006230	-2.86	-1.11	NM_147220// <i>XM_0065330</i>	<i>Abca9</i>	ATP-binding cassette, sub-family A (ABC1), member 9	0006200 // ATP catabolic process // inferred from electronic annotation//0006810 // transport // inferred from electronic annotation//0008152 // metabolic process // inferred from
1429466_s	0.001657	-2.86	-1.38	NM_176846// <i>XM_0065104</i>	<i>Exph5</i>	exophilin 5	0003334 // keratinocyte development // not recorded//0006886 // intracellular protein transport // inferred from electronic annotation//0004592 // positive regulation of exocytosis // not
1424154_a	0.009567	-2.87	-1.05	NM_028593// <i>XM_0065002</i>	<i>Cybrd1</i>	cytochrome b reductase 1	0006810 // transport // inferred from electronic annotation//0010039 // response to iron ion // inferred from direct assay//0005114 // oxidation-reduction process // not recorded
1429383_a	0.005159	-2.87	-1.37	NM_001040085// <i>NM_0010</i>	<i>Sytl2</i>	synaptotagmin-like 2	0006886 // intracellular protein transport // inferred from electronic annotation//0006887 // exocytosis // inferred from direct assay//0006887 // exocytosis // not recorded//0006904 //
1437376_a	0.007758	-2.87	-1.53	NM_001243072// <i>NM_0012</i>	<i>Sema3a</i>	sema domain, immunoglobulin domain (lg), short basic domain, secreted,	0001764 // neuron migration // inferred from mutant phenotype//0002027 // regulation of heart rate // inferred from mutant phenotype//0006915 // apoptotic process // not
1445870_a	0.001982	-2.87	-1.77	NM_001285805// <i>NM_0197</i>	<i>Zbtb20</i>	zinc finger and BTB domain containing 20	0000122 // negative regulation of transcription from RNA polymerase II promoter // inferred from direct assay//0000122 // negative regulation of transcription from RNA polymerase II
1429838_a	0.009226	-2.87	-1.39	NM_016697// <i>XM_0065414</i>	<i>Gpc3</i>	glypican 3	0001658 // branching involved in ureteric bud morphogenesis // inferred from genetic interaction//0001822 // kidney development // inferred from mutant phenotype//0008285 // negative
1434905_a	0.001155	-2.88	-1.47	NM_001081322// <i>XM_0065</i>	<i>Myo5c</i>	myosin VC	0008152 // metabolic process // inferred from electronic annotation//00032254 // establishment of secretory granule localization // not recorded
1430567_a	0.004742	-2.90	-1.40	NM_001242349// <i>NM_1786</i>	<i>Ano4</i>	anoctamin 1, calcium activated chloride channel	0006810 // transport // inferred from electronic annotation//0006811 // ion transport // inferred from electronic annotation//0006812 // cation transport // not recorded//0006821 //
1453071_s	0.001285	-2.90	-1.89	NM_001033406// <i>NM_0010</i>	<i>Mcc</i>	mutated in colorectal cancers	0010633 // negative regulation of epithelial cell migration // not recorded//00050680 // negative regulation of epithelial cell proliferation // not recorded//0009090 // negative regulation of
1449126_a	0.002623	-2.91	-1.20	NM_172859// <i>XM_0064995</i>	<i>Dzank1</i>	double zinc ribbon and ankyrin repeat domains 1	
1444086_a	0.001702	-2.92	-1.72	NM_013476	<i>Ar</i>	androgen receptor	0001701 // in utero embryonic development // inferred from mutant phenotype//0003073 // regulation of systemic arterial blood pressure // inferred from genetic interaction//0003382 //
1440992_a	0.002096	-2.94	-1.64	NM_009538	<i>Plagl1</i>	pleiomorphic adenoma gene-like 1	0006351 // transcription, DNA-templated // inferred from electronic annotation//0006357 // regulation of transcription from RNA polymerase II promoter // not recorded//0006366 //
1445427_a	0.003043	-2.94	-1.76	NM_013930	<i>Aass</i>	aminoadipate-semialdehyde synthase	0006091 // generation of precursor metabolites and energy // traceable author statement//0008152 // metabolic process // inferred from electronic annotation//0019477 // L-lysine
1422502_a	0.008230	-2.94	-1.12	NM_011254	<i>Rbp1</i>	retinol binding protein 1, cellular	0002138 // retinoic acid biosynthetic process // inferred from electronic annotation//0006810 // transport // inferred from electronic annotation//0030852 // regulation of granulocyte
1455951_a	0.002893	-2.96	-2.03	NM_021495// <i>NM_021496</i>	<i>Pu3i3</i>	poliovirus receptor-related 3	0002089 // lens morphogenesis in camera-type eye // inferred from mutant phenotype//0007155 // cell adhesion // inferred from direct assay//0007156 // homophilic cell adhesion //
1442214_a	0.003233	-2.97	-1.70	NM_011397// <i>XM_0065257</i>	<i>Slc23a1</i>	solute carrier family 23 (nucleoside transporters), member 1	0006810 // transport // inferred from electronic annotation//0006811 // ion transport // inferred from electronic annotation//0006814 // sodium ion transport // not recorded//0007420 //
1456482_a	0.006684	-2.97	-2.06	NM_001101471// <i>XM_0065</i>	<i>Akap5</i>	A kinase (PRKA) anchor protein 5	0001934 // positive regulation of protein phosphorylation // not recorded//0006605 // protein targeting // inferred from electronic annotation//0007165 // signal transduction // inferred
1438195_a	0.006638	-2.98	-1.55	NM_010140	<i>Epha3</i>	Eph receptor A3	0003197 // endocardial cushion development // inferred from mutant phenotype//0006468 // protein phosphorylation // inferred from electronic annotation//0007169 // transmembrane
1426995_a	0.005287	-2.98	-1.04	NM_008829// <i>XM_0065098</i>	<i>Pgr</i>	progesterone receptor	0001542 // ovulation from ovarian follicle // inferred from mutant phenotype//0002070 // epithelial cell maturation // inferred from mutant phenotype//0006351 // transcription, DNA-
1433566_a	0.002323	-2.99	-1.43	NM_023395	<i>Wfdc1</i>	WAP four-disulfide core domain 1	0001558 // regulation of cell growth // not recorded//0010466 // negative regulation of peptidase activity // inferred from electronic annotation//0010951 // negative regulation of
1438109_a	0.008156	-2.99	-1.54	NM_001004173// <i>XM_0064</i>	<i>Sgpp2</i>	sphingosine-1-phosphate phosphatase 2	0006670 // sphingosine metabolic process // not recorded//0010631 // dephosphorylation // not recorded
1460647_a	0.005875	-3.00	-1.34	NM_178767// <i>XM_0065151</i>	<i>Agmo</i>	alkylglycerol monoxygenase	0006633 // fatty acid biosynthetic process // inferred from electronic annotation//0006643 // membrane lipid metabolic process // not recorded//0046485 // ether lipid metabolic process //
1432092_a	0.006759	-3.00	-1.42	NM_0024263// <i>XM_0065392</i>	<i>Mxra8</i>	matrix-remodelling associated 8	0060857 // establishment of glial blood-brain barrier // inferred from expression pattern
1424948_x	0.001085	-3.01	-1.02	NM_009255// <i>XM_0064964</i>	<i>Serpine2</i>	serine (or cysteine) peptidase inhibitor, clade E, member 2	0007275 // multicellular organismal development // inferred from electronic annotation//0007399 // nervous system development // inferred from electronic annotation//0007596 // blood
1436562_a	0.000135	-3.01	-1.51	NM_026793	<i>Myct1</i>	myc target 1	
1430543_a	0.004482	-3.01	-1.40	NM_001029937	<i>Sec14l3</i>	SEC14-like 3 (S. cerevisiae)	0006810 // transport // inferred from electronic annotation
1425398_a	0.002771	-3.02	-1.00	NM_030707// <i>XM_0065023</i>	<i>Fcrl</i>	receptor-like 5, scavenger receptor	0006898 // receptor-mediated endocytosis // inferred from electronic annotation//0009967 // positive regulation of signal transduction // inferred from electronic annotation
1434049_a	0.001579	-3.03	-1.44	NM_133738	<i>Anbx2</i>	antrax toxin receptor 2	0022414 // reproductive process // inferred from mutant phenotype
1428645_a	0.005915	-3.04	-1.08	NM_009866// <i>XM_0065306</i>	<i>Cdh11</i>	cadherin 11	0007155 // cell adhesion // inferred from electronic annotation//0007156 // homophilic cell adhesion // inferred from electronic annotation//0021957 // corticospinal tract morphogenesis //
