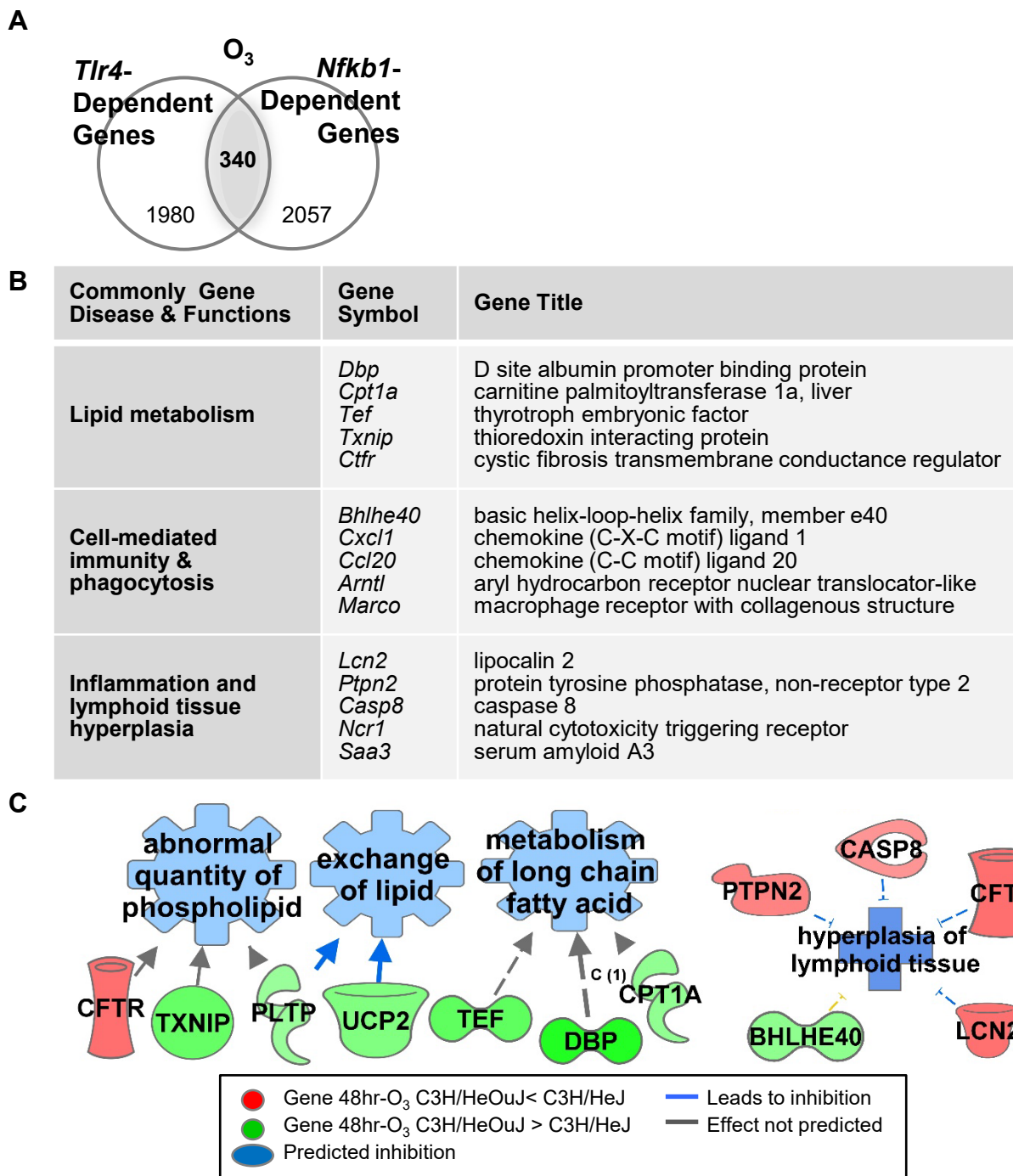
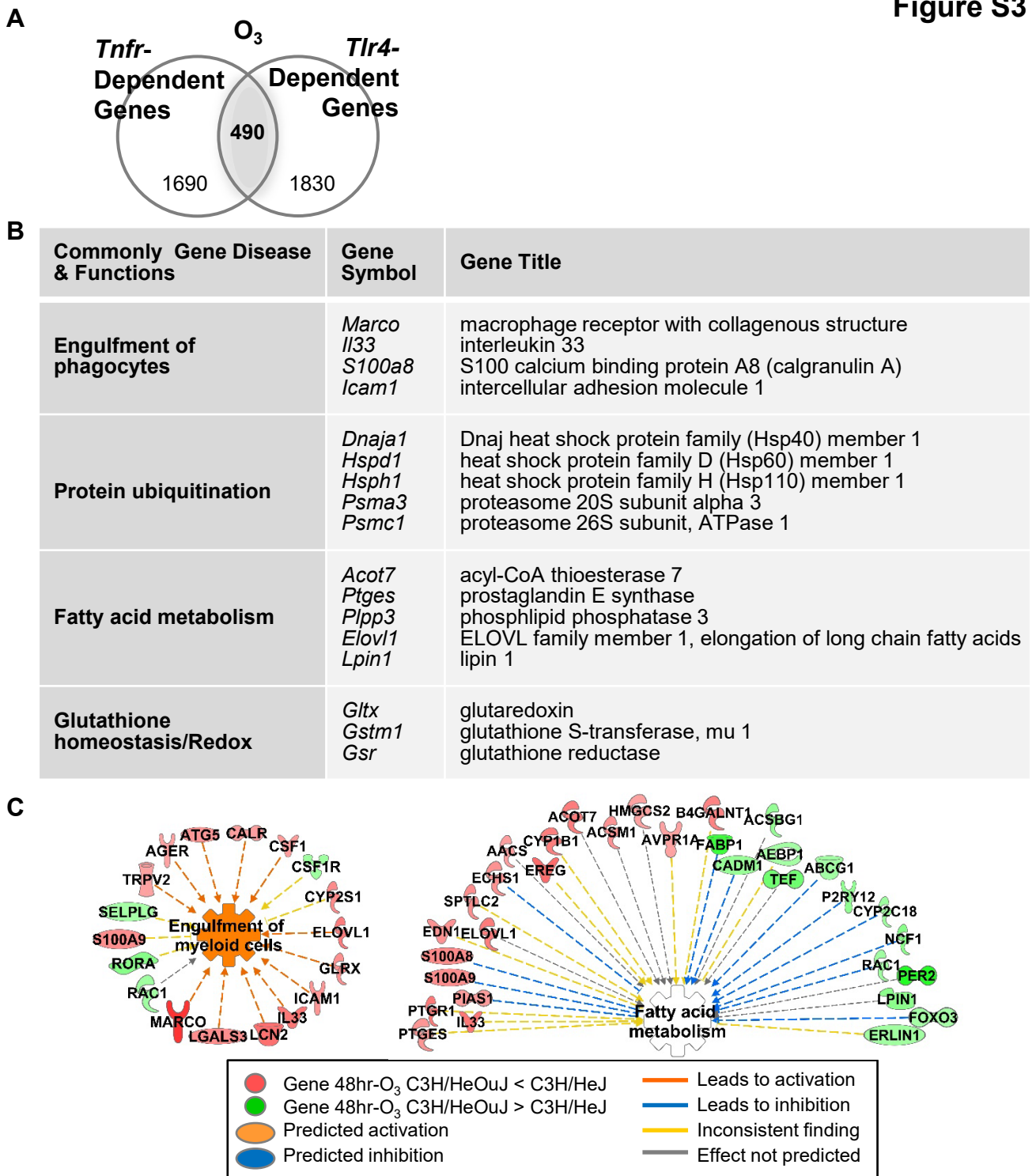


**Figure S1. Microarray analysis validation of tumor necrosis factor receptor (TNFR)- and NF- $\kappa$ B1-dependent transcriptomics in response to ozone (O<sub>3</sub>) by qRT-PCR.** (A) Differential transcript levels of TNFR-dependent tissue inhibitor of metalloproteinase 1 (*Timp1*), interleukin-33 (*Il33*) and major urinary protein 1 (*Mup1*) in *Tnfr*-deficient (*Tnfr*<sup>-/-</sup>) and wild-type (*Tnfr*<sup>+/+</sup>) mouse lungs by qRT-PCR. (B) Differential transcript levels of NF- $\kappa$ B1 (p50)-dependent immunoglobulin joining chain (*Jchain*), D site albumin promoter binding protein (*Dbp*) and serum amyloid A3 (*Saa3*) in *Nfkb1*-deficient (*Nfkb1*<sup>-/-</sup>) and wild-type (*Nfkb1*<sup>+/+</sup>) mouse lungs by qRT-PCR. (C) qRT-PCR also determined expression of common differentially regulated genes, pituitary tumor-transforming gene 1 (*Pttg1*) and *Il6*, between *Tnfr*<sup>-/-</sup> and *Tnfr*<sup>+/+</sup> mice and *Nfkb1*<sup>-/-</sup> and *Nfkb1*<sup>+/+</sup> mice. 18s rRNA-normalized group means  $\pm$  S.E.M presented (n = 3/group). \*, significantly different from genotype-matched air control mice ( $p < 0.05$ ). +, significantly different from O<sub>3</sub>-exposed wild-type mice ( $p < 0.05$ ).



**Figure S2. Common differentially regulated lung genes by toll-like receptor 4 (TLR4) and NF- $\kappa$ B1 in response to ozone (O<sub>3</sub>).** (A) Venn Diagram analysis determined common O<sub>3</sub>-responsive genes differentially expressed between C3H/HeOuJ (*Tlr4*-normal) - C3H/HeJ (*Tlr4*-mutated) and wild-type (*Nfkb1*<sup>+/+</sup>) - *Nfkb1*-deficient (*Nfkb1*<sup>-/-</sup>) mice (n=340). (B) Pathway analysis determined functions and pathways of the common genes. (C) Common genes enriched to fatty acid metabolism included *Dbp* and *Cpt1a* and to cell-mediated immunity and inflammation included *Lcn2*, *Ccl20*, and *Casp8*. Molecule colors indicated relative expression levels in C3H/HeJ mice compared to C3H/HeOuJ mice after 48 hr exposure to 0.3-parts per million O<sub>3</sub>. Analyses were done using Ingenuity Pathway Analysis and GeneSpring software.



**Figure S3. Common differentially regulated lung genes by tumor necrosis factor receptor (TNFR) and toll-like receptor 4 (TLR4) in response to ozone ( $O_3$ ).** (A) Venn Diagram analysis determined common  $O_3$ -responsive genes differentially expressed between wild-type ( $Tnfr^{+/+}$ ) -  $Tnfr$ -deficient ( $Tnfr^{-/-}$ ) mice and C3H/HeOuJ ( $Tlr4$ -normal) - C3H/HeJ ( $Tlr4$ -mutated) mice (n=490). (B-C) Pathway analysis determined top functions and pathways of the common genes. Common genes enriched to phagocytosis included *Marco*, *Il33*, and *Icam1*, to protein ubiquitination included *Dnaja1*, *Hspd1*, and *Psm3*, and to fatty acid metabolism included *Acot7*, *Ptges*, and *Elov1*. Molecule colors indicated relative expression levels in C3H/HeJ mice compared to C3H/HeOuJ mice after 48 hr exposure to 0.3-parts per million  $O_3$ . Analyses were done using Ingenuity Pathway Analysis and GeneSpring software.

**Table S1. Time-dependent changes in lung genes by 0.3-parts per million (ppm) ozone (O<sub>3</sub>) exposure in C57BL/6J mice.**

RefSeq	Transcript ID	p (24h n=60)	p (48h n=657)	p (72h n=805)	FC 24h	FC 48h	FC 72h	Gene Symbol	Gene Title	Gene Ontology Biological Process
NM_001177544	/NM_178185	1.00E-05	4.27E-05	-1.16	3.50	6.89	<b>Hist1h2ooa//Hist1h2op</b>	histone cluster 1, H2ao//histone cluster 1, H2ap	0006325 // chromatin organization // not recorded//0006342 // chromatin silencing // not recorded//0008285 // negative regulation of cell proliferation // not recorded	
NM_020509	8.10E-06	3.30E-07	2.00E-07	<b>4.32</b>	<b>6.65</b>	<b>6.74</b>	<b>Retna1</b>	retinoid like alpha	0005179 // hormone activity // inferred from electronic annotation	
NM_009264	1.38E-04	4.10E-05	1.01E-05	<b>2.26</b>	<b>4.46</b>	<b>5.56</b>	<b>Spr1a</b>	small proline-rich protein 1A	0018149 // peptide cross-linking // not recorded//0030216 // keratinocyte differentiation // not recorded//0031424 // keratinization // inferred from electronic annotation	
NM_029796	1.43E-05	2.85E-07	5.28E-05	<b>2.29</b>	<b>3.20</b>	<b>4.12</b>	<b>Lrp1</b>	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	
NM_001044384	/NM_760E-07	1.43E-07	8.61E-08	<b>3.40</b>	<b>4.45</b>	<b>3.94</b>	<b>Timp1</b>	tissue inhibitor of metalloproteinase 1	0001775 // cell activation // not recorded//0007568 // aging // inferred from electronic annotation//0008284 // positive regulation of cell proliferation // not recorded//0009725 // 0002078 // mitotic cell cycle // inferred from electronic annotation//0001556 // oocyte maturation // not recorded//0001701 // in utero embryonic development // inferred from n	
NM_172301	/NM_01	1.60E-04	1.99E-04	-1.00	<b>2.30</b>	<b>3.82</b>	<b>Ccnb3//Gm5593</b>	cyclin B1//predicted gene 5593	0002029 // protein polyubiquitination // not recorded//0006511 // ubiquitin-dependent protein catabolic process // not recorded//0007049 // cell cycle // inferred from electronic ;	
NM_026785	5.76E-06	3.03E-05	-1.03	<b>2.10</b>	<b>3.39</b>	<b>Ube2c</b>	ubiquitin-conjugating enzyme E2C	0006260 // DNA replication // inferred from electronic annotation//0009186 // deoxyribonucleoside diphosphate metabolic process // inferred from electronic annotation//000926		
NM_009104	1.42E-04	8.35E-06	<b>1.13</b>	<b>2.50</b>	<b>3.13</b>	<b>Rrm2</b>	ribonucleotide reductase M2	0006260 // DNA replication // inferred from electronic annotation//0007126 // meiotic nuclear division // inferred from direct assay//0008283 // cell proliferation // not recor		
NM_001081117	/NM_006507411//	9.76E-05	6.36E-05	<b>1.10</b>	<b>2.60</b>	<b>3.12</b>	<b>Mki67</b>	antigen identified by monoclonal antibody K1 67	0006461 // protein complex assembly // not recorded//0006468 // protein phosphorylation // inferred from direct assay//0006915 // apoptotic process // inferred from electronic ;	
NM_007659	3.11E-04	3.34E-05	<b>1.11</b>	<b>2.15</b>	<b>3.09</b>	<b>Cdk1</b>	cyclin-dependent kinase 1	0001649 // osteoblast differentiation // not recorded//0007155 // cell adhesion // inferred from electronic annotation//0007162 // negative regulation of cell adhesion // not recor		
NM_0011607	/NM_00	7.19E-05	4.07E-04	8.78E-04	<b>2.55</b>	<b>2.87</b>	<b>Tnc</b>	tenascin C	0000806 // G2/M transition of mitotic cell cycle // not recorded//0000226 // microtubule cytoskeleton organization // inferred from mutant phenotype//0000910 // cytokinesis // r	
NM_001012272	/NM_001012273//	5.06E-06	5.11E-04	-1.02	<b>2.76</b>	<b>3.03</b>	<b>Birc5</b>	baculoviral IAP repeat-containing 5	0001933 // negative regulation of protein phosphorylation // inferred from mutant phenotype//0006468 // protein phosphorylation // inferred from electronic annotation//0001631	
NM_023209	/NM_006519257	1.35E-04	6.78E-06	<b>1.12</b>	<b>1.86</b>	<b>2.74</b>	<b>Pkb</b>	PDZ binding repeat	0007173 // epidermal growth factor receptor signaling pathway // not recorded//0007186 // G-protein coupled receptor signaling pathway // not recorded//0008284 // positive reg	
NM_009704	0.00238687	8.16E-05	0.00138973	<b>1.49</b>	<b>2.42</b>	<b>2.65</b>	<b>Areg</b>	amphiregulin	0000920 // cell morphogenesis // inferred from direct assay//0000910 // cytokinesis // not recorded//0006810 // transport // inferred from electronic annotation//0007049 // cell	
NM_001177625	/NM_001177626//	0.00323483	0.00476644	1.08	1.66	2.64	<b>Ec2</b>	ect2 oncogene	0000723 // telomere maintenance // inferred from mutant phenotype//0006281 // DNA repair // inferred from mutant phenotype//0006402 // mRNA catabolic process // inferred	
NM_010479	0.00128837	0.00279063	3.62	2.32	2.58	<b>Hspa1a</b>	heat shock protein 1A	0007049 // cell cycle // inferred from electronic annotation//0045859 // regulation of protein kinase activity // inferred from electronic annotation//0051301 // cell division // infer		
NM_016904	1.86E-05	1.42E-05	1.23	2.12	2.53	<b>Cks1b</b>	CDC28 protein kinase 1b	0000281 // mitotic cytokinesis // not recorded//0002244 // hematopoietic progenitor cell differentiation // inferred from genetic interaction//0007049 // cell cycle // inferred from		
NM_028390	/NM_006510581//NM	0.001230148	7.72E-05	-1.10	<b>2.05</b>	<b>2.48</b>	<b>Anln</b>	anillin, actin binding protein	0007049 // cell cycle // inferred from electronic annotation//0007067 // mitotic nuclear division // inferred from electronic annotation//0007399 // nervous system development //	
NM_022323	2.50E-05	0.00114813	1.01	1.65	2.48	<b>Cdc20</b>	cell division cycle 20	0000709 // regulation of cyclin-dependent protein serine/threonine kinase activity // inferred from electronic annotation//0007049 // cell cycle // inferred from electronic annotation		
NM_009828	2.75E-04	1.04E-05	1.04	1.74	2.47	<b>Ccn2</b>	cyclin 2	0001701 // in utero embryonic development // inferred from mutant phenotype//0007049 // cell cycle // inferred from electronic annotation//0007067 // mitotic nuclear division //		
NM_007630	3.69E-06	4.54E-05	-1.12	<b>1.77</b>	<b>2.43</b>	<b>Ccnb2</b>	cyclin B2	0007049 // cell cycle // inferred from electronic annotation//0007127 // meiosis 1 // inferred from mutant phenotype//0016310 // phosphorylation // inferred from electronic anno		
NM_025415	0.00265037	3.27E-04	-1.02	<b>1.76</b>	<b>2.39</b>	<b>Cks2</b>	CDC28 protein kinase regulatory subunit 2	0002250 // adaptive immune response // inferred from electronic annotation//0002376 // immune system process // inferred from electronic annotation		
NM_001291892	/NM_001291893//	0.001058841	4.70E-06	1.34	1.84	2.39	<b>Lilrb4//Lilrb4a</b>	leukocyte immunoglobulin-like receptor, subfamily B, member 4b	0002376 // immune system process // inferred from electronic annotation//0006810 // transport // inferred from electronic annotation//0006811 // ion transport // inferred from	
NM_008491	4.21E-04	2.89E-06	4.51E-04	<b>1.51</b>	<b>2.31</b>	<b>Lcn2</b>	lipocalin 2	0002250 // adaptive immune response // inferred from electronic annotation//0002376 // immune system process // inferred from electronic annotation//0043123 // positive regu		
NM_001190320	/NM_001190321//	4.70E-04	8.31E-04	1.20	1.92	2.37	<b>Clec4n</b>	S100 calcium binding family 4, member n	0006915 // apoptotic process // inferred from electronic annotation//0032496 // response to lipopolysaccharide // inferred from electronic annotation//0034142 // toll-like recept	
NM_001163525	/NM_001012174	2.95E-04	1.95E-04	1.52	2.15	2.32	<b>S100a14</b>	C-type lectin domain family 4, member n	0002376 // immune system process // inferred from electronic annotation//0006221 // pyrimidine nucleotide biosynthetic process // inferred from electronic annotation//0006241	
NM_016748	/NM_00	7.70E-05	1.40E-05	2.08E-05	<b>1.81</b>	<b>2.31</b>	<b>Ctps</b>	cystidine 5'-triphosphatase	0001666 // response to hypoxia // inferred from electronic annotation//0001932 // regulation of protein phosphorylation // inferred from direct assay//0006469 // negative regulat	
NM_007707	/NM_01	2.11E-05	5.02E-06	7.01E-06	<b>1.91</b>	<b>2.45</b>	<b>Socs3</b>	suppressor of cytokine signaling 3	0000712 // resolution of meiotic recombination intermediates // not recorded//0008019 // sister chromatid segregation // not recorded//0002244 // hematopoietic progenitor cell	
NM_011623	/NM_006533153//NM	6.59E-04	4.81E-04	1.10	1.93	2.31	<b>Top2a</b>	topoisomerase (DNA) II alpha	0002185 // monocyte chemotaxis // --//0006935 // chemotaxis // traceable author statement//0006954 // inflammatory response // --//0006955 // immune response // inferre	
NM_011332	/NM_00	6.54E-05	1.55E-06	3.36E-05	<b>1.78</b>	<b>2.46</b>	<b>Ccl17</b>	chemokine (C-C motif) ligand 17	0000185 // activation of MAPKK activity // not recorded//0000186 // activation of MAPKK activity // inferred from direct assay//0006469 // negative regulation of protein kinase a	
NM_0011817	0.004028	0.00107945	0.00692808	<b>1.41</b>	<b>1.61</b>	<b>2.28</b>	<b>Gadd45g</b>	growth arrest and DNA-damage-inducible 45 gamma	0000281 // mitotic cytokinesis // not recorded//0009020 // cell separation after cytokinesis // not recorded//0007049 // cell cycle // inferred from electronic annotation//0007067	
NM_001164362	/NM_028293//NM	9.22E-04	1.54E-04	1.03	1.69	2.23	<b>Cep55</b>	centrosomal protein 55	0001525 // angiogenesis // inferred from electronic annotation//0006915 // apoptotic process // inferred from electronic annotation//0006931 // substrate-dependent cell migrat	
NM_001161746	/NM_866E-05	3.96E-04	1.50E-04	1.50	2.12	2.21	<b>Tnfrsf12a</b>	tumor necrosis factor receptor superfamily, member 12a	0001525 // ossification // inferred from electronic annotation//0001649 // osteoblast differentiation // not recorded//0006954 // inflammatory response // inferred from electronic	
NM_001204203	/NM_001204202//	5.33E-06	8.69E-04	1.05	2.26	2.19	<b>Spp1</b>	secreted phosphoprotein 1	0006810 // transport // inferred from electronic annotation//0006821 // chloride transport // not recorded//0006885 // regulation of pH // inferred from mutant phenotype//0000	
NM_011867	/NM_006515091//NM	4.86E-05	3.99E-05	1.52	1.78	2.17	<b>Slc26a8</b>	solute carrier family 26, member 4	0003209 // tumor necrosis factor-mediated signaling pathway // inferred from genetic interaction//0043000 // Golgi to plasma membrane CFTR protein transport // not recorded//h	
NM_010664	5.61E-04	2.40E-05	9.83E-07	1.26	1.73	2.15	<b>Krt18</b>	keratin 18	0001525 // angiogenesis // inferred from electronic annotation//0002062 // chondrocyte differentiation // inferred from electronic annotation//0007155 // cell adhesion // inferre	
NM_009369	0.00269734	3.06E-04	7.07E-06	1.25	1.75	2.14	<b>Tgfb1</b>	transforming growth factor, beta induced	0006260 // DNA replication // inferred from electronic annotation//0006270 // DNA replication initiation // inferred from electronic annotation//0007049 // cell cycle // inferred fr	
NM_001302540	/NM_00406378	5.53E-06	5.64E-04	1.21	1.83	2.13	<b>Mcm5</b>	minichromosome maintenance deficient 5, cell division cycle 46 S	0001938 // positive regulation of endothelial cell proliferation // not recorded//0002541 // activation of plasma trypsin involved in acute inflammatory response // not recorded//h	
NM_010171	0.00202076	6.24E-04	0.00170283	1.86	2.41	2.12	<b>F3</b>	coagulation factor III	0000724 // double-strand break repair via homologous recombination // inferred from direct assay//000724 // double-strand break repair via homologous recombination // inferre	
NM_011224	3.50E-04	5.53E-05	1.05	1.61	2.11	<b>Rad51</b>	RAD51 homolog	0005975 // carbohydrate metabolic process // inferred from electronic annotation//0006032 // chain catabolic process // not recorded//0006954 // inflammatory response // inferre		
NM_1451426	/NM_009892	0.006972907	0.0053045	-1.17	2.05	2.07	<b>Chil4//Chil3</b>	chitinase-like 4//chitinase-like 3	0006915 // apoptotic process // inferred from electronic annotation//0012189 // forebrain neuron differentiation // inferred from electronic annotation//0043065 // positive regulat	
NM_009344	/NR_871	4.17E-04	0.00103555	1.63	2.42	2.06	<b>Plhid1</b>	pleckstrin homology-like domain, family A, member 1	0001878 // transport to yeast // inferred from direct assay//0001879 // detection of yeast // inferred from direct assay//0002211 // pattern recognition receptor signaling pathway	
NM_001309637	/NM_020008//NR	0.007119291	0.00377891	1.16	2.05	2.06	<b>Clec7a</b>	C-type lectin domain family 7, member a	0009887 // organ morphogenesis // inferred from mutant phenotype//0018149 // peptide cross-linking // inferred from electronic annotation//0019538 // protein metabolic proces	
NM_001161714	/NM_00125905	3.45E-05	1.39E-04	1.47	2.12	2.05	<b>Tgm1</b>	transglutaminase 1, K, polypeptide	0001525 // angiogenesis // non-traceable author statement//0001832 // blastocyst growth // traceable author statement//0007173 // epidermal growth factor receptor signaling p	
NM_010415	6.54E-05	0.00113656	2.19E-06	1.34	1.51	2.03	<b>Hbegf</b>	heparin-binding EGF-like growth factor	0016488 // farnesyl catabolic process // not recorded//0044597 // daurorubicin metabolic process // not recorded//0044598 // doxorubicin metabolic process // not recorded//h	
NM_008012	4.52E-05	5.10E-05	1.34E-05	1.61	2.03	2.01	<b>Akr1b8</b>	aldo-keto reductase family 1, member B8	0002024 // spliceosome tri-snRNP complex assembly // not recorded//000398 // mRNA splicing, via spliceosome // not recorded//0006397 // mRNA processing // inferred from e	
NM_001110101	/NM_001204273//	3.19E-04	1.19E-06	2.00	1.59	1.69	<b>Lsm2</b>	LSM2 homolog, U6 small nuclear RNA associated (S. cerevisiae)	0008543 // fibroblast growth factor receptor signaling pathway // inferred from mutant phenotype//2000177 // regulation of neural precursor cell proliferation // inferred from mut	
NM_011369	6.27E-05	2.89E-06	1.03	1.63	1.99	<b>Schbp1</b>	SH2 domain binding protein 1	0000904 // cell morphogenesis involved in differentiation // traceable author statement//0007275 // multicellular organismal development // traceable author statement//0033205		
NM_031170	0.00207908	5.74E-04	1.35E-04	1.26	1.92	1.98	<b>Krt18</b>	keratin 8	0006882 // cellular zinc ion homeostasis // inferred from mutant phenotype//0007263 // nitric oxide mediated signal transduction // inferred from mutant phenotype//0010273 // r	
NM_008630	2.85E-06	6.98E-05	1.13E-04	3.25	2.84	1.97	<b>M2</b>	metallothionein 2	0010466 // negative regulation of peptidase activity // inferred from electronic annotation//0032496 // response to lipopolysaccharide // inferred from direct assay//0034612 // r	
NM_183249	0.003977341	7.17E-05	-1.00	1.74	1.96	<b>Wfdc21</b>	WAP four-disulfide core domain 21	0000281 // mitotic cytokinesis // not recorded//0009010 // cytokinesis // not recorded//0000920 // cell separation after cytokinesis // not recorded//0001578 // microtubule bun		
NM_001166406	/NM_184E-04	1.84E-04	1.59E-05	-1.04	1.25	1.95	<b>Kif20a</b>	kinesin family member 20A	0007339 // binding of sperm to zona pellucida // inferred from direct assay//0009408 // response to heat // inferred from direct assay//0043066 // negative regulation of apoptotic	
NM_010478	0.00991306	0.00991306	2.15	1.48	1.95	<b>Hspa1b</b>	heat shock protein 1B	0000070 // mitotic sister chromatid segregation // not recorded//0000086 // G2/M transition of mitotic cell cycle // not recorded//0001022 // negative regulation of transcription f		
NM_011121	4.59E-05	3.09E-05	1.05	1.55	1.95	<b>Plk1</b>	polo-like kinase 1	0003281 // ventricular septum development // inferred from mutant phenotype//0006766 // vitamin metabolic process // inferred from mutant phenotype//0006897 // endocytos		
NM_001081088	5.66E-04	1.81E-04	2.28E-04	1.36	1.72	1.92	<b>Lrp2</b>	low density lipoprotein receptor-related protein 2	0000079 // regulation of cyclin-dependent protein serine/threonine kinase activity // inferred from direct assay//0001836 // release of cytochrome c from mitochondria // not recor	
NM_018754	0.00146954	0.003028516	0.00477337	1.55	1.93	1.90	<b>Sfn</b>	stratifin	0000272 // mitotic cell cycle // inferred from electronic annotation//0001556 // oocyte maturation // not recorded//0001701 // in utero embryonic development // inferred from n	
NM_172301	/NM_011244665//XR	0.001493795	1.32E-04	1.01	1.38	1.89	<b>Ccnb1//Gm5593</b>	cyclin B1//predicted gene 5593	0000272 // polysaccharide catabolic process // inferred from electronic annotation//0005975 // carbohydrate metabolic process // inferred from electronic annotation//0006032 //	
NM_009892	/NM_145126	0.00298196	0.00377891	1.10	1.93	1.89	<b>Chil3//Chil4</b>	chitinase-like 3//chitinase-like 4	0042552 // myelination // not recorded//1902043 // positive regulation of extrinsic apoptotic signaling pathway via death domain receptors // inferred from direct assay	
NM_001171187	/NM_00543237	6.84E-05	4.24E-05	-1.19	1.57	1.88	<b>Moi</b>	myelin and lymphocyte protein, T, cell differentiation protein	0019058 // viral life cycle // inferred from electronic annotation	
NM_033075	/NR_871	2.03E-04	0.003982373	1.34	1.65	1.88	<b>D17H6565E-5</b>	DM segment, chr 17, human D6565 5	0006564 // L-serine biosynthetic process // inferred from electronic annotation//0008152 // metabolic process // inferred from electronic annotation//0008652 // cellular amino ac	
NM_001205339	/NM_177420	0.002927174	0.00185353	1.22	1.71	1.87	<b>Psat1</b>	phosphoserine aminotransferase 1	0007130 // cellular response to organic substance // inferred from direct assay	
NM_001291058	/NM_009853//NR	4.64E-06	0.00428983	1.04	1.99	1.87	<b>Cd68</b>	CD68 antigen	0000132 // establishment of mitotic spindle orientation // not recorded//0051382 // kinetochore assembly // not recorded//0071459 // protein localization to chromosome, centro	
NM_001302129	/NM_001302130//	0.005232663	0.0016117	-1.05	1.29	1.85	<b>Cenpa</b>	centromere protein A	0000122 // negative regulation of transcription from RNA polymerase II promoter // not recorded//0002903 // negative regulation of B cell apoptotic process // not recorded//0000	
NM_011496	/NM_006532725	3.10E-04	2.95E-05	1.02	1.41	1.85	<b>Aurkb</b>	aurora kinase B	0006260 // DNA replication // inferred from electronic annotation//0006468 // protein phosphorylation // --//0007049 // cell cycle // inferred from electronic annotation//00070	
NM_001190717	/NM_013726//NM	0.01240670	4.57E-04	1.04	1.30	1.85	<b>Dbf4</b>	B cell leukemia/lymphoma 3	0000060 // protein import into nucleus, translocation // not recorded//002268 // follicular dendritic cell differentiation // inferred from mutant phenotype//0002315 // marginal a	
NM_03360	/NM_00	3.02E-04	0.005906933	1.49	1.67	1.85	<b>Bcl3</b>	Bcl3	0000162 // negative regulation of transcription from RNA polymerase II promoter // inferred from direct assay//0000122 // negative regulation of transcription from RNA polymerase	
NM_00111078	/NM_001111079//	1.66E-05	0.00208285	1.17	1.78	1.84	<b>Uhrf1</b>	URIEN CDNA 4933413G1 gene//Rinkad box M1	0000260 // DNA replication // inferred from electronic annotation//0006268 // DNA unwinding involved in DNA replication // inferred from physical interaction//0006270 // DNA re	
NM_008021	/NM_027697	7.54E-05	1.74E-05	1.15	1.52	1.84	<b>4933413G1R1K//Foxm1</b>	RIKEN CDNA 4933413G1 gene//Rinkad box M1	0006260 // DNA replication // inferred from electronic annotation//0006268 // DNA unwinding involved in DNA replication //	