1430079_a	0.009885	-3.05	-1.39	NM_177497// <i>XM_0064996</i>	<i>Rhiz23</i>	rhizolysin domain containing 3	
1457707_a	0.000826	-3.05	-2.22	NM_134134// <i>XR_385966</i>	<i>Abhr3</i>	abhyradial domain containing 3	0008152 // metabolic process // inferred from electronic annotation
1456641_a	0.009439	-3.06	-2.07	NM_138741	<i>Sdpr</i>	serum deprivation response	0045944 // positive regulation of transcription from RNA polymerase II promoter // not recorded
1452734_a	0.001179	-3.07	-1.30	NM_178214	<i>Hist2h2be</i>	histone cluster 2, H2be	0002227 // innate immune response in mucosa // not recorded//0006334 // nucleosome assembly // inferred from electronic annotation//0019731 // antibacterial humoral response // not
1418400_a	0.004612	-3.07	-1.39	NM_007894// <i>NM_0010127</i>	<i>Ear1//Ear12//Ear2//Ear3</i>	eosinophil-associated, ribonuclease A family, member 1//eosinophi-	0008152 // metabolic process // inferred from electronic annotation//0009305 // nucleic acid phosphodiester bond hydrolysis // inferred from electronic annotation//0009502 // RNA
1437868_a	0.000564	-3.08	-1.54	NM_001145899// <i>NM_0213</i>	<i>Slc15a2</i>	solute carrier family 15 (H+peptide transporter), member 2	0006810 // transport // inferred from electronic annotation//0006851 // oligopeptide transport // inferred from direct assay//0042891 // antibiotic transport // not recorded//0042938 //
1436120_a	0.000404	-3.10	-1.50	NM_009844// <i>XM_0065072</i>	<i>Cd19</i>	CD19 antigen	0005853 // B cell receptor signaling pathway // inferred from direct assay
1438257_a	0.002557	-3.10	-1.55	NM_027294	<i>Cmtm8</i>	CKLF-like MARVEL transmembrane domain containing 8	0006935 // chemotaxis // inferred from electronic annotation
1438667_a	0.008156	-3.10	-1.56	NM_133187// <i>XM_0065019</i>	<i>Fam198b</i>	family with sequence similarity 198, member B	
1417447_a	0.003217	-3.11	-1.64	NM_029566// <i>XM_0065344</i>	<i>Mfap4</i>	microfibrillar-associated protein 4	0007155 // cell adhesion // inferred from electronic annotation//0009650 // UV protection // not recorded//0010712 // regulation of collagen metabolic process // not recorded//0043206 //
1459315_a	0.003141	-3.12	-2.57	NM_008966	<i>Ptgef</i>	prostaglandin F receptor	0007165 // signal transduction // inferred from electronic annotation//0007186 // G-protein coupled receptor signaling pathway // inferred from collagen//0032496 // response to lipopolysaccharide
1421460_a	0.000137	-3.13	-1.15	NM_013589// <i>XM_0065155</i>	<i>Ltbp2</i>	latent	

Table S7

Gene ID	p (Corr)	FC-RSV 1 d	FC-RSV 5 d	RefSeq Transcript ID	Sym	Gene Symbol	Gene Title	Gene Ontology Biological Process	
1454746_a	0.002511	-3.15	-1.96	NM_183312//NM_201639/		<i>Symt</i>	synemin, intermediate filament protein		
1446709_a	0.009316	-3.15	-1.80	NM_010358//XM_0065010		<i>Gstm1</i>	glutathione S-transferase, mu 1	0006749 // glutathione metabolic process // not recorded//0008152 // metabolic process // inferred from electronic annotation//0035690 // cellular response to drug // inferred from direct	
1452216_a	0.001251	-3.15	-1.29	NM_001290476//NM_0261		<i>Khlh13</i>	kulch-like 13	0000910 // cytokinesis // not recorded//0007049 // cell cycle // inferred from electronic annotation//0007067 // mitotic nuclear division // inferred from electronic annotation//0016567 //	
1453442_a	0.004030	-3.17	-1.92	NM_027560//NM_028450/		<i>Gulp1</i>	GULP, engulfment adaptor PTB domain containing 1	0006810 // transport // inferred from electronic annotation//0006869 // lipid transport // inferred from electronic annotation//0006909 // phagocytosis // inferred from electronic	
1453468_a	0.006137	-3.17	-1.31	NM_016719//NM_0064998		<i>Grb14</i>	growth factor receptor bound protein 14	0007165 // signal transduction // traceable author statement//0008286 // insulin receptor signaling pathway // not recorded//0009967 // positive regulation of signal transduction // inferred	
1447195_a	0.007169	-3.18	-1.82	NM_010377179//NM_1775		<i>Btla</i>	B and T lymphocyte associated	0002376 // immune system process // inferred from electronic annotation//0002768 // immune response-regulating cell surface receptor signaling pathway // inferred from mutant	
1438027_a	0.000680	-3.18	-1.54	NM_01159965//NM_0011		<i>Ralgps2</i>	Ral GEF with PH domain and SH3 binding motif 2	0007264 // small GTPase mediated signal transduction // inferred from electronic annotation//0043547 // positive regulation of GTPase activity // inferred from electronic annotation	
1460389_a	0.004566	-3.20	-1.34	NM_010097//XM_0065347		<i>Sparc1</i>	SPARC-like 1	0007165 // signal transduction // inferred from electronic annotation	
1439969_a	0.003743	-3.20	-1.60	NM_001166493//NM_2072		<i>Rasgsp3</i>	RAS, guanyl releasing protein 3	0007264 // small GTPase mediated signal transduction // inferred from electronic annotation//0007265 // Ras protein signal transduction // inferred from direct assay//0032318 // regulation	
1440264_a	0.005387	-3.20	-1.61	NM_008304		<i>Sdc2</i>	syndecan 2	0001666 // response to hypoxia // inferred from electronic annotation//0007399 // nervous system development // inferred from electronic annotation//0030154 // cell differentiation	
1452676_a	0.000636	-3.21	-1.30	NM_008343//XM_0064957		<i>Igfbp2</i>	insulin-like growth factor binding protein 2	0001558 // regulation of cell growth // inferred from electronic annotation//0006950 // response to stress // inferred from electronic annotation//0007165 // signal transduction // inferred	
1459648_a	0.002171	-3.21	-2.80	NM_013549//NM_178212		<i>Hist2h2aa1//Hist2h2aa2</i>	histone cluster 2, H2aa1//histone cluster 2, H2aa2	0006334 // nucleosome assembly // inferred from electronic annotation//0006334 // nucleosome assembly // non-traceable author statement	
1439530_a	0.003810	-3.22	-1.58	NM_026662//XM_0065286		<i>Prps2</i>	phosphoribosyl pyrophosphate synthetase 2	0006015 // 5-phosphoribose 1-diphosphate biosynthetic process // not recorded//0006167 // AMP biosynthetic process // not recorded//0009116 // nucleoside metabolic process // inferred	
1420498_a	0.000816	-3.22	1.20	NM_001080814//XM_0065		<i>Fat3</i>	FAT tumor suppressor homolog 3 (Drosophila)	0000904 // cell morphogenesis involved in differentiation // inferred from mutant phenotype//0001764 // neuron migration // inferred from mutant phenotype//0007155 // cell adhesion //	
1423745_a	0.002078	-3.23	1.06	NM_001204201//NM_0012		<i>Spp1</i>	secreted phosphoprotein 1	0001503 // ossification // inferred from electronic annotation//0001649 // osteoblast differentiation // not recorded//0006954 // inflammatory response // inferred from electronic	
1448263_a	0.004665	-3.24	-1.17	NM_011812//XM_0065158		<i>Fbln5</i>	fibulin 5	0001558 // regulation of cell growth // inferred from electronic annotation//0007155 // cell adhesion // inferred from electronic annotation//0003198 // extracellular matrix organization //	
1421241_a	0.007587	-3.24	1.16	NM_031374//XM_0065089		<i>Tex15</i>	testis expressed gene 15	0007129 // synapsis // inferred from mutant phenotype//0007130 // synaptosomal complex assembly // inferred from mutant phenotype//0007140 // male meiosis // inferred from mutant	
1430682_a	0.009043	-3.25	-1.40	NM_001001980//NM_0012		<i>Limch1</i>	limin and calponin homology domains 1	0031032 // actomyosin structure organization // inferred from electronic annotation	
1457092_a	0.002739	-3.25	-2.15	NM_001161817//NM_0012		<i>Myo1b</i>	myosin IB	0006200 // ATP catabolic process // not recorded//0008152 // metabolic process // not recorded//0030048 // actin filament-based movement // not recorded//0051017 // actin filament	
1458038_a	0.007726	-3.26	-2.31	NM_016678//XM_0065380		<i>Reck</i>	reversion-inducing-cysteine-rich protein with kazal motifs	0001955 // blood vessel maturation // inferred from genetic interaction//0001955 // blood vessel maturation // inferred from mutant phenotype//0007566 // embryo implantation //	
1440865_a	0.000916	-3.27	-1.17	NM_001193666//NM_0011		<i>Cc21a//Cc21b//Cc21c//G</i>	chemokine (C-C motif) ligand 21A (serine)//chemokine (C-C motif) ligand	0001768 // establishment of T cell polarity // inferred from sequence or structural similarity//0001771 // immunological synapse formation // inferred from direct assay//0001954 // positive	
1452770_a	0.000614	-3.28	-1.30	NM_080846//XM_0065343		<i>Higd1b</i>	HIG1 domain family, member 18		0007165 // signal transduction // inferred from electronic annotation//0007166 // cell surface receptor signaling pathway // inferred from electronic annotation//0007186 // G-protein
1439713_a	0.000490	-3.28	-1.59	NM_001002268//XM_0065		<i>Gpr126</i>	G protein-coupled receptor 126		0007528 // intramolecular junction development // inferred from mutant phenotype
1439435_a	0.002107	-3.29	-1.48	NM_001163155//NM_0077		<i>Col4a5</i>	collagen, type IV, alpha 5		0007528 // vitamin metabolic process // inferred from mutant phenotype//0006897 // endocytosis // inferred from electronic annotation//0006898 // receptor-mediated endocytosis //
1437371_a	0.005185	-3.29	-1.53	NM_001081088		<i>Lrp2</i>	low density lipoprotein receptor-related protein 2		0001504 // neurotransmitter uptake // inferred from mutant phenotype//0002026 // regulation of the force of heart contraction // inferred from mutant phenotype//0002087 // regulation
1449155_a	0.006759	-3.30	-1.20	NM_178405		<i>Atp1a2</i>	ATPase, Na+/K+ transporting, alpha 2 polypeptide		0006810 // transport // inferred from electronic annotation//0006811 // ion transport // inferred from electronic annotation//0006813 // potassium ion transport // inferred from direct
1446191_a	0.004198	-3.30	-1.78	NM_0160139//NM_0238		<i>Kcnq5</i>	potassium voltage-gated channel, subfamily Q, member 5		0001578 // microtubule bundle formation // not recorded//0031334 // positive regulation of protein complex assembly // inferred from sequence or structural similarity//0032273 // positive
1446245_a	0.009982	-3.31	-1.78	NM_182839//XM_0065174		<i>Tppp</i>	tubulin polymerization promoting protein		0006508 // proteolysis // inferred from direct assay//0006508 // proteolysis // not recorded//0006898 // receptor-mediated endocytosis // inferred from electronic annotation//0016540 //
1448590_a	0.001407	-3.31	-1.18	NM_015775//XM_0065230		<i>Tmprss2</i>	transmembrane protease, serine 2		0006182 // cGMP biosynthetic process // not recorded//0007263 // nitric oxide mediated signal transduction // not recorded//0009190 // cyclic nucleotide biosynthetic process // inferred
1457901_a	0.006128	-3.32	-2.25	NM_001161796//NM_0174		<i>Gucyl1b3</i>	guanylate cyclase 1, soluble, beta 3		0010951 // negative regulation of endopeptidase activity // inferred from electronic annotation
1421038_a	0.005079	-3.32	1.17	NM_001243008//NM_0012		<i>Col6a3</i>	collagen, type VI, alpha 3		0006334 // nucleosome assembly // inferred from electronic annotation//0002227 // innate immune response in mucosa // not recorded//0001684 // nucleosome positioning // inferred
1426377_a	0.007736	-3.33	-1.02	NM_001290466//NM_1782		<i>Hist1h2bp//Hist1h2bc//Hist1</i>	histone cluster 1, H2bp//histone cluster 1, H2bc//histone cluster 1,		0016322 // neuron remodeling // inferred from direct assay//0006068 // regulation of branching involved in salivary gland morphogenesis by extracellular matrix-epithelial cell signaling //
1456550_a	0.004213	-3.34	-2.07	NM_021320		<i>Ntn4</i>	netrin 4		0007026 // negative regulation of microtubule depolymerization // not recorded//0010976 // positive regulation of neuron projection development // not recorded//0010977 // negative
1440111_a	0.001650	-3.35	-1.61	NM_025285		<i>Stmn2</i>	stathmin-like 2		0007155 // cell adhesion // inferred from electronic annotation//0001637 // single organismal cell-cell adhesion // not recorded//0030155 // regulation of cell adhesion // inferred from
1448203_a	0.008230	-3.35	-1.17	NM_010680//XM_0065256		<i>Lama3</i>	laminin, alpha 3		0002227 // innate immune response in mucosa // not recorded//0006334 // nucleosome assembly // inferred from electronic annotation//00019731 // antibacterial humoral response // not
1426505_a	0.004618	-3.37	-1.02	NM_001097979//NM_0011		<i>Hist1h2bf//Hist1h2bj//Hist1</i>	histone cluster 1, H2bf//histone cluster 1, H2bj//histone cluster 1,		0002227 // innate immune response in mucosa // not recorded//0006334 // nucleosome assembly // inferred from electronic annotation//00019731 // antibacterial humoral response // not
1426506_a	0.004050	-3.37	-1.02	NM_001097979//NM_0011		<i>Hist1h2bf//Hist1h2bj//Hist1</i>	histone cluster 1, H2bf//histone cluster 1, H2bj//histone cluster 1,		0002053 // positive regulation of mesenchymal cell proliferation // inferred from genetic interaction//0007165 // signal transduction // inferred from electronic annotation//0008286 //
1428512_a	0.002632	-3.38	-1.35	NM_010570//XM_0064964		<i>Irs1</i>	insulin receptor substrate 1		0001525 // angiogenesis // inferred from electronic annotation//0001569 // patterning of blood vessels // inferred from mutant phenotype//0001953 // negative regulation of cell-matrix
1453942_a	0.008839	-3.39	-1.94	NM_00113148		<i>Sema3e</i>	sema domain, immunoglobulin domain (lg), short basic domain, secreted,		0002227 // innate immune response in mucosa // not recorded//0006334 // nucleosome assembly // inferred from electronic annotation//0001684 // nucleosome positioning // inferred
1426440_a	0.002052	-3.40	-1.02	NM_001097979//NM_0011		<i>Hist1h2bc//Hist1h2be//Hist1</i>	histone cluster 1, H2bc//histone cluster 1, H2be//histone cluster 1,		0001503 // ossification // inferred from electronic annotation//0001654 // eye development // not recorded//0001709 // cell fate determination // not recorded//0007275 // multicellular
1443692_a	0.008637	-3.40	-1.71	NM_001114385//NM_0312		<i>Chrd1</i>	chordin-like 1		0007275 // multicellular organismal development // inferred from electronic annotation//0001072 // embryonic body morphogenesis // inferred from mutant phenotype//0003221 //
1454646_a	0.008189	-3.40	-1.95	NM_011825//XM_0064968		<i>Grem2</i>	gremlin 2 homolog, cysteine knot superfamily (Xenopus laevis)		0001657 // uterine bud development // inferred from mutant phenotype//0001658 // branching involved in uterine bud morphogenesis // inferred from mutant phenotype//0001155 // cell
1434647_a	0.004550	-3.42	-1.46	NM_001029835//NM_0012		<i>Npr1</i>	nephrectomized		0001569 // patterning of blood vessels // inferred from direct assay//0001756 // somitogenesis // inferred from genetic interaction//0001843 // neural tube closure // inferred from genetic
1418695_a	0.006292	-3.43	1.33	NM_009144//XM_0065011		<i>Sfp2</i>	secreted frizzled-related protein 2		0001525 // angiogenesis // inferred from electronic annotation//0001525 // angiogenesis // inferred from sequence or structural similarity//0001666 // response to hypoxia // inferred from
1455726_a	0.006345	-3.43	-2.02	NM_021472//NM_201239		<i>Rnase4</i>	ribonuclease, RNase A family 4		0001539 // cilium or flagellum-dependent cell motility // inferred from electronic annotation//0006200 // ATP catabolic process // inferred from electronic annotation//0007018 //
1436520_a	0.009463	-3.44	-1.51	NM_001164669//XM_0065		<i>Dnah6</i>	dynein, axonemal, heavy chain 6		0001525 // angiogenesis // inferred from electronic annotation//0001759 // organ induction // inferred from direct assay//0001934 // positive regulation of protein phosphorylation //