RefSeq	Transcript ID	p (24h n=460)	p (48h n=657)	p (72h n=805)	FC 24h	FC 48h	FC 72h	Gene Symbol	Gene Title	Gene Ontology Biological Process
NM_001313963	/NM_758E-04	0.001150255	2.22E-04	<b>1.15</b>	<b>1.98</b>	<b>1.75</b>	<b>Krt19</b>	keratin 19	0007219 // Notch signaling pathway // inferred from direct assay//0043627 // response to estrogen // inferred from electronic annotation//0045214 // sarcomere organization // n	
NM_013602	/XM_00	1.12E-05	2.53E-04	<b>2.15</b>	<b>2.08</b>	<b>1.75</b>	<b>M1</b>	metallothionein 1	0000032 // cell wall mannoprotein biosynthetic process // --//0006486 // protein glycosylation // inferred from electronic annotation//0006493 // protein D-linked glycosylation //	
NM_007802	/XM_000500974	0.001038144	1.41E-04	<b>1.08</b>	<b>1.60</b>	<b>1.74</b>	<b>Ctsk</b>	cathepsin K	0001957 // intramembranous ossification // inferred from electronic annotation//0006508 // proteolysis // inferred from electronic annotation//00030574 // collagen catabolic proc	
NM_001113179	/NM_009772	/XM_000492327	7.74E-04	<b>-1.03</b>	<b>1.49</b>	<b>1.74</b>	<b>Bub1</b>	ubiquitin inhibited by benzimidazole 1 homolog (S. cerevisiae)	0006468 // protein phosphorylation // inferred from electronic annotation//0006915 // apoptotic process // inferred from electronic annotation//0007049 // cell cycle // inferred fr	
NM_009890	8.96E-05	2.74E-05	3.54E-04	<b>1.68</b>	<b>2.17</b>	<b>1.74</b>	<b>Ch25h</b>	cholesterol 25-hydroxylase	0006629 // lipid metabolic process // inferred from electronic annotation//0006633 // fatty acid biosynthetic process // inferred from electronic annotation//0006694 // steroid bio	
NM_000889	0.00310169	0.004915863	0.0030352	<b>1.18</b>	<b>1.42</b>	<b>1.73</b>	<b>Ppp1r14b</b>	protein phosphatase 1, regulatory (inhibitor) subunit 14B	0042325 // regulation of phosphorylation // inferred from electronic annotation//0043086 // negative regulation of catalytic activity // not recorded//0050790 // regulation of cata	
NM_009364	/XM_000505043	/NM_006131017	5.76E-05	<b>1.30</b>	<b>1.50</b>	<b>1.72</b>	<b>Tfp2j</b>	tissue factor pathway inhibitor 2	0007596 // blood coagulation // inferred from electronic annotation//0007599 // hemostasis // inferred from electronic annotation//0010466 // negative regulation of peptidase ac	
NM_001033166	/NM_001037279		0.00404433	<b>1.02</b>	<b>1.41</b>	<b>1.72</b>	<b>2700094K13Rik</b>	RIKEN cDNA 2700094K13 gene	0045454 // cell redox homeostasis // inferred from electronic annotation	
NM_001291185	/NM_011497	7.60E-04	1.40E-04	<b>1.04</b>	<b>1.34</b>	<b>1.72</b>	<b>Aurka</b>	aurora kinase A	0000212 // meiotic spindle organization // inferred from mutant phenotype//0000226 // microtubule cytoskeleton organization // inferred from genetic interaction//0000278 // mi	
NM_001159299	/NM_713E-05		0.00267216	<b>1.39</b>	<b>1.66</b>	<b>1.72</b>	<b>Ith4</b>	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//0010951 // ni	
NM_020010	7.94E-05	2.01E-06	4.44E-04	<b>1.70</b>	<b>2.03</b>	<b>1.72</b>	<b>Cyp51</b>	cytochrome P450, family 51	0006629 // lipid metabolic process // inferred from electronic annotation//0006694 // steroid biosynthetic process // not recorded//0006695 // cholesterol biosynthetic process // t	
NM_145360	/XM_00	4.63E-04	4.04E-04	<b>1.59</b>	<b>1.84</b>	<b>1.71</b>	<b>Gm38481</b>	predicted gene, 38481//isopentenyl-diphosphate delta isomerase	0006629 // lipid metabolic process // inferred from electronic annotation//0006694 // steroid biosynthetic process // inferred from electronic annotation//0006695 // cholesterol b	
NM_013492	/XM_000518503	/XM_328E-04	1.59E-04	<b>1.05</b>	<b>1.38</b>	<b>1.71</b>	<b>Cfu</b>	clusterin	0009092 // cell morphogenesis // not recorded//0001774 // microglial cell activation // not recorded//0008219 // cell death // inferred from electronic annotation//0008284 // po	
NM_008605	/XM_011242357	/XM_01242358	0.00785685	<b>1.11</b>	<b>1.47</b>	<b>1.70</b>	<b>Mmp12</b>	matrix metalloproteinase 12	0005508 // proteolysis // inferred from electronic annotation//0014070 // response to organic cyclic compound // inferred from electronic annotation//0035313 // wound healing,	
NM_010766	3.78E-05	7.05E-05	1.23E-05	<b>1.30</b>	<b>2.25</b>	<b>1.70</b>	<b>Mmpc</b>	macrophage receptor with collagenous structure	0002376 // immune system process // inferred from electronic annotation//0006897 // endocytosis // inferred from mutant phenotype//0006898 // receptor-mediated endocytosi	
NM_022430	0.007245855	0.202E-05	1.02E-05	<b>1.50</b>	<b>1.70</b>	<b>Ms40a8</b>	membrane-spanning 4-domains, subfamily A, member 8A			
NM_011239	0.00127528	0.00199509	1.11E-04	<b>1.40</b>	<b>1.70</b>	<b>Ranbp1</b>	RAN binding protein 1	0007051 // spindle organization // inferred from direct assay//0010976 // positive regulation of neuron projection development // not recorded//0035690 // cellular response to dr		
NM_145480	3.58E-04	0.00111975	1.07E-05	<b>1.45</b>	<b>1.68</b>	<b>Rfc4</b>	replication factor C (activator) 1 4	0006260 // DNA replication // inferred from electronic annotation//0006261 // DNA-dependent DNA replication // not recorded//0006281 // DNA repair // not recorded		
NM_011495	/NM_173169	/NR_00	0.003996193	<b>3.33E-04</b>	<b>1.08</b>	<b>1.40</b>	<b>Pik4</b>	polo-like kinase 4	0006468 // protein phosphorylation // inferred from electronic annotation//0007099 // centriole replication // inferred from mutant phenotype//0007099 // centriole replication //	
NM_001313914	/NM_643E-05	5.63E-04	1.41E-04	<b>2.55</b>	<b>2.41</b>	<b>1.67</b>	<b>Thbs1</b>	thrombospondin 1	0001887 // activation of MAPK activity // not recorded//0001937 // negative regulation of endothelial cell proliferation // inferred from mutant phenotype//0001937 // negative reg	
NM_011905	/XM_000510460	2.95E-04	1.71E-05	<b>1.06</b>	<b>1.50</b>	<b>1.67</b>	<b>Tir2</b>	tol-like receptor 2	0001774 // microglial cell activation // not recorded//0002224 // toll-like receptor signaling pathway // not recorded//0002237 // response to molecule of bacterial origin // infl	
NM_011568	/NM_019484	/XR_38	0.001122384	<b>1.05</b>	<b>1.35</b>	<b>1.67</b>	<b>Allyref1</b>	Ally/REF export factor 2	0006397 // mRNA processing // inferred from electronic annotation//0006406 // mRNA export from nucleus // inferred from electronic annotation//0006810 // transport // inferre	
NM_019499	/XM_000506406	0.005283785	0.00202498	<b>1.02</b>	<b>1.48</b>	<b>1.67</b>	<b>Mad21</b>	MAD2 mitotic arrest deficient-like 1	0000079 // mitotic sister chromatid segregation // inferred from mutant phenotype//0007049 // cell cycle // inferred from electronic annotation//0007067 // mitotic nuclear divisio	
NM_026014	0.002053018	1.07E-04	1.40E-06	<b>1.40</b>	<b>1.66</b>	<b>Ct1</b>	chromatin licensing and DNA replication factor 1	0000076 // DNA replication checkpoint // inferred from direct assay//0000076 // DNA replication checkpoint // not recorded//0006260 // DNA replication // inferred from electri		
NM_026835	0.0010361	1.32E-05	1.53E-05	<b>1.65</b>	<b>1.65</b>	<b>Ms40d1</b>	membrane-spanning 4-domains, subfamily A, member 6D			
NM_010295	/XM_00	3.81E-04	1.02E-04	<b>1.54</b>	<b>1.24</b>	<b>1.65</b>	<b>Glc</b>	glutamate-cysteine ligase, catalytic subunit	0006534 // cysteine metabolic process // not recorded//0006536 // glutamate metabolic process // not recorded//0006749 // glutathione metabolic process // inferred from muta	
NM_133762	/XM_000516349	/XM_000516350	0.00205482	<b>1.02</b>	<b>1.50</b>	<b>1.64</b>	<b>Ncapg2</b>	NM2 mitocendin I complex, subunit G2	0001833 // inner cell mass cell proliferation // inferred from mutant phenotype//0007049 // cell cycle // inferred from electronic annotation//0007067 // mitotic nuclear division //	
NM_011227	/XM_01	3.56E-04	1.85E-04	<b>1.43</b>	<b>1.56</b>	<b>1.63</b>	<b>Rob20</b>	RAB20, member RAS oncogene family	0006810 // transport // inferred from electronic annotation//0006886 // intracellular protein transport // not recorded//0007264 // small GTPase mediated signal transduction // i	
NM_010172	2.03E-04	1.05E-04	1.06E-04	<b>1.06</b>	<b>1.46</b>	<b>1.63</b>	<b>F7</b>	coagulation factor VII	0002690 // positive regulation of leukocyte chemotaxis // not recorded//0006508 // proteolysis // inferred from electronic annotation//0007596 // blood coagulation // inferred fr	
NM_001033484	/XM_0005101643	1.77E-04	3.76E-05	<b>1.07</b>	<b>1.40</b>	<b>1.62</b>	<b>Iqgap3</b>	IQ motif containing GTPase activating protein 3	0000082 // G1/S transition of mitotic cell cycle // inferred from mutant phenotype//0001187 // activation of MAPK activity // inferred from mutant phenotype//0001934 // positive	
NM_020047	2.41E-04	5.60E-05	0.0038563	<b>1.31</b>	<b>1.62</b>	<b>1.62</b>	<b>Tacst2</b>	tumor-associated calcium signal transducer 2	0010633 // negative regulation of epithelial cell migration // inferred from direct assay//0050678 // regulation of epithelial cell proliferation // inferred from expression pattern//00:	
NM_001297747	/NM_000298634	7.39E-04	0.0061065	<b>1.22</b>	<b>1.50</b>	<b>1.61</b>	<b>Btg3</b>	B cell translocation gene 3//B cell translocation gene 3 pseudogen	0045930 // negative regulation of mitotic cell cycle // not recorded	
NM_001316995	/NM_016750	1.08E-04	1.93E-04	<b>1.09</b>	<b>1.59</b>	<b>1.61</b>	<b>Gm203</b>	predicted pseudogene 8203//H2a histone family, member Z	0006325 // chromatin organization // not recorded//0006342 // chromatin silencing // not recorded//0007275 // multicellular organismal development // inferred from electri	
NM_010790	/XM_000537640	3.86E-04	-1.05E-05	<b>1.23</b>	<b>1.61</b>	<b>1.61</b>	<b>Meik</b>	myristic leucine zipper kinase	0006468 // protein phosphorylation // inferred from electronic annotation//0006915 // apoptotic process // not recorded//0007049 // cell cycle // inferred from electronic annotati	
NM_023284	/XM_000496958	0.00325016	1.02E-05	<b>1.35</b>	<b>1.61</b>	<b>1.61</b>	<b>Nuf2</b>	NUP2, NDC80 kinetochore complex component, homolog (S. cere	0007049 // cell cycle // inferred from electronic annotation//0007067 // mitotic nuclear division // inferred from electronic annotation//0008608 // attachment of spindle microtub	
NM_026438	0.0013035	6.85E-04	0.0023697	<b>1.25</b>	<b>1.43</b>	<b>1.61</b>	<b>Ppa1</b>	pyrophosphatase (inorganic)	0006796 // phosphate-containing compound metabolic process // inferred by curator	
NM_001077529	/NM_008705	0.001581035	4.51E-04	<b>1.06</b>	<b>1.38</b>	<b>1.60</b>	<b>Nme2</b>	NME2/23 nucleoside diphosphate kinase 2	0002762 // negative regulation of myeloid leukocyte differentiation // not recorded//0006163 // purine nucleotide metabolic process // not recorded//0006165 // nucleoside diph	
NM_010798	0.009453878	1.00E-05	0.0029498	<b>1.08</b>	<b>1.40</b>	<b>1.59</b>	<b>Mf1</b>	macrophage migration inhibitory factor	0001516 // prostaglandin biosynthetic process // not recorded//0001934 // positive regulation of protein phosphorylation // inferred from direct assay//0002035 // brain renin-ang	
NM_026410	4.05E-04	6.53E-05	1.03E-05	<b>1.43</b>	<b>1.59</b>	<b>1.59</b>	<b>Ccals5</b>	cell division cycle associated 5	0000082 // G1/S transition of mitotic cell cycle // not recorded//0006302 // double-strand break repair // not recorded//0007049 // cell cycle // inferred from electronic annotati	
NM_001145953	/NM_200E-04	9.01E-05	7.30E-05	<b>1.30</b>	<b>1.73</b>	<b>1.59</b>	<b>Lgals3</b>	lectin, galactose binding, soluble 3	0001501 // skeletal system development // inferred from genetic interaction//0002376 // immune system process // inferred from electronic annotation//0002548 // monocyte ch	
NM_025443	0.006398648	0.00593472	1.30E-05	<b>1.42</b>	<b>1.59</b>	<b>1.59</b>	<b>Pno1</b>	partner of NOB1 homolog (S. cerevisiae)		
NM_001199123	/NM_001199124	7.23E-05	4.72E-05	<b>1.12</b>	<b>1.42</b>	<b>1.59</b>	<b>Spc25</b>	SPC25, NDC80 kinetochore complex component, homolog (S. cere	0007049 // cell cycle // inferred from electronic annotation//0007052 // mitotic spindle organization // not recorded//0007059 // chromosome segregation // not recorded//0007	
NM_008102	0.00106521	0.00156661	1.39E-05	<b>1.39</b>	<b>1.45</b>	<b>1.58</b>	<b>Gch1</b>	GTP cyclohydrolase 1	0006461 // protein complex assembly // not recorded//0006729 // tetrahydrobiopterin biosynthetic process // not recorded//0006729 // tetrahydrobiopterin biosynthetic proc	
NM_016723	/NM_033607	/XM_00	0.007923941	<b>1.21</b>	<b>1.41</b>	<b>1.58</b>	<b>Uchl3</b>	ubiquitin carboxyl-terminal esterase L3 (ubiquitin thioesterase)//	0006508 // proteolysis // inferred from electronic annotation//0006915 // ubiquitin-dependent protein catabolic process // inferred from electronic annotation//0007628 // adult v	
NM_011072	0.007228755	0.007228755	1.02E-05	<b>1.30</b>	<b>1.58</b>	<b>1.58</b>	<b>Pfn1</b>	profilin 1	0001843 // neural tube closure // inferred from genetic interaction//0006357 // regulation of transcription from RNA polymerase II promoter // inferred from genetic interaction//0	
NM_011311	/XM_0005101177	/XM_0005101178	0.00139097	<b>1.17</b>	<b>1.31</b>	<b>1.58</b>	<b>S100a4</b>	S100 calcium binding protein A4	0004123 // positive regulation of I-kappaB kinase/NF-kappaB signaling // not recorded	
NM_001308227	/NM_383E-04	3.58E-04	0.0058075	<b>1.78</b>	<b>1.64</b>	<b>1.58</b>	<b>Dnajb1</b>	DnaJ (Hsp40) homolog, subfamily B, member 1	0006457 // protein folding // inferred from electronic annotation//00032781 // positive regulation of ATPase activity // not recorded//0051085 // chaperone mediated protein foldi	
NM_146171	/XM_000506531	/XM_220E-04	0.00136684	<b>-1.04</b>	<b>1.47</b>	<b>1.57</b>	<b>Ncapg2</b>	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 condensat	
NM_009841	4.27E-06	1.80E-05	9.48E-04	<b>1.61</b>	<b>1.86</b>	<b>1.57</b>	<b>Cd14</b>	CD14 antigen	0002237 // response to molecule of bacterial origin // inferred from direct assay//0002376 // immune system process // inferred from electronic annotation//0006898 // receptor-i	
NM_028128	0.00132008	6.28E-05	1.10E-05	<b>1.27</b>	<b>1.57</b>	<b>Rfc5</b>	replication factor C (activator) 1 5	0006260 // DNA replication // inferred from electronic annotation//0006261 // DNA-dependent DNA replication // not recorded//0006281 // DNA repair // not recorded		
NM_011045	0.00137512	2.49E-04	1.22E-05	<b>1.22</b>	<b>1.57</b>	<b>1.57</b>	<b>Pcna</b>	proliferating cell nuclear antigen	0001022 // negative regulation of transcription from RNA polymerase II promoter // inferred from direct assay//0006260 // DNA replication // inferred from electronic annotation//	
NM_133897	/XM_00	0.00176612	9.05E-05	<b>1.25E-04</b>	<b>1.31</b>	<b>1.74</b>	<b>Lrr8c</b>	leucine rich repeat containing 8 family, member C	0006810 // transport // inferred from electronic annotation//0006811 // ion transport // inferred from electronic annotation//0045444 // fat cell differentiation // inferred from dir	
NM_026816	0.003901336	0.00330454	1.27E-05	<b>1.41</b>	<b>1.56</b>	<b>1.56</b>	<b>Glf2f2</b>	general transcription factor IIF, polypeptide 2	0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 // regulation of transcription, DNA-templated // inferred from electronic annotation//00	
NM_197982	/XM_00	0.00690338	4.72E-05	<b>1.21</b>	<b>1.54</b>	<b>1.56</b>	<b>Ddx39</b>	DEAD (Asp-Glu-Ala-Asp) box polypeptide 39	0000398 // mRNA splicing, via spliceosome // not recorded//0006397 // mRNA processing // inferred from electronic annotation//0006406 // mRNA export from nucleus // not rec	
NM_011955	/XR_384565	6.56E-04	0.0011203	<b>1.14</b>	<b>1.38</b>	<b>1.56</b>	<b>Nubp1</b>	nucleolin binding protein 1	0006879 // cellular iron homeostasis // not recorded//0010826 // negative regulation of centrosome duplication // inferred from mutant phenotype//0016049 // cell growth //	
NM_009252	/XM_01	1.85E-04	1.10E-04	<b>1.41</b>	<b>2.01</b>	<b>1.55</b>	<b>Serpina3n</b>	serpine (or cysteine) peptidase inhibitor, clade A, member 3N	0006953 // acute-phase response // inferred from electronic annotation//0010466 // negative regulation of peptidase activity // inferred from electronic annotation//0010951 // ne	
NM_009139	0.00320978	7.29E-05	1.07E-05	<b>-1.05</b>	<b>1.48</b>	<b>1.55</b>	<b>Ccl6</b>	chemokine (C-C motif) ligand 6	0002548 // monocyte chemotaxis // --//0006935 // chemotaxis // inferred from electronic annotation//0006955 // immune response // inferred from electronic annotation//000:	
NM_001081029	7.29E-05	7.29E-05	1.23E-05	<b>1.71</b>	<b>1.54</b>	<b>1.54</b>	<b>Tmem243</b>	transmembrane protein 243, mitochondrial		
NM_026631	7.86E-04	0.00137641	4.31E-04	<b>1.25</b>	<b>1.70</b>	<b>1.54</b>	<b>Nhp2</b>	NHP2 ribonucleoprotein	0006364 // rRNA processing // inferred from electronic annotation//0031118 // rRNA pseudouridine synthesis // inferred from sequence or structural similarity//0042254 // ribosom	
NM_001159646	/NM_023595	0.004399282	1.09E-05	<b>1.25</b>	<b>1.54</b>	<b>1.54</b>	<b>Dut</b>	deoxyuridine triphosphatase	0006226 // dUMP biosynthetic process // not recorded//0043497 // regulation of protein heterodimerization activity // not recorded//0046080 // dUTP metabolic process // infer	
NM_007534	/NM_007536	/NM_00	0.00135674	<b>1.14</b>	<b>1.69</b>	<b>1.54</b>	<b>Bcl2a1a</b>	B cell leukemia/lymphoma 2 related protein A1a//B cell leukemia, peroxiredoxin 4	0001782 // B cell homeostasis // inferred from direct assay//0002903 // negative regulation of B cell apoptotic process // inferred from direct assay//0006915 // apoptotic proc	
NM_001313711	/NM_016764	/XM_000168253	3.74E-04	<b>1.00</b>	<b>1.30</b>	<b>1.54</b>	<b>Prdx4</b>	peroxiredoxin 4	0007283 // spermatogenesis // inferred from mutant phenotype//0008584 // male gonad development // inferred from mutant phenotype//0019471 // 4-hydroxyproline metaboli	
NM_001267695	/NM_021281	/XM_000500975	0.00346088	<b>-1.08</b>	<b>1.17</b>	<b>1.54</b>	<b>Css</b>	cathepsin S	0002250 // adaptive immune response // inferred from electronic annotation//0005008 // proteolysis // inferred from direct assay//0006508 // proteolysis // not recorded//0006	
NM_01109748	/NM_016871	0.00271894	0.00271894	<b>1.17</b>	<b>1.54</b>	<b>1.54</b>	<b>Tomm40</b>	translocase of outer mitochondrial membrane 40 homolog (yeast)	0006626 // protein targeting to mitochondrion // not recorded//0006810 // transport // inferred from electronic annotation//0005811 // ion transport // inferred from electri	
NM_007988	0.005565248	6.46E-04	1.08E-05	<b>1.65</b>	<b>1.53</b>	<b>1.53</b>	<b>Fasn</b>	fatty acid synthase	0001649 // osteoblast differentiation // not recorded//0006084 // acetyl-CoA metabolic process // not recorded//0006629 // lipid metabolic process // inferred from electri	
NM_001316995	/NM_016750	1.08E-04	1.05E-05	<b>1.55</b>	<b>1.53</b>	<b>1.53</b>	<b>Gm</b>			