1436074_a	0.005096	-3.45	-1.50	NM_010197//XM_0065256		<i>Fgf1</i>	fibroblast growth factor 1		0002227 // innate immune response in mucosa // not recorded//0006334 // nucleosome assembly // inferred from electronic annotation//00019731 // antibacterial humoral response // not
1427242_a	0.007058	-3.46	-1.05	NM_001177653//NM_0012		<i>Hist1h2bc//Hist1h2be//Hist1</i>	histone cluster 1, H2bc//histone cluster 1, H2be//histone cluster 1,		0006810 // transport // inferred from electronic annotation//0006811 // ion transport // inferred from electronic annotation//0003082 // bone mineralization // not recorded//0030512 //
1457260_a	0.003880	-3.46	-2.20	NM_173444//XM_0064960		<i>Nbeal1</i>	neurone beclin-like 1		0001503 // ossification // inferred from electronic annotation//0001558 // regulation of cell growth // inferred from electronic annotation//0007275 // multicellular organismal development
1437165_a	0.000176	-3.47	-1.15	NM_001172481//NM_0257		<i>Aspn</i>	asporin		0006935 // chemotaxis // inferred from direct assay//0008152 // metabolic process // inferred from electronic annotation//0009305 // nucleic acid phosphodiester bond hydrolysis //
1448394_a	0.001355	-3.47	-1.18	NM_178929//XM_0065265		<i>Kazal1</i>	Kazal-type serine peptidase inhibitor domain 1		0006116 // NADH oxidation // traceable author statement//0008152 // metabolic process // inferred from electronic annotation//0044237 // cellular metabolic process // inferred from
1418099_a	0.002052	-3.49	1.33	NM_001012766//NM_0078		<i>Eor1//Eor12//Eor2//Eor3</i>	eosinophil-associated, ribonuclease A family, member 1//eosinophi-		0043206 // extracellular fibril organization // inferred from direct assay
1432047_a	0.002462	-3.50	-1.42	NM_007621//XM_0065320		<i>Cbr2</i>	carboxyl reductase 2		0016477 // cell migration // not recorded//0032092 // positive regulation of protein binding // inferred from direct assay//0033690 // positive regulation of osteoblast proliferation // inferred
1427346_a	0.002360	-3.50	-1.05	NM_015776//XM_0065063		<i>Mjfp5</i>	microfibrillar associated protein 5		0007155 // cell adhesion // inferred from electronic annotation//0007156 // homophilic cell adhesion // inferred from electronic annotation
1460330_a	0.001017	-3.50	-1.33	NM_026516		<i>Tmem178</i>	transmembrane protein 178		0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 // regulation of transcription, DNA-templated // inferred from electronic annotation//0006357 //
1428800_a	0.003970	-3.51	-1.36	NM_145137//XM_0065329		<i>Mgl2</i>	macrophage galactose N-acetyl-galactosamine specific lectin 2		0006935 // chemotaxis // inferred from direct assay//0008152 // metabolic process // inferred from electronic annotation//0009305 // nucleic acid phosphodiester bond hydrolysis //
1423506_a	0.002663	-3.51	1.08	NM_026778//XM_0065213		<i>Cthrc1</i>	carrageen triple helix repeat containing 1		000187 // activation of MAPK activity // inferred from direct assay//0045725 // positive regulation of glycogen biosynthetic process // inferred from direct assay//0046321 // positive
1443100_a	0.000960	-3.53	-1.69	NM_001013753//XM_0065		<i>Pcdh17</i>	protocadherin 17		000898 // receptor-mediated endocytosis // inferred from electronic annotation
1433538_a	0.003035	-3.55	-1.11	NM_011542//XM_0065387		<i>Teco3</i>	transcription elongation factor A (SII), 3		0007155 // cell adhesion // inferred from electronic annotation//0007275 // multicellular organismal development // inferred from electronic annotation//0001811 // positive regulation of
1418847_a	0.005417	-3.55	1.33	NM_001012766//NM_0078		<i>Eor1//Eor12//Eor2//Eor3</i>	eosinophil-associated, ribonuclease A family, member 1//eosinophi-		0006629 // lipid metabolic process // inferred from electronic annotation//0006631 // fatty acid metabolic process // inferred from electronic annotation//0006633 // fatty acid biosynthetic
1429458_a	0.000181	-3.55	-1.38	NM_026979//XM_0065341		<i>C1qtnf2</i>	C1q and tumor necrosis factor related protein 2		0010923 // negative regulation of phosphatase activity // not recorded//0050808 // synapse organization // inferred from mutant phenotype
145421_a	0.000265	-3.57	-1.76	NM_001290633//NM_1782		<i>Reps2</i>	RALBP1 associated Eps domain containing protein 2		0006810 // transport // not recorded//0006811 // ion transport // inferred from electronic annotation//0007275 // multicellular organismal development // inferred from electronic
143832_a	0.001060	-3.58	-1.12	NM_019397		<i>Egfl6</i>	Egfr-like domain, multiple 6		0006887 // exocytosis // inferred from electronic annotation//0008152 // metabolic process // inferred from electronic annotation//00017157 // regulation of exocytosis // inferred from
1428859_a	0.002675	-3.59	-1.36	NM_009128		<i>Scd2</i>	stearoyl-Coenzyme A desaturase 2		0007275 // multicellular organismal development // inferred from electronic annotation
1426084_a	0.000126	-3.60	-1.01	NM_175522//XM_0065047		<i>Elfn1</i>	leucine rich repeat and fibronectin type III, extracellular 1		0000122 // negative regulation of transcription from RNA polymerase II promoter // inferred from direct assay//0000122 // negative regulation of transcription from RNA polymerase II
1452330_a	0.003004	-3.61	-1.29	NM_172658//XM_0065294		<i>Skca1</i>	solute carrier organic anion transporter family member 4C1		0007612 // learning // inferred from mutant phenotype//0048488 // synaptic vesicle endocytosis // inferred from mutant phenotype
1427640_a	0.000200	-3.61	-1.06	NM_145219		<i>Lgi3</i>	leucine-rich repeat LGI family, member 3		0006629 // lipid metabolic process // inferred from electronic annotation//0006637 // acyl-CoA metabolic process // traceable author statement//0008152 // metabolic process // inferred
1449429_a	0.004859	-3.62	-1.22	NM_026162//XM_0064975		<i>Pldc2</i>	plexin domain containing 2		0000122 // negative regulation of transcription from RNA polymerase II promoter // inferred from direct assay//0000122 // negative regulation of transcription from RNA polymerase II
1447122_a	0.006523	-3.62	-1.81	NM_001136061//NM_0012		<i>Ednrb</i>	endothelin receptor type B		0000122 // learning // inferred from mutant phenotype//0048488 // synaptic vesicle endocytosis // inferred from mutant phenotype
1443136_a	0.000602	-3.64	-1.69	NM_001289546//NM_1750		<i>Amph</i>	amphyphsin		0006629 // lipid metabolic process // inferred from electronic annotation//0006637 // acyl-CoA metabolic process // traceable author statement//0008152 // metabolic process // inferred
1452442_a	0.005004	-3.65	-1.29	NM_053200		<i>Ces1d</i>	carboxylesterase 1D		0000122 // negative regulation of transcription from RNA polymerase II promoter // inferred from direct assay//0006351 // transcription, DNA-templated // inferred from electronic
1443263_a	0.002007	-3.66	-1.70	NM_001289877//NM_0012		<i>Per3</i>	period circadian clock 3		0007165 // signal transduction // traceable author statement//0042325 // regulation of phosphorylation // inferred from electronic annotation//0043086 // negative regulation of catalytic
1443038_a	0.000781	-3.67	-1.69	NM_133485//XM_0065124		<i>Ppp1r14c//Gm14057</i>	protein phosphatase 1, regulatory (inhibitor) subunit 14c//Ppp1r14c		000333 // amino acid transmembrane transport // not recorded//0006810 // transport // inferred from electronic annotation//0006865 // amino acid transport // inferred from electronic
1451983_a	0.001403	-3.67	-1.28	NM_017394//XM_0065401		<i>Slc7a10</i>	solute carrier family 7 (cationic amino acid transporter, y+ system), member		0005250 // cellular amino acid metabolic process // inferred from electronic annotation//0007623 // circadian rhythm // inferred from electronic annotation//0009636 // response to toxic