RefSeq	Transcript ID	p (24h n=460)	p (48h n=657)	p (72h n=805)	FC 24h	FC 48h	FC 72h	Gene Symbol	Gene Title	Gene Ontology Biological Process
NM_001172117	XM_000215644	0.001511017	2.38E-04	<b>1.27</b>	<b>1.34</b>	<b>1.48</b>	<b>Hck</b>	hemopoietic cell kinase	0002376 // immune system process // inferred from electronic annotation//0006468 // protein phosphorylation // inferred from electronic annotation//0006887 // exocytosis // in	
NM_009226		0.00823008	1.27	1.18	<b>1.47</b>	<b>1.47</b>	<b>Snrp1</b>	small nuclear ribonucleoprotein D1	0000245 // spliceosomal complex assembly // not recorded//0000387 // spliceosomal snRNP assembly // not recorded//0002230 // positive regulation of defense response to virus	
NM_007573	0.0013884	0.009837708	<b>1.31</b>	<b>1.28</b>	<b>1.47</b>	<b>C1qbp</b>	component component 1, q subcomponent binding protein	0000122 // negative regulation of transcription from RNA polymerase II promoter // not recorded//0002250 // adaptive immune response // inferred from electronic annotation//0		
NM_001161737	XM_013929		0.00979084	<b>1.12</b>	<b>1.58</b>	<b>1.47</b>	<b>Siva1</b>	SIVA1, apoptosis-inducing factor	0006915 // apoptotic process // inferred from electronic annotation//0006924 // activation-induced cell death of T cells // not recorded//0032088 // negative regulation of NF-kapp	
NM_001290660	NM_024242		9.34E-04	<b>1.09</b>	<b>1.42</b>	<b>1.47</b>	<b>Cd302</b>	CD302 antigen	0006909 // phagocytosis // not recorded	
NM_008050	XM_006523728	XM_007315373		<b>1.06</b>	<b>1.27</b>	<b>1.46</b>	<b>LOC105242669</b> // <b>LOC105243270</b>	40S ribosomal protein S2 pseudogene//40S ribosomal protein S2-yrdc domain containing (E.coli)	0002660 // ribosomal small subunit assembly // not recorded//0001731 // formation of translation preinitiation complex // not recorded//0006412 // translation // inferred from ele	
NM_153566	7.57E-04	0.003407072	<b>1.26</b>	<b>1.24</b>	<b>1.46</b>	<b>Yrdc</b>	yrdc domain containing (E.coli)	0051051 // negative regulation of transport // not recorded		
NM_001025779	XM_01164734	XM_001022888		<b>1.07</b>	<b>1.43</b>	<b>1.46</b>	<b>Cdc6</b>	cell division cycle 6	0006260 // DNA replication // inferred from electronic annotation//0006270 // DNA replication initiation // inferred from electronic annotation//0007049 // cell cycle // inferred fr	
NM_024245	XM_006511452	XM_005921938		<b>1.06</b>	<b>1.27</b>	<b>1.46</b>	<b>Kif23</b>	kinasin family member 23	0000281 // mitotic cytokinesis // not recorded//0000910 // cytokinesis // not recorded//0007018 // microtubule-based movement // not recorded//0007049 // cell cycle // infer	
NM_031198	XM_006505035	XM_000699567		<b>1.20</b>	<b>1.48</b>	<b>1.46</b>	<b>Tjfc</b>	transcription factor EC	0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 // regulation of transcription, DNA-templated // not recorded//0006366 // transcription I	
NM_019432	XR_878316	0.001244167	5.82E-04	<b>1.09</b>	<b>1.71</b>	<b>1.46</b>	<b>Tmem37</b>	transmembrane protein 37	0006810 // transport // inferred from electronic annotation//0006811 // ion transport // inferred from electronic annotation//0006816 // calcium ion transport // inferred from ele	
NM_033073	0.00112779	0.00109445	<b>1.00</b>	<b>1.39</b>	<b>1.45</b>	<b>Krt7</b>	keratin 7	0005468 // protein phosphorylation // inferred from electronic annotation//0007093 // mitotic cell cycle checkpoint // inferred from electronic annotation//0016310 // phosphoryl		
NM_001110265	XM_001284272	XM_0094545		<b>1.21</b>	<b>1.28</b>	<b>1.45</b>	<b>Ttk</b>	TK protein kinase	0002317 // plasma cell phosphorylation // inferred from direct assay//0006915 // apoptotic process // inferred from electronic annotation//0007157 // heterophilic cell-cell adhesio	
NM_008495	0.007370463	0.00202557	<b>1.12</b>	<b>1.53</b>	<b>1.45</b>	<b>Lgals1</b>	lectin, galactose binding, soluble 1	0000054 // ribosomal subunit export from nucleus // not recorded//0000055 // ribosomal large subunit export from nucleus // not recorded//0000056 // ribosomal small subunit ex		
NM_009391	XM_006504280	XM_000249048		<b>1.14</b>	<b>1.31</b>	<b>1.45</b>	<b>LOC102641332</b> // <b>Ran</b>	GTP-binding nuclear protein Ran//RAN, member RAS oncogene fa	0006260 // DNA replication // inferred from electronic annotation//0006268 // DNA unwinding involved in DNA replication // inferred from direct assay//0006270 // DNA replicatio	
NM_008564	0.006E-04	0.00233453	<b>1.10</b>	<b>1.32</b>	<b>1.45</b>	<b>Mcm2</b>	minichromosome maintenance deficient 2 mitotin (S. cerevisiae)	0006260 // DNA replication // inferred from electronic annotation//0006268 // DNA unwinding involved in DNA replication // inferred from direct assay//0006270 // DNA replicatio		
NM_001164733	XM_001164734	2.81E-04	<b>1.13</b>	<b>1.43</b>	<b>1.45</b>	<b>Mgp6</b>	membrane protein, palmitoylated 6	0046037 // GMP metabolic process // inferred from sequence of structural similarity//0046710 // GDP metabolic process // inferred from sequence of structural similarity//004692		
NM_023587	XM_006522570	XM_001676333		<b>1.02</b>	<b>1.35</b>	<b>1.45</b>	<b>Hacd2</b>	3-hydroxyacyl-CoA dehydratase 2	0006629 // lipid metabolic process // inferred from electronic annotation//0006631 // fatty acid metabolic process // inferred from electronic annotation//0006633 // fatty acid bi	
NM_026545	0.001469113	0.00146929	<b>1.04</b>	<b>1.34</b>	<b>1.45</b>	<b>PsmA8</b>	proteasome (prosome, macropain) 26S subunit, non-ATPase, 8	0006508 // proteolysis // inferred from electronic annotation//0031647 // regulation of protein stability // not recorded//0043161 // proteasome-mediated ubiquitin-dependent pr		
NM_007413	0.000711548	0.00241723	<b>1.16</b>	<b>1.33</b>	<b>1.45</b>	<b>Adora2b</b>	adenosine A2b receptor	0001973 // adenosine receptor signaling pathway // inferred from electronic annotation//0002882 // positive regulation of chronic inflammatory response to non-antigenic stimulus		
NM_134156	XM_006515384	XM_000780949		<b>1.05</b>	<b>1.34</b>	<b>1.45</b>	<b>Actn1</b>	actinin, alpha 1	0007015 // actin filament organization // not recorded//0030220 // platelet formation // not recorded//0030865 // cortical cytoskeleton organization // traceable autor stemmen	
NM_010516	0.002322059	0.00254977	<b>-1.01</b>	<b>1.48</b>	<b>1.44</b>	<b>Cyr61</b>	cysteine rich protein 61	0001558 // regulation of cell growth // inferred from electronic annotation//0001649 // osteoblast differentiation // inferred from genetic interaction//0001934 // positive regulatio		
NM_008568	XM_006504555	XM_125E-04	0.00292747	<b>1.01</b>	<b>1.46</b>	<b>1.44</b>	<b>Mcm7</b>	minichromosome maintenance deficient 7 (S. cerevisiae)	0006260 // DNA replication // inferred from electronic annotation//0006268 // DNA unwinding involved in DNA replication // inferred from physical interaction//0006270 // DNA replic	
NM_011950	0.002006226	1.25E-04	<b>1.16</b>	<b>1.27</b>	<b>1.43</b>	<b>Mpk13</b>	mitogen-activated protein kinase 13	0001616 // MAPK cascade // not recorded//0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 // regulation of transcription, DNA-templated		
NM_016957	0.007600313	1.25E-04	<b>1.06</b>	<b>1.63</b>	<b>1.43</b>	<b>Hmgm2</b>	high mobility group nucleosomal binding domain 2	0000122 // negative regulation of transcription from RNA polymerase II promoter // inferred from mutant phenotype//0006357 // regulation of transcription from RNA polymerase I		
NM_001163476	XM_027014	XM_00143673	7.49E-04	<b>1.08</b>	<b>1.27</b>	<b>1.43</b>	<b>Gins1</b>	GINS complex subunit 1 (Psf1 homolog)	0001833 // inner cell mass cell proliferation // inferred from mutant phenotype//0006260 // DNA replication // inferred from mutant phenotype//1902983 // DNA strand elongati	
NM_027430	0.004797708	0.008045459	<b>1.08</b>	<b>1.40</b>	<b>1.43</b>	<b>Mpc2</b>	mitochondrial pyruvate carrier 2	0006909 // pyruvate metabolic process // inferred from genetic interaction//0006810 // transport // inferred from electronic annotation//0006850 // mitochondrial pyruvate elongat		
NM_001252563	XM_013592	XM_000845459		<b>-1.07</b>	<b>-1.32</b>	<b>1.43</b>	<b>Matn4</b>	matrilin 4	0048678 // response to axon injury // inferred from direct assay	
NM_008563	9.13E-04	0.00684152	<b>1.11</b>	<b>1.30</b>	<b>1.43</b>	<b>Mcm3</b>	minichromosome maintenance deficient 3 (S. cerevisiae)	0006260 // DNA replication // inferred from electronic annotation//0006270 // DNA replication initiation // inferred from electronic annotation//0007049 // cell cycle // inferred fr		
NM_133807	0.004138883	1.01E-04	<b>1.12</b>	<b>1.24</b>	<b>1.43</b>	<b>Lrrc59</b>	leucine rich repeat containing 59	0000278 // mitotic cell cycle // not recorded//0002724 // regulation of T cell cytokine production // inferred from mutant phenotype//0002730 // regulation of dendritic cell cytokin		
NM_001081363	XM_006497119	0.00111868	<b>-1.04</b>	<b>1.20</b>	<b>1.43</b>	<b>Cenpf</b>	centromere protein F	0000278 // mitotic cell cycle // not recorded//0002724 // regulation of T cell cytokine production // inferred from mutant phenotype//0002730 // regulation of dendritic cell cytokin		
NM_001163489	XM_001163490	9.64E-04	<b>1.15</b>	<b>1.29</b>	<b>1.42</b>	<b>Sema4a</b>	sema domain, immunoglobulin domain (lg), transmembrane doma	0001525 // angiogenesis // inferred from electronic annotation//0001755 // neural crest cell migration // not recorded//0002250 // adaptive immune response // inferred from elec		
NM_001287738	NM_416E-04		<b>1.35</b>	<b>1.29</b>	<b>1.42</b>	<b>Cebpb</b>	CCAAT/enhancer binding protein (CEBP), beta	0001541 // ovarian follicle development // inferred from mutant phenotype//0001892 // embryonic placenta development // inferred from genetic interaction//0002432 // granulo		
NM_001102404	XM_001102405	5.36E-04	1.89E-04	<b>1.03</b>	<b>1.49</b>	<b>1.42</b>	<b>Acp5</b>	acid phosphatase 5, tartrate resistant	0006470 // protein dephosphorylation // inferred from electronic annotation//0001631 // dephosphorylation // inferred from direct assay//0032496 // response to lipopolysacchar	
NM_001141975	XM_001141976	0.005837853	0.00813172	<b>1.06</b>	<b>1.23</b>	<b>1.42</b>	<b>Tpx2</b>	TPX2, microtubule-associated protein homolog (Xenopus laevis)	0006915 // apoptotic process // inferred from electronic annotation//0007049 // cell cycle // inferred from electronic annotation//0007067 // mitotic nuclear division // inferred fr	
NM_008892	XM_006527905	XR_878095	XR_1.04	<b>1.15</b>	<b>1.42</b>	<b>1.42</b>	<b>Polo1</b>	polymerase (DNA directed), alpha 1	0000731 // DNA synthesis involved in DNA repair // inferred from sequence of structural similarity//0006260 // DNA replication // inferred from direct assay//0006260 // DNA replic	
NM_007421	0.002353767	0.002353767	<b>1.12</b>	<b>1.69</b>	<b>1.42</b>	<b>Acss1</b>	adenylosuccinate synthetase like 1	0006163 // purine nucleotide metabolic process // inferred from direct assay//0006164 // purine nucleotide biosynthetic process // inferred from electronic annotation//0006167 //		
NM_001127382	XM_001291226	XM_139065		<b>1.04</b>	<b>1.05</b>	<b>1.42</b>	<b>Rbm17</b>	RNA binding motif protein 47	0001284 // hematopoietic progenitor cell differentiation // inferred from mutant phenotype//0001554 // cytidine to uridine editing // inferred from genetic interaction	
NM_024045	0.0062981	0.0062981	<b>1.09</b>	<b>1.32</b>	<b>1.41</b>	<b>Rab32</b>	RAB32, member RAS oncogene family	0006886 // intracellular protein transport // not recorded//0007264 // small GTPase mediated signal transduction // inferred from electronic annotation//0008152 // metabolic pro		
NM_001304758	XM_000561732	XM_000122649		<b>1.21</b>	<b>1.34</b>	<b>1.41</b>	<b>Coq7</b>	dihydroxy-7-O	0000122 // negative regulation of transcription from RNA polymerase II promoter // not recorded//0001306 // age-dependent response to oxidative stress // inferred from mutant p	
NM_023258	0.006158922	8.27E-04	<b>1.09</b>	<b>1.27</b>	<b>1.41</b>	<b>Pycard</b>	PYD and CARD domain containing	0001773 // myeloid dendritic cell activation // not recorded//0002218 // activation of innate immune response // inferred from mutant phenotype//0002218 // activation of innate		
NM_001110233	XM_001110234	XM_000945777		<b>1.43E-04</b>	<b>1.19</b>	<b>1.29</b>	<b>Nfrap1</b>	nerve growth factor receptor (TRFRS16) associated protein 1	0006915 // apoptotic process // inferred from electronic annotation//000825 // extrinsic apoptotic signaling pathway via death domain receptors // inferred from physical interacti	
NM_0010120	XM_00	2.40E-04	0.00103513	<b>1.32</b>	<b>1.30</b>	<b>1.41</b>	<b>Ejfla</b>	eukaryotic translation initiation factor 1A	0006412 // translation // inferred from electronic annotation//0006413 // translational initiation // inferred from electronic annotation	
NM_008704	0.00352848	0.001617629	<b>1.23</b>	<b>1.26</b>	<b>1.41</b>	<b>Nme1</b>	NME/NM23 nucleoside diphosphate kinase 1	0002762 // negative regulation of myeloid leukocyte differentiation // not recorded//0006163 // purine nucleotide metabolic process // not recorded//0006165 // nucleoside diph		
NM_011712	0.0039809	1.18	<b>1.15</b>	<b>1.41</b>	<b>1.41</b>	<b>Wbp5</b>	WW domain binding protein 5	0006357 // regulation of transcription from RNA polymerase II promoter // not recorded		
NM_134081	0.00228481	-1.02	<b>1.11</b>	<b>1.40</b>	<b>1.40</b>	<b>Dnaj9</b>	Dnaj (Hsp40) homolog, subfamily C, member 9	0002371 // positive regulation of ATPase activity // not recorded//0003176 // social behavior // inferred from electronic annotation		
NM_001159631	XM_0012606	XM_0003730991		<b>5.51E-04</b>	<b>1.14</b>	<b>1.27</b>	<b>Nk6</b>	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 annotat	
NM_030685	0.00627522	1.02	<b>1.19</b>	<b>1.40</b>	<b>1.40</b>	<b>Serp1</b>	serpin-associated endoplasmic reticulum protein 1	0001501 // skeletal system development // inferred from mutant phenotype//0006006 // glucose metabolic process // inferred from mutant phenotype//0006486 // protein glycos		
NM_026114	0.00613033	1.22	<b>1.35</b>	<b>1.40</b>	<b>1.40</b>	<b>Ejfs2</b>	eukaryotic translation initiation factor 2, subunit 1 alpha	0002230 // positive regulation of defense response to virus by host // not recorded//0006412 // translation // inferred from direct assay//0006413 // translational initiation // not r		
NM_008039	0.00678349	-1.00	<b>1.41</b>	<b>1.40</b>	<b>1.40</b>	<b>Fpr2</b>	formyl peptide receptor 2	0006935 // chemotaxis // inferred from electronic annotation//0007165 // signal transduction // inferred from electronic annotation//0007186 // G-protein coupled receptor signa		
NM_023203	0.004964043	3.70E-04	<b>1.11</b>	<b>1.30</b>	<b>1.40</b>	<b>Dtpp1</b>	dCTP pyrophosphatase 1	0009143 // nucleoside triphosphate catabolic process // inferred from direct assay//0051289 // protein homotetramerization // inferred from direct assay		
NM_028870	XM_006517418	0.008881584	<b>1.12</b>	<b>1.31</b>	<b>1.40</b>	<b>Ctbb</b>	clathrin, light polypeptide (Lcb)	0006886 // intracellular protein transport // inferred from electronic annotation//0016192 // vesicle-mediated transport // inferred from electronic annotation//0072583 // clathrin		
NM_013552	XM_006532276	XM_006532278		<b>7.92E-04</b>	<b>-1.02</b>	<b>1.17</b>	<b>1.40</b>	<b>Hmnr</b>	hyaluronan mediated motility receptor (RHAMM)	0000122 // negative regulation of transcription from RNA polymerase II promoter // not recorded//0001501 // skeletal system development // inferred from genetic interaction//OC
NM_001301373	XM_001301375	5.74E-04	<b>1.07</b>	<b>1.34</b>	<b>1.40</b>	<b>Fst</b>	foliostatin	0000122 // negative regulation of transcription from RNA polymerase II promoter // not recorded//0006351 // transcription, DNA-templated // inferred from electronic annotation//00		
NM_008231	XM_00	0.00589401	0.001956797	<b>1.17</b>	<b>1.24</b>	<b>1.40</b>	<b>Hdaj</b>	hepatoma-derived growth factor	0000904 // cell morphogenesis involved in differentiation // inferred from mutant phenotype//0001701 // in utero embryonic development // inferred from mutant phenotype//00	
NM_001113416	XM_145506	XM_006529397		<b>0.00646311</b>	<b>1.15</b>	<b>1.15</b>	<b>1.40</b>	<b>Epb4115</b>	erythrocyte membrane protein band 4.1 like 5	0006629 // lipid metabolic process // inferred from electronic annotation//0007283 // spermatogenesis // inferred from genetic interaction//0007283 // spermatogenesis // inferre
NM_008776	6.52E-04	1.06	<b>1.30</b>	<b>1.40</b>	<b>1.40</b>	<b>Pafah1b3</b>	platelet-activating factor acetylhydrolase, isoform 1b, subunit 3	0006260 // DNA replication // inferred from mutant phenotype//0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 // regulation of transcrip		
NM_031863	3.12E-04	-1.05	<b>1.19</b>	<b>1.40</b>	<b>1.40</b>	<b>Cenpq</b>	centromere protein Q	0006629 // lipid metabolic process // inferred from electronic annotation//0006633 // fatty acid biosynthetic process // inferred from electronic annotation//0006694 // steroid bio		
NM_009584	XM_00	0.00795411	<b>1.22</b>	<b>1.19</b>	<b>1.39</b>	<b>Dnaj2</b>	Dnaj (Hsp40) homolog, subfamily C, member 2	0007155 // cell adhesion // inferred from mutant phenotype//0007155 // cell adhesion // not recorded//0007229 // integrin-mediated signaling pathway // not recorded//000836		
NM_025436	5.88E-05	0.0017175	<b>1.40</b>	<b>1.55</b>	<b>1.39</b>	<b>Msmo1</b>	methylsterol monooxygenase 1	0001666 // response to hypoxia // inferred from electronic annotation//0005975 // carbohydrate metabolic process // inferred from electronic annotation//0006089 // lactate met		
NM_008398	XM_006513267	XM_9.65E-04	<b>0.00743213</b>	<b>1.21</b>	<b>1.47</b>	<b>1.39</b>	<b>Igsa7</b>	integrin alpha 7	0001930 // cell adhesion // inferred from mutant phenotype//0007155 // cell adhesion // not recorded//0007229 // integrin-mediated signaling pathway // not recorded//000836	
NM_001136069	XM_8.22E-04	2.17E-04	<b>1.32</b>	<b>1.42</b>	<b>1.39</b>	<b>Ldha</b>	lactate dehydrogenase A	0001666 // response to hypoxia // inferred from electronic annotation//0005975 // carbohydrate metabolic process // inferred from electronic annotation//0006089 // lactate met		
NM_008252	XM_006509524	0.00182127	<b>1.18</b>	<b>1.35</b>	<b>1.39</b>	<b>Hmgb2</b>	high mobility group box 2	0001938 // positive regulation of endothelial cell proliferation // not recorded//0002437 // inflammatory response to antigenic stimulus // inferred from mutant phenotype//00062		
NM_00130364	XM_006526707	XM_8.15E-04	<b>0.00130364</b>	<b>1.00</b>	<b>1.29</b>	<b>1.39</b>	<b>Incpap</b>	inner centromere protein	0000910 // cytokinesis // not recorded//0007049 // cell cycle // inferred from electronic annotation//0007059 // chromosome segregation // not recorded//0007067 // mitotic nu	
NM_001146057	XM_001146058	XM_133348		<b>9.16E-04</b>	<b>1.16</b>	<b>1.38</b>	<b>Acad7</b>	acyl-CoA thioesterase 7	0009062 // fatty acid catabolic process // inferred from direct assay//0015937 // coenzyme A biosynthetic process // not recorded//0035114 // medium-chain fatty-acyl-CoA catab	
NM_018865	XM_006520889	0.001789398	0.00131109	<b>1.07</b>	<b>1.25</b>	<b>1.38</b>	<b>Wisp1</b>	WT11 inducible signaling pathway protein 1	0001558 // regulation of cell growth // inferred from electronic annotation//0007155 // cell adhesion // not recorded//0007165 // signal transduction // not recorded//0007267 //	
NM_025647	0.00938079	1.07	<b>1.25</b>	<b>1.38</b>	<b>1.38</b>	<b>Cmpk1</b>	cytidine monophosphate (UMP-CMP) kinase 1	0006139 // nucleoside-containing compound metabolic process // inferred from electronic annotation//0006165 // nucleoside diphosphate phosphorylation // not recorded//0006		
NM_008638	XM_006505697	XM_011241245		<b>0.00152557</b>	<b>1.11</b>	<b>1.11</b>	<b>M</b>			