1443858_a	0.002949	-3.68	-1.71	NM_001190448//NM_0166		<i>Ddc</i>	dopa decarboxylase		0007275 // multicellular organismal development // inferred from electronic annotation//0009987 // cellular process // not recorded//0004808 // platelet-derived growth factor receptor
1446709_a	0.006379	-3.69	-1.79	NM_027924//XM_0065098		<i>Pgm1f</i>	PGM1 determining growth factor, D polypeptide		0001501 // skeletal system development // inferred from mutant phenotype//0001666 // response to hypoxia // not recorded//0001841 // neural tube formation // inferred from mutant
1431226_a	0.000218	-3.69	-1.10	NM_009328		<i>Saw1</i>	SRY (sex determining region) Y-box 4		000160 // phosphorelay signal transduction system // inferred from electronic annotation//0001662 // behavioral fear response // inferred from mutant phenotype//0006138 // cAMP
1437184_a	0.009281	-3.69	-1.53	NM_001170669//NM_1722		<i>Pde8b</i>	phosphodiesterase 8B		0009

Table S7

Gene ID	p (Corr)	FC-RSV 1 d	FC-RSV 5 d	RefSeq Transcript ID	Gene Symbol	Gene Title	Gene Ontology Biological Process
1445446_a	0.002653	-3.84	-1.76	XM_006535369//XM_0065	<i>Igh</i>	immunoglobulin heavy chain (J558 family)//Immunoglobulin heavy	0000187 // activation of MAPK activity // inferred from direct assay//0001788 // antibody-dependent cellular cytotoxicity // inferred from direct assay//0001798 // positive regulation of type
1455006_a	0.001285	-3.85	-1.32	NM_198171//XM_0065308	<i>Ces2b</i>	carboxylesterase 2B	0006508 // proteolysis // inferred from electronic annotation//0008152 // metabolic process // inferred from electronic annotation
1417790_a	0.007565	-3.86	1.54	NM_011823//XM_0065276	<i>Gpr34</i>	G protein-coupled receptor 34	0007165 // signal transduction // inferred from electronic annotation//0007186 // G-protein coupled receptor signaling pathway // inferred from electronic annotation
1434665_a	0.001500	-3.88	-1.46	NM_001025600//NM_0187	<i>Cadm1</i>	cell adhesion molecule 1	0001889 // liver development // not recorded//0002376 // immune system process // inferred from electronic annotation//0006915 // apoptotic process // inferred from electronic
1441038_a	0.002432	-3.93	-1.64	NM_009027	<i>Rasgf2</i>	RAS protein-specific guanine nucleotide-releasing factor 2	0007264 // small GTPase mediated signal transduction // inferred from electronic annotation//0032321 // positive regulation of Rho GTPase activity // inferred from electronic
1440990_a	0.001063	-3.94	-1.63	NM_144930//XR_387740	<i>Ces1f</i>	carboxylesterase 1F	0008152 // metabolic process // inferred from electronic annotation//0019626 // short-chain fatty acid catabolic process // inferred from direct assay
1456090_a	0.000460	-3.94	-2.04	NM_001002900//NM_0010	<i>Higd1c1//Mett17a1//Mett17a2</i>	HIG1 domain family, member 1C//methyltransferase like arylsulfatase K	0008152 // metabolic process // inferred from electronic annotation
1447443_a	0.007486	-3.95	-1.83	NM_029847//XM_0065174	<i>Arsk</i>	epidermal growth factor-containing fibulin-like extracellular matrix protein	0006355 // regulation of transcription, DNA-templated // not recorded//0007173 // epidermal growth factor receptor signaling pathway // not recorded//0018108 // peptidyl-tyrosine
1455259_a	0.001624	-3.98	-1.43	NM_146015//XM_0065146	<i>Efpmp1</i>	collagen, type XIV, alpha 1	0003229 // ventricular cardiac muscle tissue development // inferred from mutant phenotype//0007155 // cell adhesion // inferred from electronic annotation//0030199 // collagen fibril
1423654_a	0.001450	-3.99	1.07	NM_181277//XM_0065203	<i>CstIIa1</i>	guanylate cyclase 1, soluble, alpha 1	0006182 // cGMP biosynthetic process // inferred from mutant phenotype//006182 // cGMP biosynthetic process // not recorded//0007263 // nitric oxide mediated signal transduction //
1445238_a	0.000657	-4.01	-1.76	NM_021896//XM_0065018	<i>Gucyl1a3</i>	guanylate cyclase 1, soluble, alpha 2	0006182 // cGMP biosynthetic process // not recorded//0009190 // cyclic nucleotide biosynthetic process // inferred from electronic annotation//0030828 // positive regulation of cGMP
1448754_a	0.000029	-4.01	-1.19	NM_001033322	<i>Gucyl1a2</i>	TLR4 interactor with leucine-rich repeats	0002376 // immune system process // inferred from electronic annotation//0007218 // regulation of cytokine production involved in immune response // not recorded//0006954 //
1452540_a	0.003668	-4.05	-1.30	NM_025817	<i>Tril</i>	snail family zinc finger 2	0000122 // negative regulation of transcription from RNA polymerase II promoter // inferred from direct assay//0000122 // negative regulation of transcription from RNA polymerase II
1424495_a	0.002234	-4.05	1.04	NM_011415	<i>Sna12</i>	nuclear receptor subfamily 2, group F, member 1	0000122 // negative regulation of transcription from RNA polymerase II promoter // inferred from direct assay//0000122 // negative regulation of transcription from RNA polymerase II
1442004_a	0.004662	-4.05	-1.66	NM_010151//XM_0065170	<i>Nr2f1</i>	myosin, heavy polypeptide 10, non-muscle	0000281 // mitotic cytokinesis // inferred from mutant phenotype//0000281 // mitotic cytokinesis // not recorded//0001701 // in utero embryonic development // inferred from mutant
1431100_a	0.005241	-4.07	-1.43	NM_175260//XM_0065344	<i>Mylh10</i>	RIKEN DNA 2700079J08 gene	0000290 // deadenylation-dependent decapping of nuclear-transcribed mRNA // inferred from genetic interaction//0006397 // mRNA processing // inferred from electronic
1431142_s	0.001291	-4.07	-1.41	2700079J08Rik		potassium channel, subfamily K, member 2	0006810 // transport // inferred from electronic annotation//0006811 // ion transport // inferred from electronic annotation//0006813 // potassium ion transport // inferred from direct
1457042_a	0.002428	-4.08	-2.13	NM_001159850//NM_0012	<i>Cknk2</i>	protein tyrosine phosphatase, receptor type, D	0006470 // protein dephosphorylation // inferred from electronic annotation//0007157 // heterophilic cell-cell adhesion // inferred from direct assay//0016311 // dephosphorylation //
1435524_a	0.001360	-4.12	-1.14	NM_001014288//NM_0112	<i>Ptpnd</i>	paraoxonase 1	0006629 // lipid metabolic process // inferred from electronic annotation//0000801 // blood circulation // traceable author statement//0008203 // cholesterol metabolic process // inferred
1459289_a	0.000404	-4.13	-2.55	NM_011134//XM_0065050	<i>Pon1</i>	slit homology 2 (Drosophila)	0001656 // metanephros development // inferred from mutant phenotype//0001657 // ureteric bud development // not recorded//0001701 // in utero embryonic development // inferred
1429034_a	0.008189	-4.16	-1.36	NM_001291227//NM_0012	<i>Slit2</i>	neuronal necrosis factor receptor superfamily, member 19	0001942 // hair follicle development // inferred from genetic interaction//0043123 // positive regulation of I-kappaB kinase/NF-kappaB signaling // inferred from direct assay
1456235_a	0.006629	-4.17	-2.04	NM_001164155//NM_0138	<i>Tnfrsf19</i>	indolethylamine N-methyltransferase	0009308 // amine metabolic process // not recorded//0009636 // response to toxic substance // inferred from electronic annotation//0032259 // methylation // inferred from direct
1429407_a	0.009036	-4.21	-1.37	NM_009349	<i>Inmt</i>	carboxylesterase 1E	0008152 // metabolic process // not recorded
1444668_a	0.006337	-4.23	-1.73	NM_133660//XM_0065306	<i>Ces1e</i>	protocadherin 18	0007155 // cell adhesion // inferred from electronic annotation//0007156 // homophilic cell adhesion // non-traceable author statement//0007420 // brain development // inferred from