RefSeq	Transcript ID	p (24h n=460)	p (48h n=657)	p (72h n=805)	FC 24h	FC 48h	FC 72h	Gene Symbol	Gene Title	Gene Ontology Biological Process
NM_001113248	///NM_009188	5.85E-04	0.00715407	1.10	1.44	1.36	<b>Sin3b</b>	transcriptional regulator, SIN3B (yeast)	0001122 // negative regulation of transcription from RNA polymerase II promoter // not recorded // 0006351 // transcription, DNA-templated // inferred from electronic annotation // 0001501 // skeletal system development // inferred from mutant phenotype // 0006281 // DNA repair // inferred from electronic annotation // 0006282 // regulation of DNA repair // 0005975 // carbohydrate metabolic process // inferred from electronic annotation // 0008152 // metabolic process // inferred from electronic annotation // 0009311 // oligosaccharide	
NM_001301414	///NM_146144	0.006502939	0.00988333	1.07	1.16	1.36	<b>Usp1</b>	ubiquitin specific peptidase 1	0006810 // metabolic process // inferred from electronic annotation	
NM_013463		0.004352849	0.00464255	1.08	1.22	1.36	<b>Gla</b>	galactosidase, alpha	0005975 // carbohydrate metabolic process // inferred from electronic annotation // 0008152 // metabolic process // inferred from electronic annotation // 0009311 // oligosaccharide	
NM_026117	///NM_20	0.00720425	0.002177797	1.29	1.31	1.36	<b>Dedd2</b>	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 // 0006506 // GPI anchor biosynthetic process // inferred from mutant phenotype // 0009058 // biosynthetic process // inferred from electronic annotation	
NM_011081	///NM_006528758	0.001247793	0.00791023	1.29	1.13	1.36	<b>Piga</b>	phosphatidylinositol glycan anchor biosynthesis, class A	0006506 // GPI anchor biosynthetic process // inferred from mutant phenotype // 0009058 // biosynthetic process // inferred from electronic annotation	
NM_008608		0.00408104	-1.02	1.24	1.36	<b>Mmp14</b>	matrix metalloproteinase 14 (membrane-inserted)	0006810 // transport // inferred from electronic annotation // 0006817 // phosphate ion transport // not recorded // 0006839 // mitochondrial transport // not recorded // 0008272 // stathmin 1		
NM_019641		0.00389318	-1.03	1.12	1.36	<b>Stmn1</b>	stathmin 1	0007019 // microtubule depolymerization // not recorded // 0007052 // microtubule organization // not recorded // 0007275 // multicellular organismal development // inferred from mutant phenotype // 0006506 // transport // inferred from electronic annotation // 0006817 // phosphate ion transport // not recorded // 0006839 // mitochondrial transport // not recorded // 0008272 // stathmin 1		
NM_013770		0.007988815	0.00126833	1.05	1.32	1.36	<b>Slc25a10</b>	slc25 carrier family 25 (mitochondrial carrier, dicarboxylate trans	0006810 // transport // inferred from electronic annotation // 0006817 // phosphate ion transport // not recorded // 0006839 // mitochondrial transport // not recorded // 0008272 // stathmin 1	
NM_008363	///NM_006498795	2.49E-04	-1.08	1.07	1.35	<b>Iib1b</b>	interleukin 1 beta	0000122 // negative regulation of transcription from RNA polymerase II promoter // not recorded // 0000165 // MAPK cascade // not recorded // 0000187 // activation of MAPK activity		
NM_001311790	///NM_009982	0.006507319	0.00122507	-1.03	1.16	1.35	<b>Ctsc</b>	cathepsin C	0001913 // T cell mediated cytotoxicity // inferred from genetic interaction // 0006508 // proteolysis // inferred from mutant phenotype // 0006508 // proteolysis // not recorded // 0006810 // transport // inferred from electronic annotation // 0007264 // small GTPase mediated signal transduction // inferred from electronic annotation // 00032456 // endocytic re	
NM_177305		0.00925302	-1.01	1.21	1.35	<b>Ar4c</b>	ADP-ribosylation factor-like 4C	0006810 // transport // inferred from electronic annotation // 0007264 // small GTPase mediated signal transduction // inferred from electronic annotation // 00032456 // endocytic re		
NM_178389	///NM_006539217	0.006697938	4.93E-04	1.14	1.24	1.35	<b>Gole</b>	galactose-4-epimerase, UDP	0005975 // carbohydrate metabolic process // inferred from electronic annotation // 0006282 // DNA repair // inferred from electronic annotation // 0006282 // regulation of DNA repair // 0005975 // carbohydrate metabolic process // inferred from electronic annotation // 0008152 // metabolic process // inferred from electronic annotation // 0009311 // oligosaccharide	
NM_010344		7.82E-04	0.00190678	1.19	1.37	1.35	<b>Gsr</b>	glutathione reductase	0006749 // glutathione metabolic process // inferred by curator // 0006749 // glutathione metabolic process // not recorded // 0007283 // spermatogenesis // not recorded // 000454	
NM_133722		0.00952294	0.007355682	1.15	1.21	1.35	<b>Abhd17c</b>	abhydrolase domain containing 17C	0008152 // metabolic process // inferred from electronic annotation	
NM_010185		7.04E-04	1.05	1.22	1.35	<b>Fcer1g</b>	Fc receptor, IgE, high affinity I, gamma polypeptide	0001798 // positive regulation of type Ila hypersensitivity // inferred from mutant phenotype // 0001805 // positive regulation of type III hypersensitivity // inferred from mutant phen		
NM_001285423	///NM_5	5.90E-04	7.86E-04	0.00425993	1.33	1.46	1.35	<b>Esd</b>	esterase D/fornylglutathione hydrolase	0042694 // formaldehyde catabolic process // inferred from electronic annotation
NM_019568	///NM_00	4.98E-05	1.50	1.24	1.35	<b>Cxcl14</b>	chemokine (C-X-C motif) ligand 14	0006955 // immune response // inferred from electronic annotation // 0045662 // negative regulation of myoblast differentiation // inferred from mutant phenotype // 0048839 // m		
NM_0011479		0.00445218	2.14E-04	0.00382231	1.15	1.38	1.35	<b>Splic2</b>	serine palmitoyltransferase, long chain base subunit 2	0006629 // lipid metabolic process // inferred from electronic annotation // 0006665 // sphingolipid metabolic process // inferred from electronic annotation // 0006686 // sphingom
NM_001081212		0.00880209	1.13	1.19	1.35	<b>Irs2</b>	insulin receptor substrate 2	0002053 // positive regulation of mesenchymal cell proliferation // inferred from genetic interaction // 0002903 // negative regulation of B cell apoptotic process // inferred from mut		
NM_176979	///NM_006511706	0.006511707	8.66E-04	-1.07	1.19	1.35	<b>Topbp1</b>	topoisomerase (DNA) II binding protein 1	0006281 // DNA repair // inferred from electronic annotation // 0006974 // cellular response to DNA damage stimulus // not recorded // 0007131 // mesenchymal metaplastic recombination	
NM_001048061	///NM_010448	0.00176346	-1.06	1.14	1.35	<b>Hrrnpab</b>	heterogeneous nuclear ribonucleoprotein A/B	0001122 // negative regulation of transcription from RNA polymerase II promoter // inferred from genetic interaction // 0001837 // epithelial to mesenchymal transition // inferred fr		
NM_178376		0.00603244	-1.01	1.12	1.35	<b>Rraga</b>	Ras-related GTP binding A	0006915 // apoptotic process // inferred from electronic annotation // 0008219 // cell death // not recorded // 0009267 // cellular response to starvation // not recorded // 0010506		
NM_001177609	///NM_001177610	0.0011665	1.06	1.27	1.34	<b>LOC102641751</b>	<b>Ube2l</b>	0001122 // negative regulation of transcription from RNA polymerase II promoter // inferred from mutant phenotype // 0000122 // negative regulation of transcription from RNA pol		
NM_007793		2.35E-04	0.00707683	1.15	1.48	1.34	<b>Cstb</b>	cystatin B	0008344 // adult locomotory behavior // inferred from mutant phenotype // 0010466 // negative regulation of peptidase activity // not recorded // 0010951 // negative regulation of	
NM_025407		0.00887697	1.07	1.34	1.34	<b>Uqcrc1</b>	ubiquinol-cytochrome c reductase core protein 1	0006122 // mitochondrial electron transport, ubiquinol to cytochrome c // inferred from direct assay // 0006810 // transport // inferred from electronic annotation // 0009060 // aerc		
NM_009127		0.00303949	1.21	1.33	1.34	<b>Scd1</b>	stearoyl-Coenzyme A desaturase 1	0006629 // lipid metabolic process // inferred from electronic annotation // 0006631 // fatty acid metabolic process // inferred from electronic annotation // 0006633 // fatty acid bio		
NR_002840	///NR_028543	0.008075489	1.47	1.57	1.34	<b>Gas5</b>	<b>Snord47</b>	growth arrest specific 5 // small nucleolar RNA, C/D box 47	0007049 // cell cycle // inferred from electronic annotation // 0007067 // mitotic nuclear division // inferred from electronic annotation // 0008152 // metabolic process // inferred fr	
NM_146235		0.00234453	1.07	1.12	1.34	<b>Erc6l</b>	excision repair cross-complementing rodent repair deficiency com	0007049 // cell cycle // inferred from electronic annotation // 0007067 // mitotic nuclear division // inferred from electronic annotation // 0008152 // metabolic process // inferred fr		
NM_134122		0.00520098	-1.02	1.21	1.34	<b>Nrm</b>	neurin (nuclear envelope membrane protein)	0009966 // regulation of signal transduction // inferred from electronic annotation // 0031648 // protein destabilization // not recorded // 0043254 // regulation of protein complex		
NM_134009		0.00122125	1.03	1.15	1.34	<b>Ncln</b>	nuclear lamin homolog (zebrafish)	0009966 // regulation of signal transduction // inferred from electronic annotation // 0031648 // protein destabilization // not recorded // 0043254 // regulation of protein complex		
NM_0111333	///NM_006515598	0.006515599	0.00143837	1.05	1.21	1.34	<b>Pole2</b>	polyomerase (DNA directed), epsilon 2 (p59 subunit)	0006260 // DNA replication // inferred from electronic annotation // 0006261 // DNA-dependent DNA replication // not recorded // 0042276 // error-prone translesion synthesis // nc	
NM_009026	///NM_011248826	0.0026964	1.14	1.22	1.34	<b>Rasd1</b>	RAS, dexamethasone-induced 1	0007165 // signal transduction // inferred from electronic annotation // 0007263 // nitric oxide mediated signal transduction // not recorded // 0007264 // small GTPase mediated sig		
NM_025569	///NM_029392	2.49E-04	0.00328841	1.15	1.57	1.34	<b>Mgst3</b>	mitoxaminal glutathione S-transferase 3	0102423 // response to organonitrogen compound // inferred from electronic annotation // 0055114 // oxidation-reduction process // not recorded	
NM_001025477	///NM_001039356	0.00587571	0.00137316	1.11	1.38	1.33	<b>Hmgai1</b>	<b>Hmgai1-rs1</b>	high mobility group AT-hook 1 // high mobility group AT-hook 1, rel	
NM_016867	///NM_01	0.00494418	1.15	1.34	1.33	<b>Gipz2</b>	GIPC PDZ domain containing family, member 2	0006284 // base-excision repair // not recorded // 0006351 // transcription, DNA-templated // inferred from electronic annotation // 0006355 // regulation of transcription, DNA-tem		
NM_011662		0.00186258	-1.25	1.09	1.33	<b>Tyrbp</b>	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		
NM_138656	///NR_021	0.00438684	0.0038585	1.18	1.35	1.33	<b>Mvd</b>	mevalonate (diphospho) decarboxylase	0006629 // lipid metabolic process // inferred from electronic annotation // 0006694 // steroid biosynthetic process // inferred from electronic annotation // 0006695 // cholesterol b	
NM_001302389	///NM_001302390	0.0013024	0.00353198	1.12	1.23	1.33	<b>Ppp2c</b>	phosphoinositid phosphatase 2	0006644 // phospholipid metabolic process // not recorded // 0007155 // signal transduction // not recorded // 0003148 // sphingolipid biosynthetic process // not recorded // 000468	
NM_015897		0.002421028	0.00782959	1.12	1.30	1.33	<b>Timm23</b>	translocase of inner mitochondrial membrane 23	0006810 // transport // inferred from electronic annotation // 0006886 // intracellular protein transport // inferred from electronic annotation // 0015031 // protein transport // infer	
NM_00117752	///NM_2	3.16E-04	1.31	1.58	1.33	<b>Myc</b>	myelocytomatosis oncogene	0001122 // negative regulation of transcription from RNA polymerase II promoter // inferred from direct assay // 0000122 // negative regulation of transcription from RNA polymer		
NM_018868	///NM_00	3.43E-04	1.45E-04	1.38	1.51	1.33	<b>Nup58</b>	NOP58 ribonucleoprotein	000154 // rRNA modification // not recorded // 0006608 // snRNP protein import into nucleus // not recorded // 0004254 // rNosome biogenesis // inferred from electronic annot	
NM_021890	///NM_00527247	0.006527248	6.92E-04	-1.02	1.24	1.33	<b>Fads3</b>	fatty acid desaturase 3	0006629 // lipid metabolic process // inferred from electronic annotation // 0006631 // fatty acid metabolic process // inferred from electronic annotation // 0006623 // fatty acid bio	
NM_001163359	///NM_001163360	0.00676525	0.00237366	1.08	1.24	1.33	<b>Figln1</b>	figetin-like 1	0001649 // osteoblast differentiation // inferred from mutant phenotype // 0010569 // regulation of double-strand break repair via homologous recombination // not recorded // 0003	
NM_010188	///NM_006496658	0.006496659	0.00803502	-1.10	1.12	1.33	<b>Fcgr3</b>	Fc receptor, IgG, low affinity III	0001788 // antibody-dependent cellular cytotoxicity // inferred from mutant phenotype // 0001798 // positive regulation of type Ila hypersensitivity // inferred from mutant phenoty	
NM_025844	///NM_00	0.00209594	0.0054329	1.53	1.03	1.33	<b>Chordc1</b>	cysteine and histidine-rich domain (CHORD)-containing, zinc-bindin	0010824 // regulation of centrosome duplication // inferred from mutant phenotype // 00061077 // chaperone-mediated protein folding // inferred from direct assay // 1900034 // reg	
NM_007856	///NM_006508476	0.006508477	0.00593382	1.16	1.28	1.33	<b>Dhcr7</b>	7-dehydrocholesterol reductase	0001568 // blood vessel development // inferred from mutant phenotype // 0006629 // lipid metabolic process // inferred from electronic annotation // 0006694 // steroid biosynth	
NM_198613		0.00448233	1.00	1.24	1.32	<b>Ap2s1</b>	adaptor-related protein complex 2, sigma 1 subunit	0006810 // transport // inferred from electronic annotation // 0006886 // intracellular protein transport // inferred from electronic annotation // 0006897 // endocytosis // inferred fr		
NM_001310469	///NM_4	4.33E-05	0.00640368	1.69	1.31	1.32	<b>Osmr</b>	osteostatin M receptor	0007166 // cell surface receptor signaling pathway // traceable after interaction // 0008284 // positive regulation of cell proliferation // not recorded // 0034097 // response to cyto	
NM_007950		0.00442727	0.001884708	1.37	1.66	1.32	<b>Ereg</b>	epiregulin	0000187 // activation of MAPK activity // not recorded // 0001525 // angiogenesis // inferred from electronic annotation // 0001550 // ovarian cumulus expansion // not recorded // 000122	
NM_001199431	///NM_001199432	0.0011994	0.00999741	1.03	1.22	1.32	<b>Dnmt1</b>	DNA methyltransferase (cytosine-5) 1	0002376 // immune system process // inferred from electronic annotation // 0019886 // antigen processing and presentation of exogenous peptide antigen via MHC class II // inferred	
NM_023065		0.00112659	-1.15	1.13	1.32	<b>Ifj30</b>	interferon gamma inducible protein 30	0002376 // immune system process // inferred from electronic annotation // 0019886 // antigen processing and presentation of exogenous peptide antigen via MHC class II // inferred		
NM_001302346	///NM_001302347	0.0008773	0.00770895	1.18	1.17	1.32	<b>P2ry2</b>	purinergic receptor P2Y, G-protein coupled 2	0001701 // in utero embryonic development // inferred from electronic annotation // 0007165 // signal transduction // inferred from electronic annotation // 0007186 // G-protein cc	
NM_022415		0.00498024	7.36E-05	1.16	1.45	1.32	<b>Ptges</b>	prostaglandin H synthase	0001516 // prostaglandin biosynthetic process // not recorded // 0002526 // acute inflammatory response // inferred from electronic annotation // 0002544 // chronic inflammatory	
NM_009270		2.66E-04	1.31	1.47	1.32	<b>Sale</b>	squalene epoxidase	0006725 // cellular aromatic compound metabolic process // not recorded // 0008203 // cholesterol metabolic process // not recorded // 0010033 // response to organic substance //		
NM_001110146	///NM_021400	0.006529963	0.00204311	1.21	1.62	1.32	<b>Prg4</b>	proteoglycan 4 (megakaryocyte stimulating factor, articular super	0006898 // receptor-mediated endocytosis // inferred from electronic annotation // 0006955 // immune response // inferred from electronic annotation // 00018149 // peptide crossr	
NM_001267707	///NM_000151781	0.00058869	1.53	1.23	1.32	<b>Slc10a5</b>	slc25 carrier family 10 (anion transporter family, member 1a5	0006810 // transport // inferred from electronic annotation // 0006811 // ion transport // inferred from electronic annotation // 0008206 // bile acid metabolic process // not recorded		
NM_019553		0.004509864	1.19	1.35	1.32	<b>Ddx21</b>	DEAD (Asp-Glu-Ala-Asp) box polypeptide 21	0001649 // osteoblast differentiation // not recorded // 0006351 // transcription, DNA-templated // inferred from electronic annotation // 0006364 // rRNA processing // inferred fr		
NM_001164336	///NM_001164337	0.00715914	1.09	1.19	1.31	1.3	<b>Mar</b>	membrane-associated ring finger (C3HC4) 5	0000209 // protein polyubiquitination // not recorded // 0016567 // protein ubiquitination // inferred from electronic annotation // 0051865 // protein autoubiquitination // not recor	
NM_017373	///NM_00	0.00101011	0.001408788	1.64	1.57	1.31	<b>Nfj1b</b>	nuclear factor, interleukin 3, regulated	0001022 // negative regulation of transcription from RNA polymerase II promoter // not recorded // 0006351 // transcription, DNA-templated // inferred from electronic annotation //	
NM_001081214	///NM_1	3.1E-04	0.005732399	1.47	1.53	1.31	<b>Ppargc1r</b>	peroxisome proliferative activated receptor, gamma, coactivator-r	0006351 // transcription, DNA-templated // inferred from electronic annotation // 0006355 // regulation of transcription, DNA-templated // inferred from electronic annotation // 000	
NM_011112	///NM_006515592	0.006515593	0.00417569	-1.09	1.00	1.31	<b>Papola</b>	poly (A) polymerase alpha	0003998 // mRNA splicing, via spliceosome // -- // 0006369 // termination of RNA polymerase II transcription // -- // 0006378 // mRNA polyadenylation // not recorded // 0006397 //	
NM_024495		0.00437933	2.95E-04	1.19	1.34	1.31	<b>Cor13</b>	coronin 13	0006730 // one-carbon metabolic process // inferred from electronic annotation	
NM_001005767	///XR_384575	0.002629318	0.00329907	1.09	1.25	1.31	<b>Pari</b>	presenilin associated, rhomboid-like	0006508 // proteolysis // inferred from genetic interaction // 0006508 // proteolysis // inferred from mutant phenotype // 0006508 // proteolysis // not recorded // 0016485 // prot	
NM_028355	///NM_006503423	0.006503423	0.00329907	1.09	1.13	1.31	<b>Ndel1</b>	NDC1 transmembrane nucleoporin	0006810 // transport // inferred from electronic annotation // 0007125 // synapsis // inferred from mutant phenotype // 0007283 // spermatogenesis // inferred from mutant phenet	
NM_133757	///NM_011249288	0.00385447	0.00139282	1.12	1.28	1.31	<b>Pgs1</b>	phosphatidylglycerophosphate synthase 1	0006629 // lipid metabolic process // inferred from electronic annotation // 0006655 // phosphatidylglycerol biosynthetic process // inferred from sequence or structural similarity // 0001649 // osteoblast differentiation // inferred from electronic annotation	
NM_001001491		0.00662347	1.05	1.06	1.31	<b>Tpm4</b>	tropomyosin 4	0001924 // positive regulation of protein phosphorylation // not recorded // 0002792 // negative regulation of peptide secretion // not recorded // 0006955 // immune response // m		
NM_001136079	///NM_001170816	0.001765052	1.42	1.42	1.31	<b>Ptger4</b>	prostaglandin H receptor 4 (subtype EP4)	0002026 // pyrimidine nucleobase metabolic process // not recorded // 0006222 // UMP biosynthetic process // -- // 0006238 // CMP salvage // inferred from electronic annotation //		
NM_030724	///NM_006497039	0.006497040	9.86E-04	1.05	1.13	1.31	<b>Uck2</b>	uridine-cytidine kinase 2	0006508 // proteolysis // inferred from electronic annotation // 0006898 // receptor-mediated endocytosis // inferred from electronic annotation	
NM_145403		9.87E-04	1.22	1.37	1.31	<b>Tmprss4</b>	transmembrane protease, serine 4	0006810 // transport // inferred from electronic annotation // 0033762 // response to glucagon // not recorded // 00055114 // oxidation-reduction process // inferred from electronic		
NM_025567		0.007171161	1.00	1.26	1.31	<b>Cyc1</b>	cytochrome c-1			

RefSeq	Transcript ID	p (24h n=460)	p (48h n=657)	p (72h n=805)	FC 24h	FC 48h	FC 72h	Gene Symbol	Gene Title	Gene Ontology Biological Process
NM_013594//XM_00	0.00171644				1.31	1.18	1.29	<b>Mbd1</b>	methyl-CpG binding domain protein 1	0000122 // negative regulation of transcription from RNA polymerase II promoter // not recorded//0006346 // methylation-dependent chromatin silencing // not recorded//0006346
NM_001042513//NM	6.29E-04	0.008700395	0.00136108		1.27	1.42	1.29	<b>Tnfr1</b>	thioredoxin reductase 1	0001707 // mesoderm formation // inferred from mutant phenotype//0006979 // response to oxidative stress // not recorded//0007369 // gastrulation // inferred from mutant phenotype
NM_022325		0.00289558	-1.02	1.22	1.22	1.29	<b>Ctsz</b>	cathepsin Z	0006508 // proteolysis // inferred from electronic annotation//00051603 // proteolysis involved in cellular protein catabolic process // not recorded//0006041 // epithelial tube bran	
NM_001204875//NM	0.23871				1.12	1.11	1.29	<b>Set</b>	SET nuclear oncogene	0006334 // nucleosome assembly // inferred from electronic annotation//00043524 // negative regulation of neuron apoptotic process // not recorded//0004892 // negative regulation
NM_007825//XM_006535383//XM	1.68E-04				1.21	1.36	1.29	<b>Cyp7b1</b>	cytochrome P450, family 7, subfamily B, polypeptide 1	0006629 // lipid metabolic process // inferred from electronic annotation//0006699 // bile acid biosynthetic process // inferred from direct assay//0007586 // digestion // traceable
NM_027519//XM_00	0.00355944	0.002369367			1.39	1.41	1.29	<b>Meadg</b>	mesenteric estrogen dependent adipogenesis	0045600 // positive regulation of fat cell differentiation // inferred from mutant phenotype
NM_029959		0.00584465	1.03	1.25	1.29	<b>Pbp2</b>	phosphatidylethanolamine binding protein 2	0010033 // response to organic substance // inferred from electronic annotation//0010243 // response to organonitrogen compound // inferred from electronic annotation//00104		
NM_001013368//XM	0.00654055//XM_00654055	0.00422818	1.10	1.19	1.29	<b>E2f8</b>	E2F transcription factor 8	0000122 // negative regulation of transcription from RNA polymerase II promoter // inferred from mutant phenotype//0000122 // negative regulation of transcription from RNA pol		
NM_010253		0.0032902	1.05	1.21	1.29	<b>Gol</b>	galanin	0006954 // inflammatory response // not recorded//0007238 // neuroepithelial signaling pathway // inferred from mutant phenotype//0007399 // nervous system development // in		
NM_001291348//NM	0.001291349//	0.005597941	1.15	1.28	1.29	<b>Anapc15</b>	anaphase promoting complex C subunit 15	0007049 // cell cycle // inferred from electronic annotation//0007067 // mitotic nuclear division // inferred from mutant phenotype//00051301 // cell division // inferred from ele		
NM_001198933//NM	0.00813009		0.00472388	1.15	1.33	1.29	<b>Me1</b>	male-specific enzyme 1, NADPH-dependent, cytosolic anti-silencing function 1B histone chaperone	0006108 // malate metabolic process // not recorded//0006108 // malate metabolic process // inferred from sequence or structural similarity//0009725 // response to hormone //	
NM_024184		0.008237724	-1.06	1.22	1.29	<b>Asf1b</b>	forkhead box D1	0006333 // chromatin assembly or disassembly // inferred from electronic annotation//0006334 // nucleosome assembly // inferred from direct assay//0006335 // DNA replication		
NM_006239		0.00535609	0.007140858		1.23	1.26	1.29	<b>Foxq1</b>	forkhead box O1	0006335 // transcription, DNA-templated // inferred from electronic annotation//0006335 // regulation of transcription, DNA-templated // inferred from electronic annotation//000
NM_001033313			0.00138672		1.06	1.24	1.29	<b>Pdcp1</b>	PDGFA associated protein 1	0048008 // platelet-derived growth factor receptor signaling pathway // not recorded
NM_177638//XM_006524163//XM	0.06524164//		0.00333495		1.10	1.23	1.28	<b>Cr3b</b>	crumbs family member 3	0045198 // establishment of epithelial cell apical/basal polarity // not recorded//00045216 // cell-cell junction organization // not recorded//00072659 // protein localization to plasm
NM_133771//XM_006525109//XM	0.004369582		0.00518366		1.13	1.26	1.28	<b>Memo1</b>	mediator of cell motility 1	0032886 // regulation of microtubule-based process // not recorded
NM_007991//XM_00	0.00742847		0.00102621		1.17	1.23	1.28	<b>Fbl//LOC102643269</b>	fibrillarin//rRNA 2'-O-methyltransferase fibrillarin	0000494 // box C/D snoRNA 3'-end processing // not recorded//0001649 // osteoblast differentiation // not recorded//0006364 // rRNA processing // inferred from electronic anno
NM_024241//XR_878878//XR_878	0.002247344		1.05	1.28	1.28	<b>Tomm20</b>	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 electron		
NM_007574		0.001288241	-1.04	1.29	1.28	<b>C1qc</b>	complement component 1, q subcomponent, C chain	0002376 // immune system process // inferred from electronic annotation//0006958 // complement activation, classical pathway // inferred from electronic annotation//00038053		
NM_008062//NM_01	0.00653897	0.00191245	0.00917291		1.15	1.45	1.28	<b>G6pd//G6pd2</b>	glucose-6-phosphate dehydrogenase X-linked//glucose-6-phospho	0001816 // cytokine production // inferred from mutant phenotype//0001998 // angiotensin mediated vasoconstriction involved in regulation of systemic arterial blood pressure // u
NM_001109684//NM	0.00109685//NM_144531	0.00473739	1.21	1.29	1.28	<b>Kzn</b>	kluzin, periplakin interacting protein	0006124 // keratinization // inferred from electronic annotation		
NM_001135151//NM	8.03E-04	7.54E-04	1.29	1.28	1.28	<b>Slc39a14</b>	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		
NM_009112//XM_011251865	0.003748216		1.01	1.30	1.28	<b>S100A10</b>	S100 calcium binding protein A10 (calpactin)//protein S100-A10-l	0001176 // membrane raft assembly // not recorded//0006900 // membrane budding // not recorded//0043547 // positive regulation of GTPase activity // not recorded//0005109		
NM_007838		0.00986295	1.01	1.06	1.28	<b>Dost</b>	dolichyl-di-phosphooligosaccharide-protein glycotransferase	0006486 // protein glycosylation // inferred from sequence or structural similarity//0006486 // protein glycosylation // inferred from electronic annotation//0006487 // protein N-li		
NM_029639		3.60E-04	0.00107309		1.00	1.34	1.28	<b>Plet1</b>	platelet expressed transcript 1	0001953 // negative regulation of cell-matrix adhesion // inferred from mutant phenotype//00030154 // cell differentiation // inferred from electronic annotation//0003035 // posit
NM_029478//XM_00	0.00115548		1.36	1.31	1.27	<b>Vmp1</b>	vacuole membrane protein 1	0006887 // exocytosis // not recorded//0006914 // autophagy // inferred from electronic annotation//0007029 // endoplasmic reticulum organization // not recorded//0007030		
NM_175451		0.0014105	1.06	1.15	1.27	<b>Kcp4</b>	cytoskeleton-associated protein 4			
NM_008021//NM_027697		0.00156567	1.05	1.15	1.27	<b>Foxm1//493341G19R1K</b>	forkhead box M1//RIKEN cDNA 493341G19I	0000086 // G2/M transition of mitotic cell cycle // not recorded//0000122 // negative regulation of transcription from RNA polymerase II promoter // not recorded//0000302 // res		
NM_0113898		0.00472442	0.00271019		1.22	1.37	1.27	<b>Timm8a1</b>	translocase of inner mitochondrial membrane 8A1	0006626 // protein targeting to mitochondrion // not recorded//0006810 // transport // inferred from electronic annotation//0015031 // protein transport // inferred from electron
NR_024067		0.003965239	1.05	1.37	1.27	<b>Snhg6</b>	small nuclear RNA host gene 6			
NM_001159866//NM	0.195622//XM_004944335		1.06	1.38	1.27	<b>Uchl5</b>	ubiquitin carboxyl-terminal esterase L5	0006281 // DNA repair // inferred from electronic annotation//0006310 // DNA recombination // inferred from electronic annotation//0006351 // transcription, DNA-templated // i		
NM_023418		0.00500534	1.06	1.21	1.27	<b>Pgam1</b>	phosphoglycerate mutase 1	0006094 // gluconeogenesis // inferred from electronic annotation//0006094 // glycolytic process // not recorded//0006110 // regulation of glycolytic process // not recorded//0006740 // protein dephosphorylati		
NM_011655		0.005062215	-1.01	1.25	1.27	<b>Tubb5</b>	tubulin, beta 5 class I	0006457 // protein folding // --//0006096 // glycolytic process // not recorded//0006110 // microtubule-based process // inferred from direct assay//0007017 // microtubule-based process //		
NM_001284328//NM	0.01311113//	0.005298061	1.23	1.48	1.26	<b>Syncrip</b>	synaptotagmin binding, cytoplasmic RNA interacting protein	0001649 // osteoblast differentiation // not recorded//0006397 // mRNA processing // inferred from electronic annotation//0008380 // RNA splicing // inferred from electronic anno		
NM_023044		4.80E-05	1.01	1.47	1.26	<b>Slc15a3</b>	solute carrier family 15, member 3	0006810 // transport // inferred from electronic annotation//0006857 // oligopeptide transport // inferred from electronic annotation//0015031 // protein transport // inferred from		
NM_025380		0.00187606	1.50	1.44	1.26	<b>Eef1e1</b>	eukaryotic translation elongation factor 1 epsilon 1	0006281 // DNA repair // non-traceable author statement//0006412 // translation // inferred from electronic annotation//0006414 // translational elongation // not recorded//00		
NM_021456		1.89E-05	1.41	1.27	1.26	<b>Clp1</b>	carboxylesterase 1G	0008152 // metabolic process // inferred from electronic annotation//0010468 // regulation of gene expression // inferred from mutant phenotype//0016042 // lipid catabolic pro		
NM_009191//XM_006507488//XM	0.006507489//	0.00354966	1.11	1.08	1.26	<b>C1pb</b>	C1pb caseinolytic peptidase B	0008152 // metabolic process // inferred from electronic annotation//0034605 // cellular response to heat // not recorded		
NM_010902//NR_13	0.00233944		1.30	1.28	1.26	<b>Nfe2l2</b>	nuclear factor, erythroid derived 2, like 2	0006355 // transcription, DNA-templated // inferred from electronic annotation//0006355 // regulation of transcription, DNA-templated // inferred from direct assay//0006366 // t		
NM_008828		0.00827432	1.23	1.36	1.26	<b>Pgk1</b>	phosphoglycerate kinase 1	0005975 // carbohydrate metabolic process // not recorded//0006094 // gluconeogenesis // not recorded//0006096 // glycolytic process // inferred from direct assay//0006096 // t		
NM_001040682//NM	0.53155//NR_104435//NR	0.00592363	1.07	1.12	1.26	<b>Cmn</b>	calmin	0008285 // negative regulation of cell proliferation // inferred from direct assay//0031175 // neuron projection development // inferred from mutant phenotype		
NM_001291439//NM	9.95E-04	4.98E-04	1.28	1.87	1.26	<b>Hmgcs1</b>	3-hydroxy-3-methylglutaryl-Coenzyme A synthase 1	0001889 // liver development // inferred from electronic annotation//0006629 // lipid metabolic process // inferred from electronic annotation//0006694 // steroid biosynthesis pr		
NM_007386		0.006665054	1.12	1.29	1.26	<b>Aco1</b>	aconitase 1	0006099 // tricarboxylic acid cycle // inferred from electronic annotation//0006101 // citrate metabolic process // not recorded//0006417 // regulation of translation // inferred from		
NM_007633		0.0034679	1.08	1.19	1.26	<b>Ccne1</b>	cyclin E1	0000082 // G1/S transition of mitotic cell cycle // inferred from electronic annotation//0001547 // antral ovarian follicle growth // inferred from electronic annotation//0001889 //		
NM_009569//XM_00	0.00714783		-1.21	1.06	1.26	<b>Zfpml1</b>	zinc finger protein, multitype 1	0000122 // negative regulation of transcription from RNA polymerase II promoter // inferred from direct assay//0000122 // negative regulation of transcription from RNA polymer		
NM_009773//XM_006498622		0.00485824	-1.00	1.21	1.26	<b>Bub1b</b>	binding uninhibited by benzimidazoles 1 homolog, beta 5, cerevis	0004668 // protein phosphorylation // inferred from electronic annotation//0006915 // apoptotic process // inferred from electronic annotation//0007049 // cell cycle // inferred fr		
NM_133225		0.00571514	1.01	1.04	1.26	<b>Acd3b</b>	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 // i		
NM_001033293//XR_374072//XR_374073//XR_3	0.0014732		1.04	1.19	1.26	<b>Uup11</b>	UDP-N-acetylglucosamine pyrophosphorylase 1-like 1	0006048 // UDP-N-acetylglucosamine biosynthetic process // --//0008152 // metabolic process // inferred from electronic annotation		
NM_001242368//NM	0.007972	0.007001603	1.10	1.21	1.26	<b>F10</b>	coagulation factor X	0006508 // proteolysis // inferred from electronic annotation//0007596 // blood coagulation // not recorded//0007599 // hemostasis // inferred from electronic annotation//0003		
NM_001252578//NM	0.01252579//NM_028072//	0.00578571	-1.08	1.17	1.25	<b>Sulf2</b>	sulfatase 2	0001822 // kidney development // inferred from genetic interaction//0002063 // chondrocyte development // inferred from mutant phenotype//0003094 // glomerular filtration //		
NM_026862//XM_011250688//XM	6.07E-04		1.20	1.35	1.25	<b>Cd177</b>	CD177 antigen			
NM_001313923//NM	0.00142853		1.16	1.16	1.25	<b>Actg1</b>	actin, gamma, cytoplasmic 1	0001895 // retina homeostasis // inferred from electronic annotation//00045214 // sarcomere organization // inferred from direct assay//0051592 // response to calcium ion // infer		
NM_007634//XM_006523554		0.00964926	1.02	1.08	1.25	<b>Conf</b>	cyclin F	0000320 // re-entry into mitotic cell cycle // inferred from mutant phenotype//0001890 // placenta development // inferred from mutant phenotype//0007049 // cell cycle // infer		
NM_021274		0.0097251	1.06	1.06	1.25	<b>Cxcl10</b>	chemokine (C-X-C motif) ligand 10	0002690 // positive regulation of leukocyte chemotaxis // not recorded//0006935 // chemotaxis // not recorded//0006954 // inflammatory response // not recorded//0006955 //		
NM_001080129//NM	0.001080130//NM_001080101	0.00962911	-1.12	1.08	1.25	<b>Tmpo</b>	thymopoietin	0006355 // regulation of transcription, DNA-templated // inferred from direct assay		
NM_001165939//NM	0.00789198	0.004358608	1.24	1.35	1.25	<b>Tshb</b>	thyroid stimulating hormone, beta subunit	0033189 // response to vitamin A // inferred from electronic annotation//0043627 // response to estrogen // inferred from electronic annotation//0051592 // response to calcium i		
NM_026894//XM_006506552//XM	0.00584872		1.06	1.24	1.25	<b>Tamm41</b>	TAM41, nuclear organelle translocator assembly and maintenance pr	0006629 // lipid metabolic process // inferred from electronic annotation//0008654 // phospholipid biosynthetic process // inferred from electronic annotation//0016024 // CDP-di		
NM_026053//XM_011246581//XM	0.009550269		1.16	1.20	1.25	<b>Gem16</b>	gem, nuclear organelle associated protein 6	0000245 // spliceosomal complex assembly // inferred from electronic annotation//0000387 // spliceosomal snRNP assembly // not recorded//0006397 // mRNA processing // infer		
NM_001306205//NM	0.23556//XM_006530183//	0.00911818	1.06	1.14	1.25	<b>Mvk</b>	mevalonate kinase	0006629 // lipid metabolic process // inferred from electronic annotation//0006694 // steroid biosynthetic process // inferred from electronic annotation//0006695 // cholesterol b		
NM_009791//XM_006529108	0.006524405		1.03	1.25	1.25	<b>Aspm</b>	asp (abnormal spindle)-like, microcephaly associated (Prosophila)	0001764 // neuron migration // inferred from genetic interaction//0001764 // neuron migration // inferred from mutant phenotype//0002052 // positive regulation of neuroblast p		
NM_019980//XM_006522427//XR_005401038		0.005401038	1.16	1.29	1.25	<b>Litaf//Gm9861</b>	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 // reg		
NM_001290706//NM	0.25452//NM_006466657		1.10	1.28	1.25	<b>Tmem54</b>	transmembrane protein 54			
NM_001026213//NM_001286972//	0.005629477		1.07	1.10	1.25	<b>Dnajc19//Dnajc19-ps</b>	Dnaj (Hsp40) homolog, subfamily C, member 19//Dnaj (Hsp40) h	00056810 // transport // inferred from electronic annotation//0007601 // visual perception // not recorded//0015031 // protein transport // inferred from electronic annotation//0		
NM_011334//XR_378219		0.00897249	1.04	1.10	1.25	<b>Igfbp3</b>	integrin alpha 3	0007155 // cell adhesion // inferred from electronic annotation//0007228 // integrin-mediated signaling pathway // inferred from electronic annotation//0034113 // heterotypic cel		
NM_001042534//NM_001271395//	3.17E-05		-1.04	1.55	1.24	<b>Capp</b>	capping protein (actin filament), geloslin-like	0003013 // cell projection assembly // inferred from direct assay//0051035 // barbed-end actin filament capping // inferred from electronic annotation//0051693 // actin filament c		
NM_139149//XM_006507759//XM	0.006507760		1.14	1.25	1.24	<b>Fus</b>	fused in sarcoma	0012717 // cellular response to calcium ion // not recorded//1993506 // regulation of nucleic acid-templated transcription // inferred from electronic annotation		
NM_172845		0.00498705	1.15	1.28	1.24	<b>Adams4</b>	a disintegrin-like and metalloprotease (reprolysin type) with throm	0006508 // proteolysis // inferred from direct assay//0042742 // defense response to bacterium // inferred from genetic interaction		
NM_001311101//NM	0.026467//XM_006511383	0.00202505	1.04	1.14	1.24	<b>Rps27l</b>	ribosomal protein S27-like	0000028 // ribosomal small subunit assembly // --//0006281 // DNA repair // not recorded//0006412 // translation // not recorded//0006919 // activation of cysteine-type endop		
NM_0013470		0.007438398	1.06	1.25	1.24	<b>Anxa3</b>	annexin A3	0006909 // glycolysis // not recorded//0010595 // positive regulation of endothelial cell migration // not recorded//0021766 // hippocampus development // inferred from elect		
NM_025434		0.00607998	1.11	1.19	1.24	<b>Mps28</b>	mitochondrial ribosomal protein S28			
NM_021526		0.00564625	1.08	1.19	1.24	<b>Psmid14</b>	proteasome (prosome, macropain) 26S subunit, non-ATPase, 14	0000724 // double-strand break repair via homologous recombination // not recorded//0006281 // DNA repair // inferred from electronic annotation//0006303 // double-strand br		
NM_153576		0.00900769	9.15E-04		1.29	1.40	1.24	<b>Cxcl17</b>	chemokine (C-X-C motif) ligand 17	0001525 // angiogenesis // inferred from electronic annotation//0006935 // chemotaxis // inferred from electronic annotation//0007275 // multicellular organismal development, /
NM_153570		0.00282539	1.12	1.22	1.24	<b>Noc4l</b>	nuclear core complex associated 4 homolog (S. cerevisiae)	0042254 // ribosome biogenesis // inferred from electronic annotation		
NM_001310595//NM	0.01310596//NM_0111844//	0.00255683	1.09	1.12	1.24	<b>Psmo3</b>	proteasome (prosome, macropain) subunit, alpha type 3	0006508 // proteolysis // inferred from electronic annotation//0006511 // ubiquitin-dependent protein catabolic process // inferred from electronic annotation//0010499 // protea		
NM_001164671//NM	0.00660579		-1.45	-1.02	1.24	<b>Dnajp1</b> </				



RefSeq	Transcript ID	p (24h n=460)	p (48h n=657)	p (72h n=805)	FC 24h	FC 48h	FC 72h	Gene Symbol	Gene Title	Gene Ontology Biological Process
NM_0027352	/NM_027343	/XNM_006500155		0.00214126	1.01	1.14	1.23	<b>Gorsp2</b>	golgi reassembly stacking protein 2	0006996 // organelle organization // not recorded // 0007030 // Golgi organization // not recorded
NM_001025561	/NM_001025562	/XNM_0197000		0.00438658	1.06	1.11	1.23	<b>Pus1</b>	pseudouridine synthase 1	0001522 // pseudouridine synthesis // inferred from electronic annotation // 0008033 // tRNA processing // inferred from electronic annotation // 0009451 // RNA modification // inf
NM_0209397	/NM_170598		0.006745453		1.19	1.47	1.23	<b>Rbm12</b>	RNA binding motif protein 12	0006351 // transcription, DNA-templated // inferred from electronic annotation // 0006355 // regulation of transcription, DNA-templated // inferred from electronic annotation // 000
NM_0083606	/XNM_006510024	/XNM_00593709			1.08	1.27	1.18	<b>I18L</b>	interleukin 18	0000165 // MAPK cascade // not recorded // 0001525 // angiogenesis // not recorded // 0001525 // angiogenesis // inferred from sequence or structural similarity // 0001666 // resp
NM_1535477	/NM_17	3.08E-04	0.004201335		1.40	1.31	1.23	<b>Gn3i</b>	guanine nucleotide binding protein-like 3 (nucleolar)	0008283 // cell proliferation // not recorded // 00042127 // regulation of cell proliferation // not recorded // 00042254 // ribosome biogenesis // not recorded // 1902895 // positive reg
NM_023142			0.004574685		1.03	1.36	1.22	<b>Arpc1b</b>	actin related protein 2/3 complex, subunit 18	0030833 // regulation of actin filament polymerization // inferred from electronic annotation // 0034314 // Arp2/3 complex-mediated actin nucleation // not recorded // 1902895
NM_013562		4.82E-04	0.006719883		1.31	1.25	1.22	<b>Irf1d1</b>	interferon-related developmental regulator 1	0007275 // multicellular organismal development // inferred from electronic annotation // 0014706 // striated muscle tissue development // inferred from mutant phenotype // 0030
NM_001045863	/NM_001045864	/XNM_1385800		0.00221544	1.12	1.18	1.22	<b>Nelfe</b>	negative elongation factor complex member E, Rdbp	0000122 // negative regulation of transcription from RNA polymerase II promoter // inferred from electronic annotation // 0006351 // transcription, DNA-templated // inferred from t
NM_009112	/XNM_011251865		0.002119359		1.00	1.31	1.22	<b>LOC105242499</b>	protein S100-A10-like // S100 calcium binding protein A10 (calpain)	0001765 // membrane raft assembly // not recorded // 0006900 // membrane budding // not recorded // 0043547 // positive regulation of GTPase activity // not recorded // 0005109
NM_139002	/XNM_011248202	/XNM_011248203		0.00987496	1.04	1.07	1.22	<b>Sds1</b>	serine dehydratase-like	0005655 // L-serine catabolic process // not recorded // 0006567 // threonine catabolic process // not recorded
NM_138584	/XNM_006511222		0.008324645		1.03	1.19	1.22	<b>Spg21</b>	spastic paraplegia 21 homolog (human)	
NM_025798	/XNM_006512823	/XNM_000594041		0.00595956	1.00	1.23	1.22	<b>Hint3</b>	histidine triad nucleotide binding protein 3	0008152 // metabolic process // inferred from electronic annotation
NM_001162946	/NM_00282403		0.00282403		1.19	1.49	1.22	<b>Poa</b>	pyruvate carboxylase	0006090 // pyruvate metabolic process // not recorded // 0006094 // gluconeogenesis // not recorded // 0006107 // oxaloacetate metabolic process // not recorded // 0006629 // lip
NM_026030			0.00327023		1.12	1.14	1.22	<b>Ejfb2</b>	eukaryotic translation initiation factor 2, subunit 2 (beta)	0001701 // in utero embryonic development // inferred from mutant phenotype // 0002176 // male germ cell proliferation // inferred from mutant phenotype // 0006412 // translati
NM_026753			0.00519836		1.03	1.20	1.22	<b>Fam96b</b>	family with sequence similarity 96, member B	0007059 // chromosome segregation // not recorded // 0016226 // iron-sulfur cluster assembly // not recorded
NM_009137		0.00115586	0.00277881		1.21	1.24	1.22	<b>Ca22</b>	chemokine (C-C motif) ligand 22	0002548 // monocyte chemotaxis // not recorded // 0006935 // chemotaxis // inferred from electronic annotation // 0006954 // inflammatory response // inferred from electronic annotation //
NM_001164567	/NM_011700	/XNM_009423475		0.00423675	1.17	1.25	1.22	<b>Vill</b>	villin-like	0007101 // cytoskeleton organization // inferred from electronic annotation // 0051693 // actin filament capping // inferred from electronic annotation
NM_028315	/XNM_006519601	/XNM_006519602		0.00812882	1.13	1.16	1.22	<b>Dis3</b>	DIS3 mitotic control homolog (S. cerevisiae)	000364 // RNA processing // not recorded // 0006402 // mRNA catabolic process // not recorded // 0016075 // rRNA catabolic process // not recorded // 0043547 // positive regula
NM_025301		0.008490994	0.00326601		1.05	1.28	1.22	<b>Mrlp17</b>	mitochondrial ribosomal protein L17	0000002 // mitochondrial genome maintenance // traceable author statement // 0006412 // translation // not recorded
NM_001304719	/NM_009725	/XNM_008715484		0.008715484	1.03	1.27	1.22	<b>Atp5f1</b>	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit	0006810 // transport // inferred from electronic annotation // 0006811 // ion transport // inferred from electronic annotation // 0015986 // ATP synthesis coupled proton transport //
NM_007984		0.00769135	0.00282951		1.04	1.05	1.22	<b>Fscn1</b>	fascin homolog 1, actin bundling protein (Frogycentrotus purp	0007015 // actin filament organization // inferred from electronic annotation // 0007043 // cell-cell junction assembly // not recorded // 0010592 // positive regulation of lamellipod
NM_033079	/XNM_006505368	/XNM_006505369		0.00282951	1.03	1.09	1.22	<b>Miap</b>	meiosis 1 associated protein	0006396 // RNA processing // non-traceable author statement // 0007283 // spermatogenesis // inferred from mutant phenotype // 0007292 // female gamete generation // infer
NM_001025388	/NM_0231119	/XNM_001249618		0.001249618	1.04	1.48	1.22	<b>Eno1</b>	enolase 1, alpha non-neuron/enolase 1B, retrotransposed	0001701 // in utero embryonic development // inferred from mutant phenotype // 0006096 // glycolytic process // inferred from sequence or structural similarity // 0005109 // posit
NM_010235		0.007389488			1.16	1.24	1.22	<b>Fosl1</b>	fos-like antigen 1	0001701 // in utero embryonic development // inferred from mutant phenotype // 0006355 // regulation of transcription, DNA-templated // inferred from electronic annotation // 00
NM_026159		0.0086093			1.04	1.24	1.21	<b>Retsat</b>	retinol saturase (all trans retinol 13,14 reductase)	0042572 // retinol metabolic process // inferred from direct assay // 0055114 // oxidation-reduction process // inferred from direct assay
NM_011333		0.00835736	4.44E-04		1.20	1.36	1.21	<b>Col2</b>	chemokine (C-C motif) ligand 2	000166 // MAPK cascade // inferred from electronic annotation // 0001525 // angiogenesis // traceable author statement // 0001666 // response to hypoxia // inferred from electro
NM_022654	/XNM_006536218	/XNM_006536219		0.00499119	1.08	-1.01	1.21	<b>Pid1</b>	p53 induced death domain protein 1	0006915 // apoptotic process // inferred from electronic annotation // 0006919 // activation of cysteine-type endopeptidase activity involved in apoptotic process // inferred from ger
NM_025595		0.001052343	0.00818493		1.13	1.32	1.21	<b>Mrlp51</b>	mitochondrial ribosomal protein L51	0006412 // translation // inferred from direct assay // 0032543 // mitochondrial translation // inferred from sequence or structural similarity
NM_001310723	/NM_001310725	/XNM_0013107		0.00357863	1.05	1.12	1.21	<b>Setd8</b>	SET domain containing [lysine methyltransferase] 8	0000122 // negative regulation of transcription from RNA polymerase II promoter // not recorded // 0006351 // transcription, DNA-templated // inferred from electronic annotation //
NM_026129		0.009095989	0.00872861		1.08	1.19	1.21	<b>Erp29</b>	endoplasmic reticulum protein 29	0000187 // activation of MAPK activity // not recorded // 0001934 // positive regulation of protein phosphorylation // not recorded // 0006457 // protein folding // not recorded // 00
NM_009338	/NM_153151		0.004299975		1.14	1.26	1.21	<b>Acs2</b>	Acetyl-Coenzyme A acetyltransferase 2 // acetyl-Coenzyme A acety	0008152 // metabolic process // inferred from electronic annotation // 0045797 // positive regulation of intestinal cholesterol absorption // inferred from direct assay
NM_009253	/XNM_00	0.00116102	3.71E-05		1.28	1.78	1.21	<b>Serpin3a</b>	serpin (or cysteine) peptidase inhibitor, clade A, member 3A	0010466 // negative regulation of peptidase activity // inferred from electronic annotation // 0010951 // negative regulation of endopeptidase activity // not recorded // 0034097 // r
NM_001103618	/NM_001310619		0.009811147		1.02	1.19	1.21	<b>Ube2t</b>	ubiquitin-conjugating enzyme E2K	0007165 // signal transduction // inferred from electronic annotation // 0007186 // G-protein coupled receptor signaling pathway // inferred from electronic annotation
NM_001172100	/NM_001172101		3.73E-04		1.09	1.36	1.21	<b>Rnh1</b>	ribonuclease/angiogenin inhibitor 1	0043086 // negative regulation of catalytic activity // not recorded // 0045765 // regulation of angiogenesis // not recorded
NM_001038703	/NM_030258	/XNM_008231633		0.008231633	1.01	1.23	1.20	<b>Gpr146</b>	G-protein-coupled receptor 146	0007165 // signal transduction // inferred from electronic annotation // 0007186 // G-protein coupled receptor signaling pathway // inferred from electronic annotation
NM_016966	/NR_033590	/NR_076	0.006945512		1.01	1.23	1.20	<b>Gm8096</b>	3-phosphoglycerate dehydrogenase pseudogene // 3-phosphoglyc	0006554 // glutamine metabolic process // inferred from mutant phenotype // 0006544 // glycine metabolic process // inferred from mutant phenotype // 0006563 // L-serine metab
NM_009338	/NM_15	0.00645456	4.86E-04		1.17	1.36	1.20	<b>Acs2</b>	Acetyl-Coenzyme A acetyltransferase 2 // acetyl-Coenzyme A acety	0008152 // metabolic process // inferred from electronic annotation // 0045797 // positive regulation of intestinal cholesterol absorption // inferred from direct assay
NM_001277256	/NM_00650293		0.00650293		1.29	1.26	1.20	<b>Spre1</b>	sprout protein with EVH-1 domain 1, related sequence	0000188 // inactivation of MAPK activity // inferred from mutant phenotype // 0007275 // multicellular organismal development // inferred from electronic annotation // 0009966 //
NM_053074			0.00948157		1.07	1.23	1.20	<b>Mups2</b>	nucleoporin 62	0006351 // transcription, DNA-templated // not recorded // 0006606 // protein import into nucleus // not recorded // 0006810 // transport // inferred from electronic annotation // 00
NM_133888			0.00918714		1.19	1.20	1.20	<b>Smpd3b</b>	sphingomyelin phosphodiesterase, acid-like 3B	0006685 // sphingomyelin phospholipase // inferred from electronic annotation // 0008152 // metabolic process // inferred from electronic annotation
NM_029271		0.003213113			1.08	1.24	1.20	<b>Mpl22</b>	mitochondrial ribosomal protein L22	0006412 // translation // not recorded
NM_011132		0.008494997			1.08	1.19	1.20	<b>Pole</b>	polymerase (DNA directed), epsilon	0000082 // G1/S transition of mitotic cell cycle // not recorded // 0007331 // DNA synthesis involved in DNA repair // not recorded // 0001701 // in utero embryonic development // u
NM_001081274	/NM_025801	/XNM_006841025		0.00577521	1.10	1.38	1.20	<b>Pgd</b>	phosphogluconate dehydrogenase	0005975 // carbohydrate metabolic process // not recorded // 0006098 // pentose-phosphate shunt // not recorded // 0006739 // NADP metabolic process // not recorded // 000905
NM_0113899		0.0028944	0.002443797		1.29	1.29	1.19	<b>Timm10</b>	translocase of inner mitochondrial membrane 10	0006810 // transport // inferred from electronic annotation // 0015031 // protein transport // inferred from electronic annotation // 0045039 // protein import into mitochondrial in
NM_001253751	/NM_001253752		0.002388096		1.29	1.45	1.19	<b>Fdps</b>	farnesyl diphosphate synthetase	0006629 // lipid metabolic process // inferred from electronic annotation // 0006694 // steroid biosynthetic process // inferred from electronic annotation // 0006695 // cholesterol b
NM_008160		3.52E-04	0.005537277		1.06	1.42	1.19	<b>Gpx1</b>	glutathione peroxidase 1	0000302 // response to reactive oxygen species // inferred from mutant phenotype // 0001659 // temperature homeostasis // inferred from genetic interaction // 0001885 // endothe
NM_026033		0.00872779			-1.08	1.05	1.19	<b>Gatad1</b>	GATA zinc finger domain containing 1	0006355 // regulation of transcription, DNA-templated // inferred from electronic annotation
NM_001083904	/NM_00080166	0.003050153			1.17	1.27	1.19	<b>Fetub</b>	fetuin beta	0007338 // single fertilization // inferred from mutant phenotype // 0007339 // binding of sperm to zona pellucida // inferred from mutant phenotype // 0010466 // negative regulati
NM_009076	/XR_880074		0.00623787		-1.01	1.15	1.19	<b>LOC102635048</b>	60S ribosomal protein L12 pseudogene // ribosomal protein L12	0000062 // ribosomal large subunit assembly // not recorded // 0006412 // translation // inferred from electronic annotation
NM_001039701	/NM_001159562		0.001424126		1.03	1.30	1.19	<b>Illr1</b>	interleukin 1 receptor antagonist	0001660 // fever generation // not recorded // 0001960 // negative regulation of cytokine-mediated signaling pathway // not recorded // 0002437 // inflammatory response to antige
NM_001159421	/NM_001159422		0.001059736		1.11	1.25	1.19	<b>Ccdc58</b>	coiled-coil domain containing 58	
NM_001289591	/NM_1307		3.07E-04		1.30	1.25	1.19	<b>Tmem173</b>	transmembrane protein 173	0002218 // activation of innate immune response // inferred from mutant phenotype // 0002218 // activation of innate immune response // not recorded // 0002230 // positive regul
NM_133653	/XNM_00	1.59E-04			1.30	1.19	1.19	<b>Mat1a</b>	methionine adenosyltransferase I, alpha	0006556 // S-adenosylmethionine biosynthetic process // not recorded // 0006730 // one-carbon metabolic process // inferred from electronic annotation // 0051260 // protein hom
NM_001290810	/NM_023536	/XNM_006539162		0.00914696	1.14	1.12	1.19	<b>Mrt4</b>	mRNA turnover 4, homolog (S. cerevisiae)	0042254 // ribosome biogenesis // inferred from electronic annotation
NM_009533	/XNM_00	0.00776811			1.21	1.21	1.19	<b>Xrcc5</b>	X-ray repair complementing defective repair in Chinese hamster ce	0000237 // leptotene // inferred from mutant phenotype // 0000723 // telomere maintenance // not recorded // 0006281 // DNA repair // inferred from electronic annotation // 0000
NM_011113	/XNM_00	4.64E-04		0.00585921	1.24	1.60	1.19	<b>Plour</b>	plasminogen activator, urokinase receptor	0001934 // positive regulation of protein phosphorylation // not recorded // 0010628 // positive regulation of gene expression // not recorded // 0016310 // phosphorylation // inferr
NM_001111058	/NM_0012293	/XNM_006540590		0.00515563	1.03	1.13	1.19	<b>Cd33</b>	CD33 antigen	0007155 // cell adhesion // inferred from electronic annotation
NM_00111099	/NM_1307		3.52E-04		1.46	1.18	1.18	<b>Cdkn1a</b>	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 recorde
NM_026578	/XNM_01	0.00860914			1.16	1.13	1.18	<b>Gor1</b>	GAR1 ribonucleoprotein homolog (yeast)	0001522 // pseudouridine synthesis // inferred from electronic annotation // 0006364 // rRNA processing // inferred from electronic annotation // 0042254 // ribosome biogenesis // i
NM_007422	/XNM_00649623		0.00722469		1.11	1.23	1.18	<b>Adss</b>	adenylosuccinate synthetase, non-yeast	0006164 // purine nucleotide biosynthetic process // inferred from direct assay // 0006167 // AMP biosynthetic process // inferred from direct assay // 0006167 // AMP biosynthetic p
NM_001172146	/NM_00967711		0.00967711		1.14	1.29	1.18	<b>Aimp2</b>	aminoacyl tRNA synthetase complex-interacting multifunctional pr	0006412 // translation // inferred from electronic annotation // 0006915 // apoptotic process // inferred from electronic annotation // 0007275 // multicellular organismal developm
NM_025878	/XNM_00	0.00136003	0.00710923		1.24	1.23	1.18	<b>Mrlp518b</b>	mitochondrial ribosomal protein S18B	0006412 // translation // inferred from electronic annotation // 0032543 // mitochondrial translation // inferred from sequence or structural similarity
NM_001166672	/NM_632E-04		0.00710923		-1.30	-1.07	1.18	<b>Gm10693</b>	predicted pseudogene 10693 // predicted gene 14548 // leukocyte	0001782 // B cell homeostasis // inferred from mutant phenotype // 0002250 // adaptive immune response // inferred from electronic annotation // 0002376 // immune system proc
NM_011339	/XNM_01	0.00829025			1.24	1.18	1.18	<b>Ca22</b>	chemokine (C-C motif) ligand 12 // IC-C motif chemokine 12	0000165 // MAPK cascade // not recorded // 0001525 // angiogenesis // inferred from direct assay // 0002548 // monocyte chemotaxis // inferred from direct assay // 0002548 // m
NM_009174		0.002681195	0.006479654		1.28	1.28	1.18	<b>Slh2</b>	seven in absentia 2	0006511 // ubiquitin-dependent protein catabolic process // inferred from electronic annotation // 0006915 // apoptotic process // not recorded // 0007049 // cell cycle // inferre
NM_008465	/XNM_006527855	/XNM_008590994		0.008590994	1.03	1.19	1.18	<b>Kif4</b>	kinesin family member 4	0000281 // mitotic cytokinesis // not recorded // 0007018 // microtubule-based movement // not recorded // 0008152 // metabolic process // inferred from electronic annotation //
NM_027198		0.009409183			1.11	1.19	1.18	<b>Zswim7</b>	zinc finger SWIM-type containing 7	0007074 // double-strand break repair via homologous recombination // not recorded // 0006281 // DNA repair // inferred from electronic annotation // 0006310 // DNA recombina
NM_023058	/XNM_006524310	/XNM_006524311		0.00785748	-1.01	1.05	1.18	<b>Pkmyt1</b>	protein kinase, membrane associated tyrosine/threonine 1	0004668 // protein phosphorylation // inferred from electronic annotation // 0007049 // cell cycle // inferred from electronic annotation // 0010923 // negative regulation of phosph
NM_178614		0.00855916			1.06	1.30	1.18	<b>Samn50</b>	sorting and assembly machinery component 50 homolog (S. cerevi	0031038 // mitochondrial respiratory chain complex assembly // not recorded // 0004207 // cristae formation // not recorded // 0045040 // protein import into mitochondrial or
NM_001253883	/NM_011099	/XNM_001558087		0.001558087</						