1455884_a	0.009849	-4.26	-2.03	NM_139448//XM_0065007	<i>Pcdh18</i>	growth associated protein 43	0007275 // multicellular organismal development // inferred from electronic annotation//0007399 // nervous system development // inferred from electronic annotation//0007411 // axon
1434308_a	0.004291	-4.33	-1.45	NM_008083	<i>Gap43</i>	RIKEN DNA 1190002N15 gene	0014066 // regulation of phosphatidylinositol 3-kinase signaling // not recorded//0048199 // vesicle targeting, to, from or within Golgi // inferred by curator//0060038 // cardiac muscle cell
1458240_a	0.003161	-4.33	-2.39	NM_001033145	1190002N15Rik	SEC16 homolog B (S. cerevisiae)	0006810 // transport // inferred from electronic annotation//0007029 // endoplasmic reticulum organization // not recorded//0007031 // peroxisome organization // not
1447633_x	0.002625	-4.38	-1.83	NM_001159986//NM_0333	<i>Sec16b</i>	Hedgehog-interacting protein	0005975 // carbohydrate metabolic process // inferred from electronic annotation//0007165 // signal transduction // inferred from direct assay//0007224 // smoothened signaling pathway //
1452956_a	0.002712	-4.39	-1.89	NM_020259//XM_0065307	<i>Hhsp</i>	methyltransferase like 24	0032259 // methylation // inferred from electronic annotation
1429067_a	0.000879	-4.42	-1.36	NM_177793//XM_0065127	<i>Mett124</i>	carboxypeptidase M	0006508 // proteolysis // inferred from electronic annotation//0008152 // metabolic process // inferred from electronic annotation
1441887_x	0.000529	-4.43	-1.65	NM_027468//XM_0065140	<i>Cpm</i>	phosphodiesterase 5A, cGMP-specific	0002026 // regulation of the force of heart contraction // not recorded//0002678 // positive regulation of chronic inflammatory response // not recorded//0007165 // signal transduction //
1435134_a	0.005549	-4.44	-1.47	NM_153422//XM_0065014	<i>Pde5a</i>	potassium inwardly-rectifying channel, subfamily J, member 13	0006810 // transport // inferred from electronic annotation//0006811 // ion transport // inferred from electronic annotation//0006813 // potassium ion transport // inferred from electronic
1441769_a	0.008449	-4.46	-1.65	NM_001110227	<i>Kcnj13</i>	ADP-ribosyltransferase 4	0006471 // protein ADP-ribosylation // inferred from electronic annotation
1446636_a	0.001133	-4.48	-1.79	NM_026639	<i>Art4</i>	HIG1 domain family, member 1C//methyltransferase like angiotensin-like 2	0008152 // metabolic process // inferred from electronic annotation//0032259 // methylation // inferred from electronic annotation
1435036_a	0.002754	-4.49	-1.47	NM_001002900//NM_0010	<i>Higd1c1//Mett17a1//Mett17a2</i>	phosphate regulating endopeptidase homolog, X-linked	0001692 // vesicle-mediated transport // inferred from electronic annotation
1441589_a	0.005193	-4.54	-1.65	NM_011923//XM_0064980	<i>Angptl2</i>	post-GPI attaching to proteins 1	0006508 // proteolysis // not recorded//0019637 // organophosphate metabolic process // inferred from mutant phenotype//0030282 // bone mineralization // inferred from mutant
1425621_a	0.003344	-4.54	-1.00	NM_011077	<i>Phex</i>	secretoglobin, family 3A, member 2	0006505 // GPI anchor metabolic process // inferred from electronic annotation//0006506 // GPI anchor biosynthetic process // not recorded//0006810 // transport // inferred from
1431095_a	0.000259	-4.55	-1.41	NM_001163314//NM_1755	<i>Pgap1</i>	expressed sequence A1347460//casein kinase 1, alpha 1	0000902 // cell morphogenesis // inferred from genetic interaction//0006468 // protein phosphorylation // inferred from direct assay//0006468 // protein phosphorylation // not
1456246_x	0.009177	-4.59	-1.33	NM_001289643//NM_0012	<i>Scg3a2</i>	lectin-retinol acyltransferase (phosphatidylcholine-retinol-O-	0006653 // 1,2-diacyl-sn-glycero-3-phosphocholine metabolic process // traceable author statement//0006776 // vitamin A metabolic process // inferred from direct assay//0006776 //
1450550_a	0.003820	-4.60	-1.97	NM_146087//XM_0065263	A1347460//Csnk1a1	transmembrane and tetrapeptide repeat containing 2	0002376 // immune system process // inferred from electronic annotation
1458229_a	0.000884	-4.63	-2.39	NM_023624	<i>Lrat</i>	Fas apoptotic inhibitory molecule 3	0002376 // immune system process // inferred from electronic annotation
1455736_a	0.005475	-4.63	-2.02	NM_177368//XM_0065137	<i>Tm2c2</i>	visinin-like 1	0002376 // immune system process // inferred from electronic annotation
1454877_a	0.002550	-4.66	-1.97	NM_028671	<i>Faim3</i>	neuronal regeneration related protein	0017015 // regulation of transforming growth factor beta receptor signaling pathway // inferred from direct assay//0031103 // axon regeneration // inferred from electronic
1439899_a	0.000724	-4.67	-1.60	NM_012038//XM_0065151	<i>Vsn11</i>	ATP-binding cassette, sub-family A (ABC1), member 8a	0006200 // ATP catabolic process // inferred from electronic annotation//0006810 // transport // inferred from electronic annotation//0008152 // metabolic process // inferred from
1420465_s	0.007846	-4.70	1.20	NM_001109988//NM_0011	<i>Nrep</i>	glutamate receptor, ionotropic, AMPA1 (alpha 1)	0001919 // regulation of receptor recycling // not recorded//0006810 // transport // inferred from electronic annotation//0006811 // ion transport // inferred from electronic
1453900_a	0.009213	-4.72	-1.93	NM_153145//XM_0065330	<i>Abca8a</i>	extracellular matrix protein 2, female organ and adipocyte specific	0010811 // positive regulation of cell-substrate adhesion // inferred from direct assay//0030198 // extracellular matrix organization // inferred from direct assay
1457971_a	0.009923	-4.78	-2.26	NM_001113325//NM_0012	<i>Gria1</i>	membrane metallo endopeptidase	0001822 // kidney development // inferred from electronic annotation//0001822 // kidney development // inferred from sequence or structural similarity//0006508 // proteolysis // inferred
1457510_a	0.000404	-4.81	-2.21	NM_001012324	<i>Ecm2</i>	ABI gene family, member 3 (NESH) binding protein	0010811 // positive regulation of cell-substrate adhesion // inferred from direct assay//0030198 // extracellular matrix organization // inferred from direct assay
1444060_a	0.008156	-4.83	-1.72	NM_001289462//NM_0012	<i>Mme</i>	tubulin, beta 1 class VI	0006184 // GTP catabolic process // inferred from electronic annotation//0007017 // microtubule-based process // inferred from direct assay//0051225 // spindle assembly // inferred from
1456640_a	0.009353	-4.88	-2.07	NM_001014399//NM_0010	<i>Abi3bp</i>	BTB and CNC homology 2	0000122 // negative regulation of transcription from RNA polymerase II promoter // inferred from direct assay//0006351 // transcription, DNA-templated // inferred from electronic
1459747_a	0.000999	-4.89	-2.98	NM_001080971	<i>Tubb1</i>	nuclear receptor subfamily 1, group D, member 2	0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 // regulation of transcription, DNA-templated // inferred from direct assay//0019216 // regulation
1459461_a	0.005121	-4.91	-2.63	NM_001109661//NM_0075	<i>Bach2</i>	membrane-spanning 4-domains, subfamily A, member 1	0042113 // B cell activation // inferred from electronic annotation
1459749_s	0.001703	-5.20	-2.99	NM_011584	<i>Nr1d2</i>	phosphatidylinositol-3,4,5-trisphosphate-dependent Rac exchange factor 2	0007186 // G-protein coupled receptor signaling pathway // not recorded//0008344 // adult locomotory behavior // inferred from mutant phenotype//0032314 // regulation of Rac GTPase
1457201_a	0.002342	-5.26	-2.19	NM_007641	<i>Msa4a1</i>	tetraspanin 2	0006954 // inflammatory response // inferred from genetic interaction//0007420 // brain development // inferred from electronic annotation//0014002 // astrocyte development // inferred