RefSeq	Transcript ID	p (24h n=460)	p (48h n=657)	p (72h n=805)	FC 24h	FC 48h	FC 72h	Gene Symbol	Gene Title	Gene Ontology Biological Process
NM_001163290//NM_023341//XM_008151176					-1.04	-1.19	1.01	<b>Adck3</b>	aarF domain containing kinase 3	0006744 // ubiquinone biosynthetic process // not recorded//0016310 // phosphorylation // not recorded
NM_009008					-1.32	1.06	-1.01	<b>Rac2</b>	RAS-related C3 botulinum substrate 2	0006935 // chemotaxis // inferred from direct assay//0007015 // actin filament organization // not recorded//0007186 // G-protein coupled receptor signaling pathway // inferred f
NM_016974//XM_00_1.81E-04					-1.94	-1.29	-1.02	<b>Ddbp</b>	D site albumin promoter binding protein	0011889 // liver development // inferred from electronic annotation//0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 // regulation of tra
NM_013559//XM_0065049191//XM_0004626031					1.03	-1.90	-1.02	<b>Hsp1h</b>	heat shock 105kDa/110kDa protein 1	0006986 // response to unfolded protein // traceable author statement//0043524 // negative regulation of neuron apoptotic process // traceable author statement//0045345 // po
NM_013560					-1.54	-1.96	-1.05	<b>Hspb1</b>	heat shock protein 1	0011895 // retina homeostasis // inferred from electronic annotation//0006469 // negative regulation of protein kinase activity // inferred from direct assay//0006986 // response t
NM_145459	3.63E-04				-1.32	-1.04	-1.05	<b>Zfp503</b>	zinc finger protein 503	0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 // negative regulation of transcription, DNA-templated // inferred from electronic annotation//000
NM_029809					-1.05	-1.21	-1.05	<b>Rnf225</b>	ring finger protein 225	0051973 // positive regulation of telomerase activity // not recorded
NM_145562					1.02	-1.20	-1.05	<b>Parm1</b>	prostate androgen-regulated mucin-like protein 1	0002227 // innate immune response in mucosa // not recorded//0006334 // nucleosome assembly // not recorded//0019731 // antibacterial humoral response // not recorded//0
NM_001097979//NM_000617165					-1.44	-1.48	-1.06	<b>Hist1h2bc//Hist1h2be//Hist1h</b>	histone cluster 1, H2bc/histone cluster 1, H2be//histone cluster	0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 // regulation of transcription, DNA-templated // inferred from electronic annotation//000
NM_001302338//NM_000452163					-1.17	-1.11	-1.06	<b>Nfe2l3</b>	nucleic factor, erythroid derived 2	0007155 // cell adhesion // inferred from electronic annotation//0019221 // cytokine-mediated signaling pathway // inferred from electronic annotation//0030593 // neutrophil ch
NM_001252651//NM_9.84E-04					-1.25	-1.13	-1.06	<b>Csf3r</b>	colony stimulating factor 3 receptor (granulocyte)	0002329 // pre-B cell differentiation // inferred from mutant phenotype//0006810 // transport // inferred from electronic annotation//0006811 // ion transport // inferred from ele
NM_177725	0.00192245				-1.15	-1.13	-1.06	<b>ErbB2</b>	leucine rich repeat containing 2	0001889 // liver development // inferred from electronic annotation//0001934 // positive regulation of protein phosphorylation // inferred from mutant phenotype//0006351 // tra
NM_001003817	0.00473034				-1.21	-1.18	-1.07	<b>Igf1</b>	immunoglobulin kappa chain complex	0006898 // receptor-mediated endocytosis // --//0006910 // phagocytosis, recognition // --//0006911 // phagocytosis, engulfment // --//0006958 // complement activation, clas
NM_026065//XM_006516946					1.04	-1.28	-1.07	<b>Cap2</b>	CAP, adenylate cyclase-associated protein, 2 (yeast)	0009092 // cell morphogenesis // inferred from electronic annotation//0007010 // cytoskeleton organization // inferred from electronic annotation
NM_009621	0.00628537				1.34	-1.03	-1.07	<b>Adamts1</b>	a disintegrin-like and metalloproteinase (reprolysin type) with throm	0001542 // ovulation from ovarian follicle // inferred from mutant phenotype//0001822 // kidney development // inferred from mutant phenotype//0006508 // proteolysis // infer
NM_008610//NM_006530751					-1.11	-1.27	-1.08	<b>Mmp2</b>	matrix metalloproteinase 2	0001525 // angiogenesis // inferred from electronic annotation//0001542 // ovarian follicle development // not recorded//0001666 // response to hypoxia // inferred from direct a
NM_001160215//NM_000949219					-1.14	-1.18	-1.08	<b>Fcrla</b>	Fc receptor-like A	0003154 // cell differentiation // inferred from electronic annotation
NM_031172//NM_17_000359042					-1.25	-1.07	-1.08	<b>Hist3h2a//Trim17</b>	histone cluster 3, H2a//tripeptide motif-containing 17	0006325 // chromatin organization // not recorded//0006337 // nucleosome disassembly // not recorded//0006342 // chromatin silencing // not recorded//0006914 // autophagy
NM_025828					-1.13	-1.22	-1.08	<b>Lman2</b>	lectin, mannose-binding 2	0006810 // transport // inferred from electronic annotation//0006890 // retrograde vesicle-mediated transport, Golgi to ER // not recorded//0015031 // protein transport // infer
NM_054094//XM_00_000566332					1.28	-1.02	-1.08	<b>AcsM1</b>	acyl-CoA synthetase medium-chain family member 1	0006629 // lipid metabolic process // inferred from electronic annotation//0006631 // fatty acid metabolic process // inferred from electronic annotation//0006633 // fatty acid bio
NM_008584	0.00111336				-1.28	-1.19	-1.09	<b>Meox2</b>	mesenchyme homeobox 2	0001525 // angiogenesis // inferred from mutant phenotype//0001757 // somitite specification // inferred from genetic interaction//0006351 // transcription, DNA-templated // infer
NM_001316360//NM_6.01E-04					-1.31	1.02	-1.09	<b>Bmp4</b>	bone morphogenetic protein 4	0001022 // negative regulation of transcription from RNA polymerase II promoter // inferred from direct assay//0000122 // negative regulation of transcription from RNA polymer
NM_001013392//NM_000130643					-1.20	-1.11	-1.09	<b>Rreb1</b>	RAS responsive element binding protein 1	0001022 // negative regulation of transcription from RNA polymerase II promoter // inferred from mutant phenotype//0001022 // negative regulation of transcription from RNA pol
NM_001005846//NM_0004561					-1.23	-1.15	-1.09	<b>Mcoln2</b>	mucoilin 2	0006810 // transport // inferred from electronic annotation//0006811 // ion transport // inferred from electronic annotation
NM_001111043//NM_001111044//4.20E-04					-1.24	-1.65	-1.09	<b>Serpinh1</b>	serine (or cysteine) peptidase inhibitor, clade H, member 1	0003433 // chondrocyte development involved in endochondral bone morphogenesis // inferred from mutant phenotype//0010951 // negative regulation of endopeptidase activity ,
NM_008788//XM_006504558					-1.07	-1.28	-1.10	<b>Poace</b>	procollagen C-endopeptidase enhancer protein	0006508 // proteolysis // inferred from direct assay//0010952 // positive regulation of peptidase activity // not recorded
NM_019564	0.001425422				-1.19	-1.30	-1.10	<b>Htra1</b>	HtrA serine peptidase 1	0011558 // regulation of cell growth // inferred from electronic annotation//0001890 // placenta development // inferred from mutant phenotype//0006508 // proteolysis // inferri
NM_010882	0.009879425				-1.04	-1.27	-1.10	<b>Ndn</b>	necladin	0001764 // neuron migration // inferred from mutant phenotype//0003016 // respiratory system process // inferred from mutant phenotype//0006351 // transcription, DNA-templ
NM_028044	0.005925631				-1.01	-1.21	-1.10	<b>Cnn3</b>	calponin 3, acidic	0003855 // epithelial cell differentiation // inferred from electronic annotation//0031032 // actomyosin structure organization // inferred from electronic annotation//0032780 // n
NM_015786	3.87E-04				-1.38	-1.08	-1.10	<b>Hist1h1c</b>	histone cluster 1, H1c	0000122 // negative regulation of transcription from RNA polymerase II promoter // inferred from genetic interaction//0006334 // nucleosome assembly // inferred from electronic ;
NM_007464//XM_00_000106683					1.25	1.05	-1.11	<b>Birc3</b>	baculoviral IAP repeat-containing 3	0006915 // apoptotic process // inferred from electronic annotation//0016567 // protein ubiquitination // not recorded//0003198 // positive regulation of protein ubiquitination//000
NM_022319//XM_006511334					-1.05	-1.19	-1.11	<b>Cstn2</b>	calsyn2	0011575 // cell adhesion // inferred from electronic annotation//0007156 // homophilic cell adhesion via plasma membrane adhesion molecules // inferred from electronic annotati
NM_009789	0.009267952				-1.07	-1.26	-1.11	<b>S100g</b>	S100 calcium binding protein G	0000187 // activation of MAPK activity // inferred from direct assay//0007165 // signal transduction // inferred from electronic annotation//0007186 // G-protein coupled receptor
NM_001290486//NM_010336//NM_003096117					1.03	-1.22	-1.11	<b>Lpar1</b>	lysophosphatidic acid receptor 1	0002836 // glomerular basement membrane development // inferred from mutant phenotype//0032836 // glomerular basement membrane development // not recorded
NM_007735//NM_01_000484402					-1.24	-1.27	-1.11	<b>Col4a4</b>	collagen, type IV, alpha 4	0006839 // mitochondrial transport // not recorded//0035865 // cellular response to potassium ion // not recorded//0043653 // mitochondrial fragmentation involved in apoptotic
NM_008730	0.003843463				-1.13	-1.25	-1.11	<b>Nptx1</b>	neuronal pentraxin 1	0000122 // negative regulation of transcription from RNA polymerase II promoter // inferred from direct assay//0006351 // transcription, DNA-templated // inferred from electronic
NM_001008542//NM_8.43E-05					-1.20	-1.03	-1.11	<b>Mx1</b>	MAX interactor 1, dimerization protein	0001606 // immunoglobulin mediated immune response // inferred from mutant phenotype//0016446 // somatic hypermutation of immunoglobulin genes // inferred from mutant c
NM_010104	0.008150942				-1.12	-1.43	-1.12	<b>Edn1</b>	endothelin 1	0000122 // negative regulation of transcription from RNA polymerase II promoter // not recorded//0011501 // skeletal system development // inferred from mutant phenotype//000
NM_020581	0.00779299				1.29	1.02	-1.12	<b>Angrp14</b>	angiotensin-like 4	0001525 // angiogenesis // inferred from electronic annotation//0001666 // response to hypoxia // inferred from electronic annotation//0003267 // cellular response to starvation,
NM_053195//XM_006500452					-1.05	-1.18	-1.12	<b>Slc24a3</b>	solute carrier family 24 (sodium/potassium/calcium exchanger), m	0001189 // liver development // inferred from electronic annotation//0006811 // ion transport // inferred from electronic annotation//0006812 // cation transport // not recorded//00068
NM_020495//NM_178235//NM_0C_000757671					-1.09	-1.19	-1.12	<b>Slc1b2</b>	solute carrier organic anion transporter family, member 1b2	0001889 // liver development // inferred from electronic annotation//0006810 // transport // inferred from electronic annotation//0006811 // ion transport // inferred from electr
NM_008626//XM_006532406					-1.08	-1.37	-1.12	<b>Mrc2</b>	mannose receptor, C type 2	0001649 // osteoblast differentiation // not recorded//0006897 // endocytosis // inferred from electronic annotation//0003074 // collagen catabolic process // not recorded
NM_001285812//NM_000613731					-1.16	-1.08	-1.13	<b>Tmem53</b>	transmembrane protein 53	0000122 // negative regulation of transcription from RNA polymerase II promoter // not recorded//0005978 // glycogen biosynthetic process // inferred from mutant phenotype//0
NM_145434	2.70E-05				-1.80	-1.38	-1.13	<b>Nr1d1</b>	nuclear receptor subfamily 1, group D, member 1	0043086 // negative regulation of catalytic activity // inferred from electronic annotation
NM_013712//XM_011247596//XM_000813078					-1.05	-1.21	-1.13	<b>Itg1b1p2</b>	integrin beta 1 binding protein 2	0000724 // double-strand break repair via homologous recombination // inferred from sequence or structural similarity//0000737 // DNA catabolic process, endonucleolytic // not r
NM_00103257//NM_001195065//NM_00819721					1.00	-1.25	-1.13	<b>Phactr2</b>	phosphatase and actin regulator 2	0006613 // cotranslational protein targeting to membrane // inferred from direct assay
NM_015792//XM_006497505//XM_0007663231					-1.12	-1.18	-1.13	<b>Fbxo18</b>	F-box protein 18	0016055 // Wnt signaling pathway // inferred from electronic annotation//0016567 // protein ubiquitination // not recorded//0003178 // negative regulation of Wnt signaling path
NM_019419	0.0097243				-1.16	-1.21	-1.13	<b>Ar1p61</b>	ADP-ribosylation factor-like 6 interacting protein 1	0010977 // negative regulation of neuron projection development // inferred from genetic interaction//0014043 // negative regulation of neuron maturation // inferred from genetic
NM_172448//XM_00_000818185					-1.21	-1.11	-1.13	<b>Rnf43</b>	ring finger protein 43	
NR_028264	0.002430072				-1.21	-1.33	-1.13	<b>Dreu2</b>	deleted in lymphocytic leukemia, 2	
NM_027416	0.00471647				1.17	-1.03	-1.13	<b>Calm13</b>	calmodulin-like 3	
NM_001099308//NM_001099349//NM_006185873					-1.04	-1.31	-1.13	<b>Gm11007//Gm14308//Gm143</b>	predicted gene 11007//predicted gene 14308//predicted gene 1	0006355 // regulation of transcription, DNA-templated // inferred from electronic annotation
NM_001042605//NM_000685659					-1.28	-1.22	-1.13	<b>Cd74</b>	CD74 antigen (invariant polypeptide of major histocompatibility co	0000187 // activation of MAPK activity // not recorded//0001516 // prostaglandin biosynthetic process // not recorded//0001961 // positive regulation of cytokine-mediated sign
NM_013912	0.006826226				-1.05	-1.24	-1.13	<b>Apln</b>	apelin	0002026 // regulation of the force of heart contraction // not recorded//0007165 // signal transduction // inferred from electronic annotation//0007186 // G-protein coupled recep
NM_029436//XM_00_000648036					-1.18	-1.11	-1.14	<b>Klhl24</b>	kelch-like 24	0016567 // protein ubiquitination // not recorded//200312 // regulation of kainate selective glutamate receptor activity // inferred from electronic annotation
NM_010217	0.00849896				1.35	1.03	-1.14	<b>Ctcf</b>	connective tissue growth factor	0001502 // cartilage condensation // inferred from direct assay//0001503 // ossification // inferred from mutant phenotype//0001525 // angiogenesis // inferred from direct assay,
NM_001122892//NM_000254945					-1.18	-1.30	-1.14	<b>Fyn</b>	Fyn proto-oncogene	0001764 // neuron migration // inferred from genetic interaction//0001764 // neuron migration // inferred from mutant phenotype//0002250 // adaptive immune response // infer
NM_001276383//NM_153060//XM_5.97E-04					-1.11	-1.37	-1.14	<b>Spns2</b>	spinster homolog 2	0001782 // B cell homeostasis // inferred from mutant phenotype//0002260 // lymphocyte homeostasis // inferred from mutant phenotype//0002920 // regulation of humoral imm
NM_011948//XM_006523329					-1.10	-1.18	-1.14	<b>Mkp3k4</b>	mitogen-activated protein kinase kinase kinase 4	0000165 // MAPK cascade // not recorded//0000186 // activation of MAPK activity // not recorded//0000187 // activation of MAPK activity // not recorded//0001890 // placenta
NM_172398//XM_00_000854638					-1.19	-1.10	-1.14	<b>Akr1b10</b>	aldo-keto reductase family 1, member B10 (aldose reductase)	00055114 // oxidation-reduction process // inferred from electronic annotation
NM_013737//XM_00_000645464					-1.14	-1.04	-1.14	<b>Pis2g7</b>	phospholipase A2, group VII (platelet-activating factor acetylhydro	0006629 // lipid metabolic process // inferred from electronic annotation//0006954 // inflammatory response // traceable author statement//0016042 // lipid catabolic process // h
NM_010391//NM_01_00016031					-1.24	-1.18	-1.14	<b>H2-Q10</b>	histocompatibility 2, Q region locus 10	0002376 // immune system process // inferred from electronic annotation//0002474 // antigen processing and presentation of peptide antigen via MHC class II // not recorded//000
NM_021534	0.00343374				-1.19	-1.13	-1.14	<b>Pmp4</b>	peroxisomal membrane protein 4	
NM_007903	0.004087877				-1.05	-1.22	-1.14	<b>Edn3</b>	endothelin 3	0001755 // neural crest cell migration // inferred from mutant phenotype//0002690 // positive regulation of leukocyte chemotaxis // not recorded//0003100 // regulation of system
NM_001163640//NM_000511251					1.21	1.06	-1.14	<b>Chn2</b>	chimerin 2	0007165 // signal transduction // inferred from electronic annotation//0035556 // intracellular signal transduction // inferred from electronic annotation//0043547 // positive regul
NM_001122899//NM_010704//NM_009543374					-1.10	-1.28	-1.15	<b>Lepr</b>	leptin receptor	0001525 // angiogenesis // not recorded//0007165 // signal transduction // traceable author statement//0007186 // G-protein coupled receptor signaling pathway // not recorded,
NM_001281852//NM_3.36E-04					-2.85	-1.69	-1.15	<b>S100a9</b>	S100 calcium binding protein A9 (calgranulin B)	0002376 // immune system process // inferred from electronic annotation//0002523 // leukocyte migration involved in inflammatory response // not recorded//0002544 // chronic
NM_008520//XM_00_000353953					-1.22	-1.29	-1.15	<b>Ltbp3</b>	latent transforming growth factor beta binding protein 3	0001501 // skeletal system development // inferred from mutant phenotype//0007179 // transforming growth factor beta receptor signaling pathway // inferred from mutant pheno
NM_025785//XM_00_000447636					-1.16	-1.12	-1.15	<b>Fbxo25</b>	F-box protein 25	0016567 // protein ubiquitination // inferred from direct assay
NM_133351//XM_00_000308314					-1.25	-1.08	-1.15	<b>Prss8</b>	protease, serine 8 (prostinin)	0001942 // hair follicle development // inferred from mutant phenotype//0006508 // proteolysis // inferred from electronic annotation//0010765 // positive regulation of sodium ic
NM_001048054//NM_1.99E-04					1.28	1.13	-1.15	<b>Dusp16</b>	dual specificity phosphatase 16	0000188 // inactivation of MAPK activity // inferred from direct assay//0006470 // protein dephosphorylation // not recorded//0016310 // phosphorylation // inferred from electro
NM_012026//XM_00_000298236					-1.22	-1.19	-1.15	<b>Arhgef28</b>	Rho guanine nucleotide exchange factor (GEF) 28	0021955 // central nervous system neuron axonogenesis // inferred from mutant phenotype//0003154 // cell differentiation // inferred from electronic annotation//00035023 // reg
NM_001159329//NM_025332//NM_00630718					-1.15	-1.27	-1.15	<b>Gtppb8</b>	GTP-binding protein 8 (putative)	0000917 // barrier septum assembly // inferred from electronic annotation
NM_152895//XM_01_000348007					-1.18	-1.22	-1.16	<b>Kdms5b</b>	lysine (K)-specific demethylase 5B	0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 // regulation of transcription, DNA-templated // inferred from electronic annotation//000
NM_001164059//NM_0009107					-1.15	-1.16	-1.16	<b>Sell</b>	selectin, lymphocyte	0007155 // cell adhesion // inferred from electronic annotation//003198 // response to ATP // inferred from direct assay//0004201 // response to oleic acid // inferred from electr
NM_025786	0.00187184				-1.30	-1.24	-1.16	<b>Rnf186</b>	ring finger protein 186	
NM_001201413//NM_001201414//NM_0016										

RefSeq	Transcript ID	p (24h n=460)	p (48h n=657)	p (72h n=805)	FC 24h	FC 48h	FC 72h	Gene Symbol	Gene Title	Gene Ontology Biological Process	
NM_001081309	//NM_00589131				-1.15	-1.12	-1.17	<b>Pik3r4</b>	phosphatidylinositol 3 kinase, regulatory subunit, poly peptide 4, p1	0006468 // protein phosphorylation // not recorded // 0006623 // protein targeting to vacuole // not recorded // 0016236 // macroautophagy // not recorded // 0016310 // phospho	
NM_001304475	//NM_145446//NM_175337//Xv				-1.10	-1.06	-1.17	<b>Mh3</b>	muti homology 3 (E coli)	0006298 // mismatch repair // inferred from genetic interaction // 0006298 // mismatch repair // inferred from mutant phenotype // 0006974 // cellular response to DNA damage str	
NM_001033127	//NM_001111011//NM_177311//				1.04	-1.04	-1.17	<b>Serac1</b>	serine activator site containing 1	0006629 // lipid metabolic process // inferred from electronic annotation // 0008654 // phospholipid biosynthetic process // inferred from electronic annotation // 0030198 // extrac	
NM_0169177	//XM_00081068				-1.15	-1.10	-1.17	<b>Slc40a1</b>	serine carrier family 40 (iron-regulated transporter), member 1	0006269 // lymphocyte homeostasis // inferred from mutant phenotype // 0003158 // endothelium development // inferred from mutant phenotype // 0006810 // transport // inf	
NM_008729	//XM_006520032//XM_0007134052				-1.03	-1.23	-1.17	<b>Ctndd2</b>	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 // regu	
NM_011812	//XM_006515864//XM_006529001//				-1.13	-1.44	-1.17	<b>Fbln5</b>	fibulin 5	0001755 // regulation of cell growth // inferred from electronic annotation // 0007155 // cell adhesion // inferred from electronic annotation // 0003198 // extracellular matrix organi	
NM_001114385	//NM_031258//XM_006529001//				0.00810582	-1.04	1.01	<b>Chrd1l</b>	chordin-like 1	0001503 // ossification // inferred from electronic annotation // 0001654 // eye development // not recorded // 0001709 // cell fate determination // not recorded // 0007275 // muli	
NM_133858	//NM_19_000886008				-1.15	-1.11	-1.17	<b>Fam36a</b>	family with sequence similarity 63, member A		
NM_001290745	//NM_016965//XM_006499881//				0.00861665	-1.07	-1.13	<b>Nckap1</b>	NCK-associated protein 1	0001701 // in utero embryonic development // inferred from mutant phenotype // 0001756 // somitogenesis // inferred from mutant phenotype // 0001843 // neural tube closure //	
NM_001146275	//NM_00288293				-1.69	-1.31	-1.17	<b>Interf</b>	interferon inducible GTPase 1	0002376 // immune system process // inferred from electronic annotation // 0008152 // metabolic process // inferred from electronic annotation // 0010506 // regulation of autoph	
NM_011657	//XM_006505909//XR_0008048018				0.0065621	-1.06	-1.17	<b>Tulp3</b>	tubby-like protein 3	0001841 // neural tube formation // inferred from mutant phenotype // 0001843 // neural tube closure // inferred from mutant phenotype // 0007275 // multicellular organismal dev	
NM_015732	//XM_00_0009297946				-1.18	-1.17	-1.17	<b>Axin2</b>	axin2	0001756 // somitogenesis // inferred from direct assay // 0001934 // positive regulation of protein phosphorylation // not recorded // 0001957 // intramembranous ossification // inf	
NM_001081300	//NM_00730591				-1.15	-1.19	-1.18	<b>Tshz1</b>	teashirt zinc finger family member 1	0006351 // transcription, DNA-templated // inferred from electronic annotation // 0006355 // regulation of transcription, DNA-templated // inferred from electronic annotation // 000	
NM_051385	//XM_011247883				0.00667963	-1.02	-1.15	<b>Col4a6</b>	collagen, type IV, alpha 6	0003198 // extracellular matrix organization // inferred from direct assay // 0071230 // cellular response to amino acid stimulus // inferred from direct assay	
NM_010453	5_74E-05 001072674				-1.48	-1.43	-1.18	<b>Hoxa5</b>	homeobox A5	001150 // skeletal system development // inferred from mutant phenotype // 0002009 // morphogenesis of an epithelium // inferred from mutant phenotype // 0003016 // respirat	
NM_001079824	//XM_00457865 006742058				-1.18	-1.22	-1.18	<b>Hnrnp3</b>	heterogeneous nuclear ribonucleoprotein H3	0030855 // epithelial cell differentiation // inferred from electronic annotation	
NM_00117773	//NM_001177774//NM_080428//				0.00759114	-1.05	-1.13	<b>Fbxw7</b>	F-box and WD-40 domain protein 7	0001570 // vasculogenesis // inferred from mutant phenotype // 0001944 // vasculature development // traceable author statement // 0006355 // regulation of transcription, DNA-te	
NM_007792	0.00960092				1.01	1.11	-1.18	<b>Csrp2</b>	cysteine and glycine-rich protein 2	0007275 // multicellular organismal development // inferred from electronic annotation // 0030154 // cell differentiation // inferred from electronic annotation // 0045445 // myobla	
NM_029738	//XM_006522701//NM_006522702//				0.00654555	-1.02	-1.15	<b>Ctup1</b>	clustern associated protein 1	0001843 // neural tube closure // inferred from mutant phenotype // 0001947 // heart looping // inferred from mutant phenotype // 0007224 // smoothed signaling pathway // inf	
NM_001313939	//NM_3_58E-04				-1.41	-1.27	-1.19	<b>Cd79b</b>	CD79B antigen	0002250 // adaptive immune response // inferred from electronic annotation // 0002376 // immune system process // inferred from electronic annotation // 0007166 // cell surface r	
NM_010706	//XM_006539566				0.00960752	1.01	-1.10	<b>Lgals4</b>	lectin, galactose binding, soluble 4		
NM_001162532	5.10E-04				-1.17	-1.45	-1.19	<b>Fam174b</b>	family with sequence similarity 174, member B		
NM_011748	//NM_178733//XM_006539948//XM				0.00608039	-1.06	-1.12	<b>Zfp14</b>	zinc finger protein 14	0006355 // regulation of transcription, DNA-templated // not recorded	
NM_001306088	//NM_00093547				-1.15	-1.08	-1.19	<b>Dnmbp</b>	dynamid binding protein 1	0030203 // regulation of Rho protein signal transduction // inferred from electronic annotation // 0035556 // intracellular signal transduction // inferred from electronic annotat	
NM_00117778	//NM_001177779//				0.009131226	-1.12	-1.18	<b>Dlg3</b>	discs, large homolog 3 (Drosophila)	0001736 // establishment of planar polarity // inferred from mutant phenotype // 0007268 // synaptic transmission // not recorded // 0007399 // nervous system development // not	
NM_021719	0.00454522				-1.06	-1.17	-1.19	<b>Cldn15</b>	claudin 15	0006810 // transport // inferred from electronic annotation // 0006811 // ion transport // inferred from electronic annotation // 0016338 // calcium-independent cell-cell adhesion vi	
NM_001085515	//XM_00037944				-1.22	-1.19	-1.19	<b>Al64131</b>	expressed sequence A464131	0005975 // carbohydrate metabolic process // inferred from electronic annotation // 0008152 // metabolic process // inferred from electronic annotation // 0043558 // positive regul	
NM_025347	//NM_02_00966351				-1.21	-1.09	-1.19	<b>Ype3</b>	ypocell-like 3 (Drosophila)	0006915 // apoptotic process // inferred from electronic annotation // 2000774 // positive regulation of cellular senescence // not recorded	
NM_001136076	//NM_011031//XM_0001857876				-1.22	-1.37	-1.19	<b>P4ha2</b>	procollagen-proline, 2-oxoglutarate 4-dioxygenase (proline 4-hydr	0018401 // peptidyl-proline hydroxylation to 4-hydroxy-L-proline // inferred from direct assay // 0055114 // oxidation-reduction process // inferred from electronic annotation	
NM_133238	0.00948798 0.006270198				-1.18	-1.43	-1.19	<b>Cd20a</b>	CD20a antigen	0006897 // endocytosis // inferred from electronic annotation // 0010468 // regulation of gene expression // not recorded // 0003193 // regulation of blood coagulation // not record	
NM_010225	0.00195853 0.004991675				-1.22	-1.23	-1.19	<b>Foxj2</b>	forkhead box F2	0006351 // transcription, DNA-templated // inferred from electronic annotation // 0006355 // regulation of transcription, DNA-templated // inferred from electronic annotation // 000	
NM_001285446	//NM_09823//NM_172860//Xv				0.00982678	-1.00	-1.15	<b>Cbfa2i2</b>	core-binding factor, runt domain, alpha subunit 2, translocated to,	0006351 // transcription, DNA-templated // inferred from electronic annotation // 0006355 // regulation of transcription, DNA-templated // inferred from electronic annotation // 00	
NM_033373	0.00622604				-1.17	-1.12	-1.19	<b>Krt23</b>	keratin 23		
NM_001109988	//NM_001109989//				0.003853193	-1.15	-1.49	<b>Nrep</b>	neuronal regeneration related protein	0017015 // regulation of transforming growth factor beta receptor signaling pathway // inferred from direct assay // 0031103 // axon regeneration // inferred from electronic annotat	
NM_020608	//XM_006524699//XM_006524702//				0.00983801	-1.02	-1.17	<b>Cramp1l</b>	Crn, cramped-like (Drosophila)		
NM_008984	//XM_006523864//XM_0002538469				-1.04	-1.29	-1.19	<b>Ptprm</b>	protein tyrosine phosphatase, receptor type, M	0001937 // negative regulation of endothelial cell proliferation // not recorded // 0006470 // protein dephosphorylation // not recorded // 0007155 // cell adhesion // inferred from el	
NM_022814	0.0088749				1.05	-1.01	-1.19	<b>Svep1</b>	sushi, von Willebrand factor type A, EGF and pentraxin domain con	0007155 // cell adhesion // inferred from electronic annotation	
NM_0119306	0.00771691				-1.03	-1.04	-1.19	<b>Adamts8</b>	a disintegrin-like and metalloproteinase (reprolysin type) with throm	0006508 // proteolysis // inferred from electronic annotation	
NM_007655	0.00117669				-1.50	-1.32	-1.19	<b>Cd79a</b>	CD79A antigen (immunoglobulin-associated alpha)	0002250 // adaptive immune response // inferred from electronic annotation // 0006355 // immune system process // inferred from electronic annotation // 0007166 // cell surface r	
NM_001167884	//NM_001167885//NM_0011678				0.00577843	-1.05	-1.12	<b>Suv420h1</b>	suppressor of variegation 4-20 homolog 1 (Drosophila)	0006351 // transcription, DNA-templated // inferred from electronic annotation // 0006355 // regulation of transcription, DNA-templated // inferred from electronic annotation // 000	
NM_011020	//XM_006500766//NM_002094866				-1.23	-1.78	-1.20	<b>Hspad1</b>	heat shock protein 4 like	0006457 // protein folding // not recorded // 0006886 // response to unfolded protein // not recorded	
NM_009061	0.00943916				-1.12	-1.32	-1.20	<b>Rgs2</b>	regulator of G-protein signaling 2	0006471 // regulation of translation // inferred from electronic annotation // 0007049 // cell cycle // inferred from electronic annotation // 0007186 // G-protein coupled receptor sig	
NM_001285793	//NM_019804//XM_0009403271				-1.10	-1.35	-1.20	<b>Bqalnt4</b>	UDP-Gal-beta-GlcNAc beta 1,4-galactosyltransferase, poly peptide 4	0005975 // carbohydrate metabolic process // inferred from electronic annotation // 0006486 // protein glycosylation // inferred from electronic annotation	
NM_007533	//XM_006539486//XR_881644				0.00936886	-1.15	1.04	<b>Bdkha</b>	branched chain ketocacid dehydrogenase E1, alpha polypeptide	0007584 // response to nutrient // inferred from electronic annotation // 0008152 // metabolic process // inferred from electronic annotation // 0009083 // branched-chain amino ac	
XM_357640	//XM_99_4.71E-05				-1.46	1.03	-1.20	<b>Igk-v28//Igkc//Igk1//Igkv1</b>	immunoglobulin kappa chain variable 28 (V28) // immunoglobulin	0006898 // receptor-mediated endocytosis // not recorded // 0006910 // phagocytosis, recognition // not recorded // 0006911 // phagocytosis, engulfment // not recorded // 000695	
NM_008256	0.00476513				-1.12	-1.02	-1.20	<b>Hmgcs2</b>	3-hydroxy-3-methylglutaryl-Coenzyme A synthase 2	0008122 // kidney development // inferred from electronic annotation // 0001889 // liver development // inferred from electronic annotation // 0006629 // lipid metabolic process //	
NM_023799	//XM_01_000745062				-1.16	-1.34	-1.20	<b>Mgea5</b>	meningioma expressed antigen 5 (hyaluronidase)	0006044 // N-acetylglucosamine metabolic process // not recorded // 0006517 // protein deglycosylation // not recorded // 0006612 // protein targeting to membrane // not record	
NM_013905	0.00369991				-1.43	1.11	-1.20	<b>Heyl</b>	hairly/enhancer-of-split related with YRPW motif-like	0003151 // outflow tract morphogenesis // inferred from genetic interaction // 0003181 // atrioventricular valve morphogenesis // inferred from genetic interaction // 0003184 // pul	
NM_001302559	//NM_000129079 0.008755075				-1.44	-1.01	-1.20	<b>Igkv1//Iglc1</b>	immunoglobulin lambda variable 1 // immunoglobulin lambda constant 1		
NM_148938	0.00913573				-1.08	-1.14	-1.20	<b>Slc1a3</b>	solute carrier family 1 (glial high affinity glutamate transporter), m	0002230 // positive regulation of defense response to virus by host // not recorded // 0006536 // glutamate metabolic process // inferred from mutant phenotype // 0006537 // gluta	
NM_001127351	//NM_001177804//NM_022433//				0.00605833	-1.00	-1.09	<b>Sirt3</b>	sirtuin 3	0006476 // protein deacetylation // inferred from direct assay // 0006476 // protein deacetylation // not recorded // 0007568 // aging // inferred from electronic annotation // 00090	
NM_001285917	//NM_029653//NM_005758764				-1.12	-1.24	-1.20	<b>Dapk1</b>	death associated protein kinase 1	0006417 // regulation of translation // inferred from electronic annotation // 0006468 // protein phosphorylation // inferred from direct assay // 0006468 // protein phosphorylation,	
NM_019819	//XM_00_00038857				-1.21	1.07	-1.20	<b>Dusp14</b>	dual specificity phosphatase 14	0001888 // inactivation of MAPK activity // inferred from electronic annotation // 0006470 // protein dephosphorylation // inferred from electronic annotation // 0016311 // dephosp	
NM_018883	//XM_006533760//XM_0002545798				-1.26	-1.30	-1.20	<b>Camk1k</b>	calmodulin/calmodulin-dependent protein kinase kinase 1, alpha	0006468 // protein phosphorylation // inferred from electronic annotation // 0016310 // phosphorylation // inferred from electronic annotation // 0032147 // activation of protein kin	
NM_001102455	//NM_001102456//				-1.08	-1.25	-1.20	<b>Aplp2</b>	amyloid beta (A4) precursor-like protein 2	0001967 // suckling behavior // inferred from genetic interaction // 0006878 // cellular copper ion homeostasis // inferred from mutant phenotype // 0007176 // regulation of epider	
NM_001310659	//NM_008342//XM_0007797964				-1.09	-1.27	-1.20	<b>Igf2bp2</b>	insulin-like growth factor binding protein 2	0001558 // regulation of cell growth // inferred from electronic annotation // 0007165 // signal transduction // inferred from electronic annotation // 0007565 // female pregnancy //	
NM_029869	//NM_133906//XM_00_004646215				-1.05	-1.28	-1.20	<b>Zksan1</b>	zinc finger with KRAB and SCAN domains 1	0006351 // transcription, DNA-templated // inferred from electronic annotation // 0006355 // regulation of transcription, DNA-templated // not recorded	
NM_001162973	//NM_001162974//NM_027053//				0.00608147	1.00	-1.16	<b>Lrrc51</b>	leucine rich repeat containing 51		
NM_010062	0.00931373				-1.11	-1.10	-1.21	<b>Dnase2a</b>	deoxyribonuclease II alpha	0000737 // DNA catabolic process, endonucleolytic // inferred from mutant phenotype // 0006259 // DNA metabolic process // inferred from electronic annotation // 0006308 // DNA	
NM_011782	//XM_011246127				0.00749509	-1.11	-1.14	-1.21	<b>Adamts5</b>	a disintegrin-like and metalloproteinase (reprolysin type) with throm	0006508 // proteolysis // inferred from electronic annotation // 0042742 // defense response to bacterium // inferred from genetic interaction
NM_025510	//XM_006533940				0.00698212	-1.07	-1.14	-1.21	<b>Adpm</b>	ADP-ribose/CDP-alcohol diphosphatase, manganese dependent	0008152 // metabolic process // inferred from electronic annotation
NM_001170537	//NM_00914076				0.00994408	-1.14	-1.27	-1.21	<b>Mef2c</b>	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 pol
NM_001037098	//NM_026495//XM_006498259//				0.00475203	-1.03	-1.04	-1.21	<b>Nucx2</b>	nucleus accumbens associated 2, BEN and BTB (PO2) domain cont	0002885 // negative regulation of cell proliferation // not recorded // 0010608 // posttranscriptional regulation of gene expression // not recorded // 0016575 // histone deacetylato
NM_174847	//XM_006522976//XM_0002111516				-1.02	-1.29	-1.21	<b>Ctcd2</b>	C2 calcium-dependent domain containing 2		
NM_010382	0.002069863				-1.25	-1.28	-1.21	<b>H2-Eb1</b>	histocompatibility 2, class II antigen E beta		
NM_001285928	//NM_001285929//				-1.06	-1.17	-1.21	<b>Ubxn10</b>	UBX domain protein 10	0002376 // immune system process // inferred from electronic annotation // 0002504 // antigen processing and presentation of peptide or polysaccharide antigen via MHC class II // u	
NM_008091	//NM_00_00129949				-1.28	-1.03	-1.21	<b>Gata3</b>	GATA binding protein 3	0000122 // negative regulation of transcription from RNA polymerase II promoter // inferred from direct assay // 0000902 // cell morphogenesis // inferred from mutant phenotype //	
NM_001171147	//NM_009534//XM_0008853333				-1.01	-1.22	-1.21	<b>Yap1</b>	yes-associated protein 1	0000902 // cell morphogenesis // inferred from mutant phenotype // 0001570 // vasculogenesis // inferred from mutant phenotype // 0003143 // embryonic heart tube morphogene	
NM_177775	//XM_006511221//XM_0002958888				0.00655575	-1.14	-1.24	-1.21	<b>Eys13</b>	extended synaptotagmin-like protein 3	0006810 // transport // inferred from electronic annotation // 0006869 // lipid transport // inferred from electronic annotation
NM_009210	//NM_14_000718989				-1.20	-1.15	-1.21	<b>Hrf</b>	heparanase-like transcription factor	0000209 // protein polyubiquitination // inferred from electronic annotation // 0006301 // postreplication repair // inferred from electronic annotation // 0006351 // transcription, DT	
NM_028306	//XM_00_000314892 1.73E-04				-1.39	-1.61	-1.21	<b>Hspa12b</b>	heat shock protein 12B		
NM_001081225	//XM_000284439				1.16	1.02	-1.21	<b>Fam178a</b>	family with sequence similarity 178, member A	0006281 // DNA repair // inferred from electronic annotation // 0006974 // cellular response to DNA damage stimulus // not recorded // 0031334 // positive regulation of protein con	
NM_001013373	//XM_006510132//				0.00191935	-1.08	-1.18	-1.21	<b>Trpmss13</b>	transmembrane protease, serine 13	0006508 // proteolysis // inferred from electronic annotation // 0006898 // receptor-mediated endocytosis // inferred from electronic annotation // 0061436 // establishment of skin
NM_											



RefSeq	Transcript ID	p (24h n=460)	p (48h n=657)	p (72h n=805)	FC 24h	FC 48h	FC 72h	Gene Symbol	Gene Title	Gene Ontology Biological Process	
NM_009811					0.00465104	-1.11	-1.14	<b>-1.27 Casp6</b>	caspase 6	0002525 // acute inflammatory response to non-antigenic stimulus // not recorded // 0006508 // proteolysis // not recorded // 0006508 // proteolysis // inferred from reviewed com	
NM_001290740	//NM_011723	//NM_030560	//NM_00687366		0.00687366	-1.02	-1.08	<b>-1.27 Cwc22</b> // <b>-1.27 Xdh</b>	CWC22 spliceosome-associated protein homolog (S. cerevisiae) //	0000398 // mRNA splicing, via spliceosome // not recorded // 0001933 // negative regulation of protein phosphorylation // not recorded // 0001937 // negative regulation of endothe	
NM_177727	//NM_006500661	//NM_006500618			0.0088671	-1.12	-1.26	<b>-1.27 Lsm14b</b>	LSM14 homolog B (SCD5, S. cerevisiae)	0006417 // regulation of translation // inferred from electronic annotation // 0007275 // multicellular organismal development // inferred from electronic annotation	
NM_002868			0.00951198	0.004995458		-1.20	-1.24	<b>-1.27 Hmx5</b>	homeobox B5	0006351 // transcription, DNA-templated // inferred from electronic annotation // 0006355 // regulation of transcription, DNA-templated // inferred from direct assay // 0006366 // t	
NM_001110009	//NM_00180989					-1.27	-1.06	<b>-1.27 Apoc1</b>	apolipoprotein C-I	0006641 // triglyceride metabolic process // inferred from mutant phenotype // 00006810 // transport // inferred from electronic annotation // 0006869 // lipid transport // inferred fr	
NM_008609			0.00644142			-1.11	-1.27	<b>-1.27 Mmp15</b>	matrix metalloproteinase 15	0006508 // proteolysis // inferred from electronic annotation // 0032355 // response to estradiol // inferred from electronic annotation // 0035987 // endometrial cell differentiation,	
NM_025638	//NM_006533944		0.00152505			-1.08	-1.13	<b>-1.27 Gdpd1</b>	glycerophosphodiester phosphodiesterase domain containing 1	0006071 // glycerol metabolic process // inferred from electronic annotation // 0006629 // lipid metabolic process // inferred from electronic annotation	
NM_027494	//NM_006530457	//NM_011248240			0.00447972	-1.08	-1.12	<b>-1.28 Zcch8</b>	zinc finger, CCHC domain containing 8	0006399 // mRNA processing // inferred from electronic annotation // 0008380 // RNA splicing // inferred from electronic annotation	
NM_001289782	//NM_00497211	2.11E-04				-1.21	-1.38	<b>-1.28 Cryab</b>	crystallin, alpha B	0001666 // response to hypoxia // inferred from mutant phenotype // 0002088 // lens development in camera-type eye // inferred from genetic interaction // 0006457 // protein fold	
NM_153198	//NM_17	0.00377578				-1.35	-1.27	<b>-1.28 Hbp1</b>	high mobility group box transcription factor 1	0006351 // transcription, DNA-templated // inferred from electronic annotation // 0006355 // regulation of transcription, DNA-templated // inferred from electronic annotation // 000	
NM_001161763	//NM_001161765	//NM_010232			0.00104899	-1.06	-1.11	<b>-1.28 Fmo5</b>	flavin containing monooxygenase 5	0017144 // drug metabolic process // not recorded // 00055114 // oxidation-reduction process // not recorded	
NM_001166597	//NM_00052117		0.00395366			-1.20	-1.23	<b>-1.28 Dgkz</b>	diacylglycerol kinase zeta	0007205 // protein kinase C-activating G-protein coupled receptor signaling pathway // inferred from electronic annotation // 0016310 // phosphorylation // not recorded // 0031571	
NM_001311122	//NM_00602292		0.00578565			-1.22	-1.12	<b>-1.28 Lrrc16a</b>	leucine rich repeat containing 16A	0016477 // cell migration // not recorded // 0030032 // lamellipodium assembly // not recorded // 0030335 // positive regulation of cell migration // inferred from mutant phenotype	
NM_011902			0.00161931			-1.03	-1.03	<b>-1.28 Tek2</b>	tek2n 2	0030030 // cell projection organization // inferred from electronic annotation // 0030317 // sperm motility // inferred from mutant phenotype // 0036159 // inner dynein arm assem	
NM_001025432	//NM_006521751		5.33E-04			-1.01	-1.34	<b>-1.28 Crebbp</b>	CREB binding protein	0001222 // negative regulation of transcription from RNA polymerase I promoter // not recorded // 0006351 // transcription, DNA-templated // inferred from electronic annotation // 0001525 // angiogenesis // inferred from electronic annotation // 0001938 // positive regulation of endothelial cell proliferation // not recorded // 0002376 // immune system process	
NM_000858	//NM_006515566		8.40E-05			0.00187625	-1.08	-1.50	<b>-1.28 Prkd1</b>	protein kinase D1	0001503 // ossification // inferred from electronic annotation // 0001525 // angiogenesis // inferred from electronic annotation // 0001938 // positive regulation of endothelial cell pr
NM_001252653	//NM_007895	//NM_006500984			0.00565337	-1.09	-1.06	<b>-1.28 Ecm1</b>	extracellular matrix protein 1	0001503 // ossification // inferred from electronic annotation // 0001525 // angiogenesis // inferred from electronic annotation // 0001938 // positive regulation of endothelial cell pr	
NM_001093149	//NM_001285885	//NM_006968951				-1.15	-1.34	<b>-1.28 Gm12942</b> // <b>-1.28 Zmym6</b>	predicted gene 12942 // zinc finger, MYM-type 6 cytochrome P450, family 2, subfamily d, polypeptide 22	0007010 // cytoskeletal organization // not recorded // 0002260 // regulation of cell morphogenesis // not recorded // 0001503 // positive regulation of endothelial cell pr	
NM_001163472	//NM_019823		0.00457534			-1.08	-1.11	<b>-1.28 Cyp2d2</b>	cytochrome P450, family 2, subfamily d, polypeptide 22	0006805 // xenobiotic metabolic process // not recorded // 0007565 // female pregnancy // inferred from electronic annotation // 0010033 // response to organic substance // infer	
NM_025933			0.00291985			-1.02	-1.04	<b>-1.28 Higd2a</b>	HIG1 domain family, member 2A	0006810 // transport // inferred from electronic annotation // 0043066 // negative regulation of apoptotic process // not recorded // 0005114 // oxidation-reduction process // infer	
NM_009780	//NM_006523531	//NM_006523532			0.00130037	-1.03	-1.07	<b>-1.29 Cab1</b> // <b>-1.29 LOC102643089</b>	complement component 4B (Chido blood group) // complement C	0002376 // immune system process // inferred from electronic annotation // 0006954 // inflammatory response // inferred from electronic annotation // 0006956 // complement act	
NM_001313757	//NM_007397	//NM_006511925			0.00400254	-1.07	-1.22	<b>-1.29 Acriv2b</b>	actin receptor IB	0000122 // negative regulation of transcription from RNA polymerase I promoter // not recorded // 0001501 // skeletal system development // inferred from genetic interaction // OC	
NM_001291903	//NM_009623	//NM_006520319			0.00774957	<b>1.02</b>	-1.09	<b>-1.29 Adcy8</b>	adenylyate cyclase 8	0006171 // cAMP biosynthetic process // not recorded // 0007189 // adenylyate cyclase-activating G-protein coupled receptor signaling pathway // not recorded // 0007193 // adenyly	
NM_007881			7.89E-04			-1.03	-1.01	<b>-1.29 Atn1</b>	atrophin 1	0000122 // negative regulation of transcription from RNA polymerase I promoter // inferred from direct assay // 0000122 // negative regulation of transcription from RNA polymer	
NM_011401	//NM_006505822	//NM_006525647			0.0021223	-1.15	-1.26	<b>-1.29 Slc2a3</b>	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 fr	
NM_001044751	//NM_008288	//NM_006497227			0.00261837	-1.04	-1.11	<b>-1.29 Hsd11b1</b>	hydroxysteroid 11-beta dehydrogenase 1	0006629 // lipid metabolic process // inferred from electronic annotation // 0006704 // glucocorticoid biosynthetic process // not recorded // 0006713 // glucocorticoid catabolic pro	
NM_137344	//NM_00	0.00198241			0.00917043	-1.20	-1.09	<b>-1.29 Tdrp</b>	testis development related protein	0007283 // spermatogenesis // not recorded	
NM_133237			5.95E-04			-1.16	-1.30	<b>-1.29 Apcd1</b>	adenomatous polyposis col down-regulated 1	0001942 // hair follicle development // not recorded // 0016055 // Wnt signaling pathway // inferred from electronic annotation // 0003178 // negative regulation of Wnt signaling pa	
NM_133898	//NM_00	6.10E-04	0.003046447		0.00249839	-1.28	-1.34	<b>-1.29 Ntbp21</b>	NEDD4 binding protein 2-like 1	0006520 // cellular amino acid metabolic process // inferred from electronic annotation // 0007623 // circadian rhythm // inferred from electronic annotation // 0009636 // response	
NM_001190448	//NM_016672	//NM_001337507			0.00109191	-1.16	-1.40	<b>-1.29 Ddc</b>	dopa decarboxylase	0006351 // transcription, DNA-templated // inferred from electronic annotation // 0006355 // regulation of transcription, DNA-templated // inferred from electronic annotation // 000	
NM_144837	//NM_01124451	//XR_382437			0.00165726	-1.05	-1.15	<b>-1.29 Icel1</b>	interactor of the cell elongation complex ELL subunit 1	0006520 // cellular amino acid metabolic process // inferred from electronic annotation // 0007623 // circadian rhythm // inferred from electronic annotation // 0009636 // response	
NM_145394			0.007113169		0.00165529	-1.18	-1.23	<b>-1.29 Slc44a3</b>	solute carrier family 4A, member 3	0002376 // immune system process // inferred from electronic annotation // 0002523 // leukocyte migration involved in inflammatory response // not recorded // 0002526 // acute i	
NM_013650		2.29E-04				-2.98	-1.81	<b>-1.29 S100a8</b>	S100 calcium binding protein A8 (calgranulin A)	0002376 // immune system process // inferred from electronic annotation // 0002523 // leukocyte migration involved in inflammatory response // not recorded // 0002526 // acute i	
NM_029933	//NM_00	0.00409769	0.002907983		0.00732456	-1.20	-1.26	<b>-1.30 Bcl9</b>	B cell CLL/lymphoma 9	0014908 // myotube differentiation involved in skeletal muscle regeneration // inferred from genetic interaction // 00016055 // Wnt signaling pathway // inferred from electronic anno	
NM_009626	//NM_006500919	//NM_006500920			0.00251234	-1.17	-1.10	<b>-1.30 Num1a</b>	alcohol dehydrogenase 7 (class IV), mu or sigma polypeptide	0001503 // retinoid metabolic process // not recorded // 0006067 // ethanol metabolic process // not recorded // 0006068 // ethanol metabolic process // inferred from mutant phen	
NM_133947	//NM_00	0.00532344			0.00458652	-1.11	-1.22	<b>-1.30 Fx6b</b>	nuclear mitotic apparatus protein 1	0001372 // establishment of mitotic spindle orientation // inferred from mutant phenotype // 00051321 // meiotic cell cycle // inferred from electronic annotation // 00060487 // lung e	
NM_001162494	//NM_008056	//NM_006520438			0.00153224	-1.01	-1.17	<b>-1.30 Higd1b</b>	HIG1 domain family, member 1B	0006469 // negative regulation of protein kinase activity // inferred from direct assay // 0035556 // intracellular signal transduction // not recorded // 0061099 // negative regulati	
NM_08084	//NM_006534395	//NM_006534396			0.00185491	-1.10	-1.21	<b>-1.30 Sk3bp5</b>	SK3-domain binding protein 5 (BTK-associated)	0006469 // negative regulation of protein kinase activity // inferred from direct assay // 0035556 // intracellular signal transduction // not recorded // 0061099 // negative regulati	
NM_011884	//NM_006519013	//NM_006519015			0.00533577	-1.03	-1.10	<b>-1.30 Cytb5d1</b>	cytochrome b5 domain containing 1	0006469 // negative regulation of protein kinase activity // inferred from direct assay // 0035556 // intracellular signal transduction // not recorded // 0061099 // negative regulati	
NM_001045525	//NM_011249073		0.00423348			-1.31	-1.18	<b>-1.30 Tspyl4</b>	TSPY-like 4	0006334 // nucleosome assembly // inferred from electronic annotation	
NM_030203		0.00220143			0.00329473	-1.20	-1.25	<b>-1.30 Spnat13</b>	spermatogenesis associated 13	0006334 // nucleosome assembly // inferred from electronic annotation	
NM_001032372	//NM_00765177		0.00372383		1.12	-1.18	-1.30	<b>-1.30 Mertk</b>	c-met proto-oncogene tyrosine kinase	0016477 // cell migration // not recorded // 0030032 // lamellipodium assembly // not recorded // 0030334 // regulation of cell migration // not recorded // 0035023 // regulation of	
NM_008578	//NM_006498860		0.0055816			-1.04	-1.15	<b>-1.30 Dmd</b>	dystrophin, muscular dystrophy	0001779 // natural killer cell differentiation // inferred from genetic interaction // 0006468 // protein phosphorylation // not recorded // 0006909 // phagocytosis // not recorded // 00	
NM_001314034	//NM_001314033	//NM_001314040			0.0055816	-1.04	-1.15	<b>-1.30 Dmd</b>	dystrophin, muscular dystrophy	0001954 // positive regulation of cell-matrix adhesion // inferred from mutant phenotype // 0002027 // regulation of heart rate // inferred from mutant phenotype // 0002027 // regu	
NM_001197321	//NM_3.25E-04	4.51E-04			0.00982258	-1.28	-1.41	<b>-1.30 Foxp1</b>	forkhead box P1	0000122 // negative regulation of transcription from RNA polymerase I promoter // inferred from direct assay // 0000122 // negative regulation of transcription from RNA polymer	
NM_018884	//NM_00	0.00525579	1.98E-04		0.00232707	-1.23	-1.46	<b>-1.30 Pdzn3</b>	PDZ domain containing RING finger 3	0006810 // neuromuscular junction development // inferred from mutant phenotype // 0016567 // protein ubiquitination // inferred from direct assay	
NM_001159529	//NM_00981256		0.00489347		-1.22	-1.13	-1.30	<b>-1.30 Cox7a2l</b>	cytochrome c oxidase subunit VIIa polypeptide 2-like	0002082 // regulation of oxidative phosphorylation // inferred from mutant phenotype // 00097250 // mitochondrial respiratory chain supercomplex assembly // inferred from direct	
NM_177242			0.00251847		-1.01	-1.06	-1.30	<b>-1.30 Pptc7</b>	PPTC7 protein phosphatase (S. cerevisiae)	0006470 // protein dephosphorylation // inferred from electronic annotation // 0008152 // metabolic process // inferred from electronic annotation	
NM_133218	//NM_006530055		0.00467643		1.03	-1.17	-1.30	<b>-1.30 Zfp704</b>	zinc finger protein 704	00051607 // defense response to virus // inferred from electronic annotation	
NM_001243916	//NM_00039332		0.00414976		-1.02	-1.27	-1.30	<b>-1.30 Antxr1</b>	atriaxin toxin receptor 1	0007165 // signal transduction // not recorded // 0022414 // reproductive process // inferred from mutant phenotype // 0031532 // actin cytoskeleton reorganization // not recorded	
NM_178626	//NM_006534320		0.00891308		-1.02	-1.18	-1.30	<b>-1.30 Cdc42e2</b>	CDH2 small effector 2	0006909 // phagocytosis // inferred from electronic annotation // 0007165 // signal transduction // not recorded // 0008360 // regulation of cell shape // inferred from electronic an	
NM_026347	//NM_006515175	//NM_006515176			0.0036121	-1.20	-1.04	<b>-1.30 Iah1</b>	isoamyl acetate-hydrolyzing esterase 1 homolog (S. cerevisiae)	0006629 // lipid metabolic process // inferred from electronic annotation // 0016042 // lipid catabolic process // inferred from electronic annotation	
NM_026141	//NM_006512832	//XR_380072			0.00169483	-1.06	-1.15	-1.30	<b>-1.30 Ppil4</b>	peptidylprolyl isomerase (chaperin)-like 4	0000413 // protein peptidyl-prolyl isomerization // not recorded // 0006457 // protein folding // inferred from electronic annotation // 1901407 // regulation of phosphorylation of Rf
NM_001039184	//NM_006529900	//NM_006529900			0.00905664	-1.00	-1.09	-1.30	<b>-1.30 Cep350</b>	centrosomal protein 350	0034453 // microtubule anchoring // inferred from electronic annotation
NM_007818		0.00607943			1.30	-1.42	-1.31	<b>-1.31 Cyp3a11</b>	cytochrome P450, family 3, subfamily a, polypeptide 11	0005114 // oxidation-reduction process // inferred from electronic annotation	
NM_001123327	//NM_006500458	//NM_006500454			0.00109792	-1.03	-1.24	-1.31	<b>-1.31 Qser1</b>	glutamine and serine rich 1	0006351 // transcription, DNA-templated // inferred from electronic annotation // 0006355 // regulation of transcription, DNA-templated // inferred from electronic annotation
NM_009672	//NM_006510778	//NM_006510778			0.00801359	-1.12	-1.31	<b>-1.31 Anp32a</b>	acidic (leucine-rich) nuclear phosphoprotein 32 family, member A	0006468 // protein phosphorylation // not recorded // 0006979 // response to oxidative stress // inferred from direct assay // 0007346 // regulation of mitotic cell cycle // not recorde	
NM_133985	//NR_045693	//NM_006511919	//NM_006511919		0.00540533	-1.04	-1.11	-1.31	<b>-1.31 Oxsr1</b>	oxidative-stress responsive 1	0007165 // signal transduction // inferred from electronic annotation // 0007264 // small GTPase mediated signal transduction // not recorded // 0008360 // regulation of cell shape //
NM_176837	//NM_006512885	//NM_011243213			0.00510432	-1.04	-1.15	-1.31	<b>-1.31 Arhgap18</b>	Rho GTPase activating protein 18	0000187 // activation of MAPK activity // inferred from direct assay // 0006979 // response to oxidative stress // inferred from direct assay // 0007165 // signal transduction // inferre
NM_001301298	//NM_000865401	0.003944993			0.00187503	-1.17	-1.24	-1.31	<b>-1.31 Gobi1</b>	growth factor receptor bound protein 2-associated protein 1	0007049 // cell cycle // inferred from electronic annotation // 0007050 // cell cycle arrest // not recorded // 0008285 // negative regulation of cell proliferation // not recorded // 001
NM_031392		0.00143825			-1.09	-1.05	-1.31	<b>-1.31 Wdr6</b>	WD repeat domain 6	0007095 // mitochondrion organization // non-traceable author statement // 0007052 // mitotic spindle organization // inferred from direct assay // 0008610 // lipid biosynthetic pro	
NM_001293757	//NM_001293758	//NM_001293757			0.00309847	-1.06	-1.05	-1.31	<b>-1.31 Dctn6</b>	dyctn6 (never in mitosis gene a)-related expressed kinase 9	0006468 // protein phosphorylation // not recorded // 0007049 // cell cycle // inferred from electronic annotation // 0007052 // mitotic nuclear division // inferred from electronic an
NM_001039530	//NM_00652392	//NM_006523929			0.0020614	-1.13	-1.13	-1.31	<b>-1.31 Parp14</b>	poly (ADP-ribose) polymerase family, member 14	0006351 // transcription, DNA-templated // inferred from electronic annotation // 0006355 // regulation of transcription, DNA-templated // inferred from electronic annotation // 000
NM_001081069			0.00251007		-1.14	-1.23	-1.31	<b>-1.31 Rgs11</b>	regulator of G-protein signaling 11	0007186 // G-protein coupled receptor signaling pathway // traceable author statement // 0009968 // negative regulation of signal transduction // inferred from electronic annotation	
NM_144551	//NM_006515054	//NM_006515055			0.00231598	-1.01	-1.21	-1.31	<b>-1.31 Trib2</b>	tribbles homolog 2 (Drosophila)	0006468 // protein phosphorylation // inferred from electronic annotation // 0032436 // positive regulation of proteasomal ubiquitin-dependent protein catabolic process // inferred i
NM_001109690	//NM_001109691	//NM_138755			0.0026076	-1.11	-1.12	-1.31	<b>-1.31 Phf21a</b>	PHD finger protein 21A	0000122 // negative regulation of transcription from RNA polymerase I promoter // not recorded // 0001967 // sucking behavior // inferred from mutant phenotype // 0006351 // tr
NM_026639		6.38E-04			9.62E-04	-1.10	-1.32	-1.31	<b>-1.31 Arta</b>	ADP-ribosyltransferase 4	0006471 // protein ADP-ribosylation // inferred from electronic annotation
NM_0261											