1453395_a	0.009725	-5.26	-1.92	NM_001033636//NM_0295	<i>Prex2</i>	epoxide hydrolase 1, microsomal	0001889 // liver development // inferred from electronic annotation//0006725 // cellular aromatic compound metabolic process // inferred from mutant phenotype//0009636 // response to
1458640_a	0.006155	-5.30	-2.46	NM_001243132//NM_0275	<i>Tspan2</i>	chitinase-like 4//chitinase-like 3	0005975 // carbohydrate metabolic process // inferred from electronic annotation//0006032 // chitin catabolic process // inferred from electronic annotation//0006954 // inflammatory
1456539_a	0.000085	-5.32	-2.06	NM_010145	<i>Ephx1</i>	Ctla and tumor necrosis factor related protein 7	0005126 // protein homooligomerization // inferred from direct assay
1418545_a	0.003064	-5.49	1.37	NM_145126//NM_009892	<i>Chil4//Chil3</i>	hemolytic complement	0001701 // in utero embryonic development // inferred from genetic interaction//0002376 // immune system process // inferred from electronic annotation//0002523 // leukocyte migration
1427056_a	0.004225	-5.51	-1.04	NM_009893//XM_0065009	<i>Chil3//Chil4</i>	histocompatibility 2, O region beta locus//uncharacterized LOC102633400	0002376 // immune system process // inferred from electronic annotation//0002504 // antigen processing and presentation of peptide or polysaccharide antigen via MHC class II // inferred
1457227_a	0.001396	-5.54	-2.19	NM_001135712//NM_1754	<i>Ctla7</i>	nuclear receptor subfamily 1, group D, member 1	0000122 // negative regulation of transcription from RNA polymerase II promoter // not recorded//0005978 // glycine biosynthetic process // inferred from mutant phenotype//0006351 //
1424470_a	0.002351	-5.76	1.04	NM_175366	<i>Mex3b</i>	brain expressed X-linked 2	0006915 // apoptotic process // inferred from electronic annotation//0007049 // cell cycle // inferred from electronic annotation//0045944 // positive regulation of transcription from RNA
1434282_a	0.001733	-5.77	-1.12	NM_010406//XR_374061//Hc		alanine and arginine rich domain containing protein	0030324 // lung development // inferred from electronic annotation
1444668_a	0.006337	-5.88	-1.74	NM_010389//XM_0065236	<i>H2-Ob//LOC102633400</i>	solute carrier family 4, sodium bicarbonate cotransporter, member 5	0002064 // epithelial cell development // inferred from mutant phenotype//0003014 // renal system process // inferred from mutant phenotype//0003073 // regulation of systemic arterial
1458589_a	0.007974	-5.95	-2.45	NM_145434	<i>Nr1d1</i>	hemectin 1	0003333 // amino acid transmembrane transport // not recorded//0015804 // neutral amino acid transport // not recorded//0015816 // glycine transport // not recorded//1902475 // L-
1447993_a	0.005612	-6.20	-1.87	NM_009749	<i>Bex2</i>	growth differentiation factor 10	0040007 // growth // inferred from electronic annotation//0045444 // fat cell differentiation // inferred from mutant phenotype//0045669 // positive regulation of osteoblast differentiation
1440372_a	0.002563	-6.22	-1.61	NM_175503	<i>Aard</i>	neuron-derived neurotrophic factor	0001764 // neuron migration // not recorded//0007399 // nervous system development // inferred from electronic annotation//0010811 // positive regulation of cell-substrate adhesion //
1458552_a	0.001938	-6.35	-2.45	NM_001166067//XM_0065	<i>Sk4a5</i>	integrin alpha 8	0001656 // metanephros development // inferred from genetic interaction//0001656 // metanephros development // inferred from mutant phenotype//0007155 // cell adhesion // inferred
1420077_a	0.006878	-6.69	-1.34	NM_001024720//XM_0065	<i>Hmcn1</i>	sodium channel, voltage-gated, type VII, alpha	0006810 // transport // inferred from electronic annotation//0006811 // ion transport // inferred from electronic annotation//0006814 // sodium ion transport // inferred from electronic
1452306_a	0.007879	-6.96	-1.29	NM_172479//XM_0065275	<i>Sk3a5</i>	kinesin family member 26B	0007018 // microtubule-based movement // inferred from electronic annotation//0007275 // multicellular organismal development // inferred from electronic annotation//0008152 //
1439818_a	0.004010	-7.02	-1.60	NM_145741	<i>Gdf10</i>	tubulointerstitial nephritis antigen	0006508 // proteolysis // inferred from electronic annotation//0006898 // receptor-mediated endocytosis // inferred from electronic annotation//0006955 // immune response // inferred
1426422_a	0.003759	-7.13	-1.02	NM_172399//XM_0065065	<i>Ndnf</i>	signal peptide, CUB domain, EGF-like 2	0055114 // oxidation-reduction process // inferred from direct assay
1440053_a	0.001001	-7.17	-1.61	NM_001001309//XM_0064	<i>Itha8</i>	aldehyde oxidase 3	0006810 // transport // inferred from electronic annotation//0006811 // ion transport // inferred from electronic annotation//0006813 // potassium ion transport // inferred from electronic
1455538_a	0.004662	-7.18	-2.00	NM_009135	<i>Scn7a</i>	potassium voltage-gated channel, Isk-related subfamily, gene 2	0005634 // response to stilbenoid // inferred from expression pattern//0002168 // heme metabolic process // inferred from direct assay//0055114 // oxidation-reduction process // inferred
1457459_a	0.007961	-7.26	-2.20	NM_001161665//NM_1777	<i>Kl26b</i>	cytochrome P450, family 2, subfamily A, polypeptide 4//cytochrome P450,	0006810 // transport // inferred from electronic annotation//0006811 // ion transport // inferred from electronic annotation//0006814 // sodium ion transport // not recorded//0007399 //
1431037_a	0.001927	-7.36	-1.10	NM_012033//XM_0065112	<i>Tna3</i>	sodium channel, voltage-gated, type III, beta	0001666 // response to hypoxia // inferred from electronic annotation//0001889 // liver development // inferred from electronic annotation//0006778 // porphyrin-containing compound
1450366_a	0.005529	-7.45	-1.24	NM_020052	<i>Scube2</i>	osteoglycin	0007155 // cell adhesion // inferred from electronic annotation
1458768_a	0.005975	-7.46	-2.49	NM_023611//XM_0064962	<i>Arag</i>	procollagen C-endopeptidase enhancer 2	0010952 // positive regulation of peptidase activity // not recorded
1444748_a	0.006995	-7.70	-1.75	NM_134110//XM_0065230	<i>Kcne2</i>	S100 calcium binding protein G	0001889 // liver development // inferred from electronic annotation//0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 // regulation of transcription,
1460061_a	0.009077	-7.87	-3.70	NM_007812//NM_009997	<i>Cyp2a4//Cyp2a5</i>	D site albumin promoter binding protein	0019800 // peptide cross-linking via chondroitin 4-sulfate glycosaminoglycan // inferred from direct assay
1434264_a	0.006583	-8.30	-1.45	NM_001083917//NM_0012	<i>Scn3b</i>	Mamdc2	0006810 // transport // inferred from electronic annotation//0008284 // positive regulation of cell proliferation // inferred from electronic annotation//0015909 // long-chain fatty acid
1458000_a	0.001272	-9.05	-2.29	NM_008760	<i>Ogn</i>	fatty acid binding protein 1, liver	
1459775_a	0.001287	-9.67	-3.07	NM_001136059//NM_0099	<i>Cyp1a1</i>		
1433481_a	0.009709	-9.99	-1.43	NM_001271019//NM_1455	<i>Siglec5</i>		
1444177_a	0.003254	-10.75	-1.72	NM_029620	<i>Pcalce2</i>		
1423392_a	0.005014	-12.41	1.08	NM_009789	<i>S100g</i>		
1459687_x	0.006367	-12.57	-2.87	NM_016974//XM_0065405	<i>Dbp</i>		
1437361_a	0.007984	-12.61	-1.53	NM_174857//XM_0065273	<i>Mamdc2</i>		
14							

Table S7

Gene ID	p (Corr)	FC-RSV 1 d	FC-RSV 5 d	RefSeq Transcript ID	Gene Symbol	Gene Title	Gene Ontology Biological Process
1447344_a	0.002468	-24.17	-1.83	NM_018732//XM_0064990	Scn3a	sodium channel, voltage-gated, type III, alpha	0006810 // transport // inferred from electronic annotation//0006811 // ion transport // inferred from electronic annotation//0006813 // potassium ion transport // inferred from electronic

Table S8. Representative lung genes with different basal expressions in inbred strains compared to C3H/HeOuJ (OuJ) mice.

Strain	FD	Symbol	Title	Strain	FD	Symbol	Title
B6	23.6	<i>Ctca3</i>	chloride channel calcium activated 3	BALBc	44.05	<i>Nppa</i>	natriuretic peptide type A
	21.0	<i>Nppa</i>	natriuretic peptide type A		33.80	<i>Serpina1b</i>	serine (or cysteine) peptidase inhibitor, clade A, member 1B
	20.3	<i>Nxpe4</i>	neurexophilin and PC-esterase domain familv. member		12.22	<i>H2-D1</i>	histocompatibility 2, D region locus
	17.7	<i>Rperin1</i>	retinitis pigmentosa GTPase regulator interacting protein 1		11.54	<i>Slc12a4</i>	solute carrier family 12, member 4
	15.9	<i>H2-D1</i>	histocompatibility 2, D region locus 1		9.9	<i>Muc5b</i>	mucin 5, subtype B, tracheobronchial
	15.2	<i>Mir1931</i>	microRNA 1931		9.4	<i>Ltf</i>	lactotransferrin
	11.9	<i>Trim12a</i>	tripartite motif-containing 12A		9.2	<i>Reg3g</i>	regenerating islet-derived 3 gamma
	11.1	<i>Klra21</i>	killer cell lectin-like receptor subfamily A, member 21		7.1	<i>Cyth1</i>	cytohesin 1
	8.9	<i>Ang</i>	angiogenin, ribonuclease, RNase A familv. 5		-16.8	<i>Rbp7</i>	retinol binding protein 7, cellular
	8.7	<i>Zfp874a</i>	zinc finger protein 874a		-15.6	<i>H2-Q4</i>	histocompatibility 2, Q region locus 4
	8.1	<i>Tlr1</i>	toll-like receptor 1		-15.4	<i>Krt79</i>	keratin 79
	5.9	<i>Trim5</i>	tripartite motif-containing 5		-13.9	<i>Acox1</i>	acyl-Coenzyme A oxidase-like
	-20.5	<i>H2-Ea-ps</i>	histocompatibility 2, class II antigen E alpha, pseudogene		-11.4	<i>Igh-VJ558</i>	immunoglobulin heavy chain (J558 family)
	-10.3	<i>Ifi202b</i>	interferon activated gene 202B		-9.4	<i>Fabp1</i>	fatty acid binding protein 1, liver
	-10.3	<i>Rbp7</i>	retinol binding protein 7, cellular		-9.3	<i>Arl2bp</i>	ADP-ribosylation factor-like 2 binding protein
	-9.0	<i>Ifi202b</i>	interferon activated gene 202B		-8.3	<i>Chil4</i>	chitinase-like 4
	-8.9	<i>Clec2d</i>	C-type lectin domain family 2, member d		-7.8	<i>Klk1b22</i>	kallikrein 1-related peptidase b22
	-8.1	<i>Tnfrsf14</i>	tumor necrosis factor receptor superfamily, member 7		-6.7	<i>H60c</i>	histocompatibility 60c
	-8.0	<i>Klk1b22</i>	kallikrein 1-related peptidase b22		-5.8	<i>Nrn1</i>	neuritin 1
	-7.8	<i>Krt79</i>	keratin 79		-5.2	<i>Akr1c19</i>	aldo-keto reductase family 1, member C19
AKR	115.8	<i>Mela</i>	melanoma antigen	D2	78.4	<i>Serpina1b</i>	serine (or cysteine) peptidase inhibitor, clade A, member 1b
	22.1	<i>Serpina1b</i>	serine (or cysteine) peptidase inhibitor, clade A, member 1b		22.2	<i>Nppa</i>	natriuretic peptide type A
	13.0	<i>Nptx1</i>	neuronal pentraxin 1		19.7	<i>Stab2</i>	stabilin 2
	10.1	<i>Slc12a4</i>	solute carrier family 12, member 4		18.1	<i>H2-D1</i>	histocompatibility 2, D region locus
	6.5	<i>Nr4a1</i>	nuclear receptor subfamily 4, group A, member 1		9.0	<i>Slc12a4</i>	solute carrier family 12, member 4
	5.4	<i>Ctse</i>	cathepsin E		8.8	<i>Mela</i>	melanoma antigen
	-135.6	<i>Bpifa1</i>	BPI fold containing family A, member 1		8.0	<i>Pdk2</i>	pyruvate dehydrogenase kinase, isoenzyme 2
	-24.1	<i>Gbp2b</i>	guanylate binding protein 2b		6.8	<i>C4a</i>	complement component 4A
	-18.4	<i>Cyp2a4</i>	cytochrome P450, family 2, subfamily a, polypeptide 4		6.5	<i>Colla1</i>	collagen, type I, alpha 1
	-14.1	<i>Cd200r4</i>	CD200 receptor 4		6.1	<i>Ctse</i>	cathepsin E
	-13.0	<i>Adipoq</i>	adiponectin, C1Q and collagen domain containing		4.0	<i>Npr1</i>	natriuretic peptide receptor 1
	-11.3	<i>Car3</i>	carbonic anhydrase 3		-32.0	<i>Gbp2b</i>	guanylate binding protein 2b
	-11.0	<i>Scgb3a1</i>	secretoglobin, family 3A, member 1		-17.2	<i>Klrd1</i>	killer cell lectin-like receptor, subfamily D, member 1
	-10.9	<i>Clec3b</i>	C-type lectin domain family 3, member b		-12.1	<i>Krt79</i>	keratin 79
	-10.2	<i>Mndal</i>	myeloid nuclear differentiation antigen like		-10.3	<i>Clec2d</i>	C-type lectin domain family 2, member d
	-9.9	<i>Stk25</i>	serine/threonine kinase 25 (yeast)		-8.4	<i>Cyt11</i>	cytokine-like 1
	-9.7	<i>Chil1</i>	chitinase-like 1		-7.2	<i>Klk1b22</i>	kallikrein 1-related peptidase b22
	-9.7	<i>Pcdhb9</i>	protocadherin beta 9		-5.8	<i>Tnfrsf14</i>	tumor necrosis factor receptor superfamily, member 7
	-9.3	<i>H2-Q4</i>	histocompatibility 2, Q region locus 4		-5.6	<i>Igf2bp2</i>	insulin-like growth factor binding protein 2
	-8.7	<i>Neur13</i>	neuralized homolog 3 homolog (Drosophila)		-5.5	<i>Cd68</i>	CD68 antigen

Table S9. Genetic variation between C3H/HeJ (HeJ) and C3H/HeOuJ (OuJ) mice profiled from public databases.

Chr location GRCm38 mm10	dbSNP 142 annotation	C3H/HeJ	C3H/HeOuJ	dbSNP ID	Observed	Source	# map
1:74436995	U3:Usp37	T	H	rs32450500	C/T	1, 2, 3, 4	
2:12537037		T	C	rs27130564	C/T	4, 5	1
2:16685831	I:Plxdc2	--	C	rs13476359	A/G	7, 8, 9	1
2:30200638	I:Ccbl1	A	G	rs27209253	A/G	4, 10	1
2:80631020	Cn:Dusp19: (GR:218)	C (ArG:R)	G (Gly:G)	rs4223249	C/G	1, 4	
3:155381683		G	C	rs30265767	C/G	1, 2, 3, 4	
4:35884831	I:Lingo2	C	G	rs27803280	C/G	4, 11	1
4:66841106	Cn:Tlr4: (PH:712)	A (His:H)	C (Pro:P)	rs3023006	A/C	4, 8, 12	
5:78220474		T	C	rs3715999	C/T	4, 13	
6:60591379	NC:Gm35386	G	C	rs13478783	A/G	7, 8, 9, 14	1
8:79983947	I:Hhip	G	C	rs6296891	C/G	4, 9, 15	
9:19881764		C or H	C	rs29794988	A/C	1, 4, 18	
10:22267450	I:Gm26740	T	H	rs13480537	C/T	4, 7	1
11:93164961	I:Car10	A	T	rs3089065	C/T	1, 6, 18	
12:107898573		A	T	rs3663172	A/T	1, 2, 4, 18	
13:33047356		A	T	rs3023380	A/G	8, 16	1
13:89748045	I:Gm4117	A	C	rs6397550	A/G	7, 8	1
13:116177492		G	C	rs3088696	A/G	8, 9, 15, 16	1
14:19409254		T	H	rs13482083	A/C/T	4	
14:75283060	I:Cpb2	G	A	rs47236847	A/G	1, 2, 4, 18	
15:30475011	I:Ctnnd2	A	G	rs33001692	A/G	4, 17	1
15:56184744		C	A	rs33554600	A/C	4, 19	1
15:58508677		T	C	rs49553868	C/T	4, 20	1
16:57292484	I:Tmem30c I:LOC105246122	G	C	rs4189277	A/G	7, 8, 9, 14	1
17:60868278		A	C	rs6251286	A/C	4, 9, 15	1
17:69303335		T	G	rs45762357	G/T	1, 2, 4	
X:93486170	I:Pola1 NC:Pola1	G	C	rs13483882	C/G	1, 2, 3, 4, 18	
X:159376175	I:Eif1ax	A	G	rs29312788	A/G	4, 21	1

SNPs obtained from the Mouse Phenome Database (<https://phenome.jax.org>). I = intron; U3 = 3'-untranslated; NC = non-coding; Cn = non-synonymous coding (amino acid location and change shown in parentheses in bold). Data sets are pulled from the following sources:

1 = Sanger1; 2 = Perlegen2; 3 = CGD-MDA1; 4 = Chicago1; 5 = NES08813828; 6 = JAXSNP1; 7 = GNF2; 8 = TJL3; 9 = WTCHG1; 10 = NES08761336; 11 = NES09474121; 12 = Dbsnp1; 13 = 5-76988137; 14 = CNB1; 15 = Merck1; 16 = TLJ2; 17 = NES12608404; 18 = Broad2; 19 = NES12656279; 20 = NES15622060; 21 = NES09737451