RefSeq	Transcript ID	p (24h n=460)	p (48h n=657)	p (72h n=805)	FC 24h	FC 48h	FC 72h	Gene Symbol	Gene Title	Gene Ontology Biological Process	
NM_175518	/NM_006537925	/NM_011250037			0.00170902	-1.08	-1.14	-1.32	<b>Tmem245</b>	transmembrane protein 245	
NM_197999	/NM_006531391	/NM_006531392			4.12E-04	-1.05	-1.32	-1.32	<b>Ces2g</b>	carboxylesterase 2G	00081152 // metabolic process // inferred from electronic annotation
NM_001013414	/NM_001291118	/NM_001291118			0.00465085	-1.04	-1.18	-1.32	<b>Neur4f</b>	neuronal E3 ubiquitin protein ligase 4	
NM_001077361	/NM_001077362	/NM_001021287			0.00229826	-1.10	-1.20	-1.32	<b>Fhl1</b>	four and a half LIM domains 1	00032554 // regulation of membrane depolarization // not recorded // 0007275 // multicellular organismal development // inferred from electronic annotation // 0010972 // negative
NM_176737	/NM_006538825				5.40E-04	1.02	-1.12	-1.32	<b>Cep104</b>	centrosomal protein 104	
NM_011663		0.002148202				-1.11	-1.25	-1.32	<b>Zrsr1</b>	zinc finger (CCCH type), RNA binding motif and serine/arginine rich 1	
NM_175309					0.00509452	-1.05	-1.03	-1.32	<b>Upk3b</b>	uroplakin 3B	0010629 // negative regulation of gene expression // not recorded // 0046325 // negative regulation of glucose import // inferred from mutant phenotype
NM_010474		0.00344019			0.00668088	-1.28	1.15	-1.32	<b>Hs3t1</b>	heparan sulfate (glucosamine) 3-O-sulfotransferase 1	0008152 // metabolic process // inferred from electronic annotation
NM_031257	/NM_006509227	/NM_006509227			8.86E-04	-1.02	-1.34	-1.33	<b>Plekha2</b>	pleckstrin homology domain-containing, family A (phosphoinositid	00019954 // positive regulation of cell-matrix adhesion // not recorded
NM_025290		0.003556988				1.02	-1.26	-1.33	<b>RspH1</b>	radial spoke head 1 homolog (Chlamydomonas)	0035082 // axoneme assembly // not recorded // 0051321 // meiotic cell cycle // inferred from electronic annotation
NM_001199059	/NM_019983	/NM_006504446			0.00801718	-1.06	-1.07	-1.33	<b>Rabgef1</b>	RAB guanine nucleotide exchange factor (GEF) 1	0001933 // negative regulation of protein phosphorylation // inferred from mutant phenotype // 0002686 // negative regulation of leukocyte migration // inferred from mutant phen
NM_199029	/NM_00101378				0.00845424	-1.17	-1.15	-1.33	<b>Zfp395</b>	zinc finger protein 395	0006353 // regulation of transcription from RNA polymerase II promoter // not recorded
NM_001113333	/NM_000837567	0.001752195			0.00262895	-1.21	-1.38	-1.33	<b>Cp2</b>	cryptochrome 2 (photolyase-like)	0001122 // negative regulation of transcription from RNA polymerase II promoter // not recorded // 0006381 // DNA repair // inferred from electronic annotation // 0006351 // trans
NM_053200					0.00404769	-1.07	-1.02	-1.33	<b>Ces1d</b>	carboxylesterase 1D	0006629 // lipid metabolic process // inferred from electronic annotation // 0006637 // acyl-CoA metabolic process // traceable author statement // 0009636 // response to toxic sub
NM_001037136	/NM_178119				0.00357796	-1.08	-1.12	-1.33	<b>Aagp1</b>	ArfGAP with GTPase domain, ankyrin repeat and PH domain 1	0006810 // transport // inferred from electronic annotation // 0007165 // signal transduction // inferred from electronic annotation // 0007264 // small GTPase mediated signal trans
NM_001305284	/NM_001305286	0.004262139				-1.06	-1.37	-1.33	<b>Mpd2</b>	multiple PDZ domain protein	0007155 // cell adhesion // inferred from direct assay // 0042552 // myelination // not recorded
NM_001159367	/NM_000217006					1.28	-1.10	-1.33	<b>Per1</b>	period circadian clock 1	0001122 // negative regulation of transcription from RNA polymerase I promoter // inferred from direct assay // 0000122 // negative regulation of transcription from RNA polymer
NM_001277970	/NM_000481572	6.88E-04				-1.23	-1.53	-1.33	<b>Itna6</b>	integrin alpha 6	0007155 // cell adhesion // inferred from electronic annotation // 0007160 // cell-matrix adhesion // inferred from mutant phenotype // 0007229 // integrin-mediated signaling pathw
NM_001040187	/NM_152806	/NM_008353866			0.0039879	-1.07	-1.26	-1.33	<b>Dxk17</b>	DEAD (Asp-Glu-Ala-Ser) box polypeptide 17	0006351 // transcription, DNA-templated // inferred from electronic annotation // 0006355 // regulation of transcription, DNA-templated // inferred from electronic annotation // 000
NM_001005740	/NM_001005748	/NM_001301026			0.0024098	-1.04	-1.23	-1.33	<b>Phactr1</b>	phosphatase and actin regulator 1	0031032 // actomyosin structure organization // inferred from mutant phenotype // 0003103 // actomyosin structure organization // not recorded // 0031532 // actin cytoskeleton r
NM_000829	/NM_006505459	/NM_006505460			0.00369307	-1.21	-1.21	-1.34	<b>Cnd2</b>	cyclin D2	0000082 // G1/S transition of mitotic cell cycle // not recorded // 0001934 // positive regulation of protein phosphorylation // not recorded // 0007049 // cell cycle // inferred from el
NM_001309390	/NM_028783	/NM_006510644			0.00791583	-1.08	-1.14	-1.34	<b>Robo4</b>	roundabout homolog 4 (Drosophila)	0001525 // angiogenesis // not recorded // 0007275 // multicellular organismal development // inferred from electronic annotation // 0030154 // cell differentiation // inferred from e
NM_016737		0.009858104				-1.11	-1.56	-1.34	<b>Stip1</b>	stress-induced phosphoprotein 1	
NM_145584		0.0020224			0.00318655	-1.19	-1.11	-1.34	<b>Spon1</b>	spondin 1, (f-spondin) extracellular matrix protein	0007155 // cell adhesion // inferred from electronic annotation
NM_001081149	/NM_006509112	/NM_006509112			0.00199466	-1.05	-1.19	-1.34	<b>Kat6a</b>	Klysine1 acetyltransferase 6A	0003007 // heart morphogenesis // inferred from genetic interaction // 0003007 // heart morphogenesis // inferred from mutant phenotype // 0006334 // nucleosome assembly // in
NM_001291910	/NM_009624	/NM_007432137			0.00136432	-1.03	-1.20	-1.34	<b>Adcy1</b>	adenylate cyclase 9	0006171 // cAMP biosynthetic process // inferred from direct assay // 0006173 // cAMP biosynthetic process // not recorded // 0006171 // cAMP biosynthetic process // traceable au
NM_001311123	/NM_011643	/NM_006511053			0.00129362	-1.06	-1.15	-1.34	<b>Trcp1</b>	transient receptor potential cation channel, subfamily C, member 1	0006810 // transport // inferred from electronic annotation // 0006811 // ion transport // inferred from electronic annotation // 0006816 // calcium ion transport // inferred from ele
NM_139300	/NM_006521702	/NM_00606755			0.0050602	-1.04	-1.36	-1.34	<b>Myik</b>	myosin, light polypeptide kinase	0002230 // positive regulation of defense response to virus by host // not recorded // 0006468 // protein phosphorylation // inferred from electronic annotation // 0006939 // smooth
NM_020590		0.00696564			-1.15	-1.09	-1.34	<b>Gaporap1</b>	gamma-aminobutyric acid (GABA) A receptor-associated protein-III	0000045 // autophagosome assembly // not recorded // 0000422 // mitophagy // not recorded // 0006914 // autophagy // inferred from electronic annotation // 0044804 // nucleop	
NM_001025566	/NM_001271496	/NM_013490			8.30E-04	1.02	-1.07	-1.34	<b>Chka</b>	choline kinase alpha	0006580 // ethanolamine metabolic process // not recorded // 0006629 // lipid metabolic process // inferred from electronic annotation // 0006646 // phosphatidylethanolamine bio
NM_001013370	/NM_001162908	9.25E-04			0.00861679	-1.08	-1.33	-1.34	<b>Sesn1</b>	serine 1	0051896 // regulation of protein kinase B signaling // inferred from direct assay // 1901031 // regulation of response to reactive oxygen species // inferred from electronic annota
NM_001293701	/NM_027241				4.35E-04	-1.07	-1.09	-1.35	<b>Polr3gl</b>	polymerase (RNA) III (DNA directed) polymerase G like	0006359 // regulation of transcription from RNA polymerase III promoter // inferred from electronic annotation // 0006384 // transcription initiation from RNA polymerase III promot
NM_001253885	/NM_000497973				0.00231874	-1.23	-1.15	-1.35	<b>Abpb1</b>	amyloid beta (A4) precursor protein-binding, family B, member 1	0001764 // neuron migration // inferred from genetic interaction // 0006302 // double-strand break repair // inferred from mutant phenotype // 0006302 // double-strand break repa
NM_001472	/NM_201239				8.11E-04	-1.14	-1.22	-1.35	<b>Rnase4</b>	ribonuclease, RNase A family 4	
NM_145586	/NM_006507682				0.00200493	-1.07	-1.12	-1.35	<b>Tmem159</b>	transmembrane protein 159	0001525 // angiogenesis // inferred from electronic annotation // 0001525 // angiogenesis // -- // 0001525 // angiogenesis // inferred from sequence or structural similarity // 00016
NM_007409		0.001428181				-1.17	-1.27	-1.35	<b>Adh1</b>	alcohol dehydrogenase 1 (class I)	0001523 // retinoid metabolic process // inferred from mutant phenotype // 0006068 // ethanol catabolic process // inferred from direct assay // 0006068 // ethanol catabolic proces
NM_133663	/NM_006532457				0.00255569	-1.15	-1.10	-1.35	<b>Pdk2</b>	pyruvate dehydrogenase kinase, isoenzyme 2	0005979 // carbohydrate metabolic process // inferred from electronic annotation // 0006006 // glucose metabolic process // inferred from electronic annotation // 0006111 // regul
NM_007382		0.00351396			0.00351396	-1.09	-1.05	-1.35	<b>Acdm</b>	acyl-Coenzyme A dehydrogenase, medium chain	0001889 // liver development // inferred from mutant phenotype // 0005978 // glycogen biosynthetic process // inferred from mutant phenotype // 0006082 // organic acid metaboli
NM_001033460		0.003626539			8.32E-04	-1.03	-1.22	-1.35	<b>Dcx1</b>	dyx1in regulatory complex subunit 1	0007368 // determination of left/right symmetry // inferred from mutant phenotype // 0007507 // heart development // inferred from mutant phenotype // 0006285 // cilium-depen
NM_001193271	/NM_377E-05	0.001450011			6.43E-04	-1.49	-1.30	-1.35	<b>Meis1</b>	Meis homeobox 1	0001525 // angiogenesis // inferred from mutant phenotype // 0002088 // lens morphogenesis in camera-type eye // inferred from mutant phenotype // 0006351 // transcription, DN
NM_011723	/NM_011246381	/NM_001290740			0.00409524	-1.09	-1.03	-1.35	<b>Xdh1/Cwc22</b>	xanthine dehydrogenase // CWC22 spliceosome-associated protei	0001923 // angiogenesis // inferred from mutant phenotype // not recorded // 0001937 // negative regulation of endothelial cell proliferation // not recorded // 0006919 // activation o
NM_001081237	/NM_000420363	0.007821989			0.00169184	-1.19	-1.31	-1.35	<b>Klhl42</b>	kelch-like 42	0002029 // protein polyubiquitination // not recorded // 0007049 // cell cycle // inferred from electronic annotation // 0007067 // mitotic nuclear division // inferred from electr
NM_138590	/NM_177027	/NM_006537984	/NM_00042718		2.63E-04	-1.01	-1.16	-1.35	<b>Zcch7c</b>	zinc finger, CCHC domain containing 7	
NM_0012718		0.00394075			-1.31	-1.58	-1.35	<b>Ms4a4b</b>	membrane-spanning 4-domains, subfamily A, member 4B		
NM_001290817	/NM_009242	5.14E-04			3.54E-04	-1.15	-1.29	-1.36	<b>Sparc</b>	secreted acidic cysteine rich glycoprotein	0001503 // ossification // inferred from electronic annotation // 0001937 // negative regulation of endothelial cell proliferation // not recorded // 0007165 // signal transduction // inf
NM_017376	/NM_153484	/NM_006520744	/NM_0007817		0.00274866	-1.18	-1.12	-1.36	<b>Tef</b>	tryptophan embryonic factor	0006351 // transcription, DNA-templated // inferred from electronic annotation // 0006355 // regulation of transcription, DNA-templated // inferred from electronic annotation // 000
NM_007817		0.004945			-1.03	-1.19	-1.36	<b>Cyp2f2</b>	cytochrome P450, family 2, subfamily f, polypeptide 2	0006805 // xenobiotic metabolic process // not recorded // 0009636 // response to toxic substance // inferred from mutant phenotype // 0018931 // naphthalene metabolic process //	
NM_001199141	/NM_144516	/NM_006516491			0.00274866	-1.18	-1.12	-1.36	<b>Tef</b>	tryptophan embryonic factor	0006351 // transcription, DNA-templated // inferred from electronic annotation // 0006355 // regulation of transcription, DNA-templated // inferred from electronic annotation // 000
NM_008304		0.00736489			-1.08	-1.29	-1.36	<b>Sdc2</b>	syndecan 2	0007399 // nervous system development // inferred from electronic annotation // 0016477 // cell migration // not recorded // 0030154 // cell differentiation // inferred from elect	
NM_009284		0.0073247			-1.16	-1.30	-1.36	<b>Stat6</b>	signal transducer and activator of transcription 6	0000122 // negative regulation of transcription from RNA polymerase II promoter // inferred from direct assay // 0000122 // negative regulation of transcription from RNA polymer	
NM_012042	/NM_000569502				0.00546097	-1.22	-1.19	-1.36	<b>Cul1</b>	cullin 1	0006511 // ubiquitin-dependent protein catabolic process // inferred by curator // 0006513 // protein monoubiquitination // inferred from genetic interaction // 0006915 // apoptotic
NM_028763		0.00680922			-1.09	-1.10	-1.36	<b>Cbx6</b>	chromobox 6	0000122 // negative regulation of transcription from RNA polymerase II promoter // not recorded // 0006351 // transcription, DNA-templated // inferred from electronic annotation //	
NM_001081362	/NM_006504781	/NM_00650478			0.00219987	-1.03	-1.09	-1.37	<b>Trap</b>	transformation/transcription domain-associated protein	0006281 // DNA repair // not recorded // 0006351 // transcription, DNA-templated // inferred from electronic annotation // 0006355 // regulation of transcription, DNA-templated //
NM_001286468	/NM_000212396	0.003012689			0.001005	-1.41	-1.40	-1.37	<b>Arhgap24</b>	Rho GTPase activating protein 24	0006351 // angiogenesis // inferred from electronic annotation // 0007165 // signal transduction // inferred from electronic annotation // 0007275 // multicellular organismal develop
NM_001163557	/NM_000322478	0.002404311			0.00169824	-1.29	-1.31	-1.37	<b>Ppfibp2</b>	PTPRF interacting protein, binding protein 2 (liprin beta 2)	
NM_023186		0.00887344			-1.31	-1.51	-1.37	<b>Chia1</b>	chitinase, acidic 1	0000272 // polysaccharide catabolic process // inferred from electronic annotation // 0002376 // immune system process // inferred from electronic annotation // 0002532 // produc	
NM_001206367	/NM_001206368	/NM_00120636			9.21E-04	-1.07	-1.11	-1.37	<b>Gsn</b>	gelsolin	0006911 // phagocytosis, engulfment // inferred from mutant phenotype // 0006915 // apoptotic process // not recorded // 0007568 // aging // inferred from electronic annotation // 000
NM_001113213	/NM_001113214	/NM_0011776			0.00909863	-1.11	-1.12	-1.37	<b>Odf2</b>	outer dense fiber of sperm tails 2	0007275 // multicellular organismal development // inferred from electronic annotation // 0007283 // spermatogenesis // inferred from electronic annotation // 0007286 // spermat
NM_008481	/NM_006512566	/NM_011243134			9.78E-04	-1.11	-1.18	-1.37	<b>Lama2</b>	laminin, alpha 2	0007155 // cell adhesion // inferred from electronic annotation // 0007411 // axon guidance // inferred from genetic interaction // 0022013 // myelination in peripheral nervous syste
NM_001033481	/NM_006526927	6.35E-04			6.57E-04	-1.13	-1.32	-1.37	<b>Myf1</b>	myelin regulatory factor	0006351 // transcription, DNA-templated // inferred from electronic annotation // 0006355 // regulation of transcription, DNA-templated // inferred from electronic annotation // 000
NM_175692		0.00147914			-1.05	-1.16	-1.37	<b>Snhg11</b>	small nucleolar RNA host gene 11		
NM_001304744	/NM_007714	/NM_006532111			0.00622726	1.00	-1.19	-1.37	<b>Cik4</b>	CDC like kinase 4	0006468 // protein phosphorylation // inferred from electronic annotation // 0016310 // phosphorylation // inferred from electronic annotation // 0018108 // peptidyl-tyrosine phosph
NM_001040113	/NM_001040113	/NM_027180			0.00348318	-1.09	-1.11	-1.37	<b>Arp1</b>	ArfGAP with RhoGAP domain, ankyrin repeat and PH domain 1	0001921 // positive regulation of receptor recycling // not recorded // 0007165 // signal transduction // inferred from electronic annotation // 0007179 // transforming growth factor
NM_197986	/NM_00654001	0.00369614			-1.40	-1.33	-1.37	<b>Tmem140</b>	transmembrane protein 140		
NM_001253755	/NM_172605	/NM_006518909			0.00656467	-1.13	-1.25	-1.37	<b>Tdrd5</b>	tudor domain containing 5	0006397 // mRNA processing // inferred from electronic annotation // 0016568 // chromatin modification // inferred from electronic annotation // 1903506 // regulation of nucleic a
NM_001243132	/NM_520E-04				0.00107842	-1.31	-1.25	-1.37	<b>Tspan2</b>	tetraspanin 2	0006954 // inflammatory response // inferred from genetic interaction // 0007166 // cell surface receptor signaling pathway // not recorded // 0007420 // brain development // infer
NM_023402		0.001264852			0.00826063	-1.09	-1.32	-1.38	<b>Myh12b</b>	myosin, light chain 12B, regulatory	0008360 // regulation of cell shape // inferred from mutant phenotype // 0007057 // platelet aggregation // not recorded
NM_001163748	/NM_008804	/NM_008764171			0.00108919	-1.20	-1.21	-1.38	<b>Pde9a</b>	phosphodiesterase 9A	0007165 // signal transduction // inferred from electronic annotation // 0010613 // positive regulation of cardiac muscle hypertrophy // inferred from mutant phenotype // 0046068 //
NM_001083929	/NM_008161				0.00114975	-1.10	1.03	-1.38	<b>Gpx3</b>	glutathione peroxidase 3	0006749 // glutathione metabolic process // not recorded // 0006979 // response to oxidative stress // inferred from electronic annotation // 0042744 // hydrogen peroxide catabolic
NM_009349		0.00154834			-1.05	1.01	-1.38	<b>Inmt</b>	indolethylamine N-methyltransferase	0009308 // amine metabolic process // not recorded // 00	

RefSeq	Transcript ID	p (24h n=460)	p (48h n=657)	p (72h n=805)	FC 24h	FC 48h	FC 72h	Gene Symbol	Gene Title	Gene Ontology Biological Process
NM_001286728	/NM_337E-04				0.00321229	-1.32	-1.22	-1.39	<i>Glkci1</i>	glucocorticoid induced transcription 1
NM_011546	/NM_006525767	/NM_006525769			0.00624649	1.06	-1.14	-1.39	<i>Zeb1</i>	zinc finger E-box binding homeobox 1
NM_001013786	/NM_006516710	/NM_00651671			0.00163829	-1.05	-1.12	-1.39	<i>Zscan26</i>	zinc finger and SCAN domain containing 26
NM_145220	/NM_006513508	/NM_006513509			0.00470725	1.04	1.00	-1.39	<i>Appl2</i>	apoferritin protein, phosphotyrosine interaction, PH domain and leuc
NM_019427	/NM_000872323				6.86E-04	-1.15	-1.18	-1.39	<i>Epb414b</i>	erythrocyte membrane protein band 4.1 like 4b
NM_010197	/NM_006525641	/NM_008898494			4.76E-04	-1.16	-1.29	-1.39	<i>Fg1</i>	fibroblast growth factor 1
NM_011416	/NM_026003	/NM_000559034			0.00665594	-1.01	-1.30	-1.39	<i>Smarca2</i>	SWI/SNF related, matrix associated, actin dependent regulator of c
NM_00131148	/NM_021605	/NM_006529770			0.00665594	-1.02	-1.08	-1.39	<i>Nek7</i>	NIMA (never in mitosis gene a)-related expressed kinase 7
NM_133871	/NM_006502485	/NM_006502486			0.00827549	-1.01	-1.56	-1.39	<i>Ifi44</i>	interferon-inducible protein 44
NM_001289490	/NM_001289491	/NM_207219			0.00186866	-1.13	-1.25	-1.39	<i>Oard1</i>	O-acyl-ADP-ribose deacylase 1
NM_013785					0.00107573	-1.15	-1.11	-1.40	<i>Ip6k1</i>	inositol hexaphosphate kinase 1
NM_212457					0.0011152	-1.15	-1.08	-1.40	<i>Be4</i>	brain expressed gene 4
NM_133738		0.00948514			6.03E-04	1.00	-1.49	-1.40	<i>Artx2</i>	antitoxin receptor 2
NM_145492	/NM_006525819	/NM_006525820			0.00306098	1.02	-1.10	-1.40	<i>Zfp521</i>	zinc finger protein 521
NM_173781	/NM_006511736	/NM_006511737			0.00656108	-1.14	-1.09	-1.40	<i>Rab6b</i>	RAB6B, member RAS oncogene family
NM_001310837	/NM_010656	/NM_003679679			7.98E-04	-1.11	-1.37	-1.40	<i>Ssn</i>	sarcospan
NM_001199136	/NM_001199137	/NM_0040695			5.02E-04	-1.14	-1.29	-1.40	<i>Mucf1</i>	microtubule-actin crosslinking factor 1
NM_0021883	/NM_006537772	/NM_006537773			1.64E-04	-1.16	-1.23	-1.40	<i>Tmod1</i>	tropomodulin 1
NM_133829	/NM_178081	/NM_006496374	/NM_000105510		0.0041381	-1.11	-1.29	-1.41	<i>Msf6</i>	major facilitator superfamily domain containing 6
NM_001005510					0.0037105	-1.15	-1.08	-1.41	<i>Syne2</i>	spectrin repeat containing, nuclear envelope 2
NM_001154799	/NM_007796	/NM_001145801			0.0034878	-1.06	-1.50	-1.41	<i>Ctla2b</i>	cytotoxic T lymphocyte-associated protein 2 alpha//cytotoxic T ly
NM_138756	/NM_006510870	/NM_006510871			0.00397328	-1.16	-1.29	-1.41	<i>Slc25a36</i>	solute carrier family 25, member 36
NM_146126					0.0041585	-1.13	-1.17	-1.41	<i>Sord</i>	sorbitol dehydrogenase
NM_001081188	/NM_006512207	/NM_00651220			0.00883526	-1.12	-1.24	-1.41	<i>Exoc7</i>	exosome component 7
NM_016678	/NM_006538086				0.0083015	-1.04	-1.15	-1.41	<i>Reck</i>	reversion-inducing-cysteine-rich protein with kazal motifs
NM_025817		0.00135585	3.71E-04		0.00533326	-1.36	-1.52	-1.41	<i>Tril</i>	TLR intracellular with leucine-rich repeats
NM_017394	/NM_006540196	/NM_001890356			0.0023255	-1.13	-1.34	-1.42	<i>Slc7a10</i>	solute carrier family 7 (cationic amino acid transporter, y+ system)
NM_011542	/NM_006538710	/NM_006538711			0.00128194	-1.09	-1.10	-1.42	<i>Tec3</i>	transcription elongation factor A [SII], 3
NM_001168620	/NM_032003	/NM_006367763			-1.19	-1.36	-1.42	<i>Enpp5</i>	ectonucleotide pyrophosphatase/phosphodiesterase 5	
NM_001199187	/NM_026937	/NM_008646874			-1.06	-1.25	-1.42	<i>Ascl1</i>	activating signal integrator 1 complex subunit 1	
NM_0027144	/NM_006510586	/NM_011242597			3.40E-04	-1.08	-1.10	-1.42	<i>Arhgef12</i>	Rho guanine nucleotide exchange factor (GEF) 12
NM_001271407	/NM_001271408	/NM_0012714			0.0070907	-1.14	-1.19	-1.42	<i>Sorbs3</i>	sorbin and SH3 domain containing 3
NM_001112725	/NM_626E-04				1.31	1.01	-1.42	<i>Aldehyde3</i>	aldehyde dehydrogenase family 3, subfamily A1	
NM_001164155	/NM_013869	0.00166157			0.0015411	-1.16	-1.32	-1.42	<i>Tnfrsf19</i>	tumor necrosis factor receptor superfamily, member 19
NM_001004468	/NM_021314	/NM_003823771			8.26E-04	-1.15	-1.35	-1.42	<i>Tacc2</i>	transforming, acidic coiled-coil containing protein 2
NM_009531		0.00212137	-1.22	-1.23	-1.42	-1.23	-1.43	<i>Xpc</i>	xeroderma pigmentosum, complementation group C	
NM_007823		2.45E-04	-1.01	-1.02	-1.43	-1.02	-1.43	<i>Cyp4b1</i>	cytochrome P450, family 4, subfamily B, polypeptide 1	
NM_009776	/NM_006498623				0.001715	-1.11	-1.14	-1.43	<i>Serpin1</i>	serine (or cysteine) peptidase inhibitor, clade G, member 1
NM_001159632	/NM_133699	/NM_006515194			2.11E-04	-1.05	-1.05	-1.43	<i>Atg16l2</i>	ATPase, H+ transporting, lysosomal V1 subunit C2
NM_001081039	/NM_001128307	/NM_00112828			5.16E-04	-1.17	-1.17	-1.43	<i>Dock9</i>	dedicator of cytokinesis 9
NM_001253752	/NM_001253753	/NM_144842			0.00325849	-1.10	-1.12	-1.43	<i>Zmyx5</i>	zinc finger, MYM-type 5
NM_009546		0.00162946	-1.08	-1.22	-1.43	-1.22	-1.43	<i>Trim25</i>	tripartite motif-containing 25	
NM_0027707	/NM_201232	/NM_006519994	/NM_001145959	/NM_00203915	0.00155424	-1.00	-1.14	-1.44	<i>Nupbl</i>	Nipped-B homolog (Drosophila)
NM_001166067	/NM_006505963	3.96E-04			0.00196813	-1.07	-1.27	-1.44	<i>Prdm1</i>	PR domain containing 1, with ZNF domain
NM_007548	/NM_006512502	/NM_006512503			0.00177863	-1.11	-1.09	-1.44	<i>Syf2</i>	SyF2 homolog, RNA splicing factor (S. cerevisiae)
NM_001004359	/NM_001005385	1.95E-04			0.00467485	-1.18	-1.69	-1.44	<i>Grasp1</i>	G-protein-coupled receptor associated sortin protein 1
NM_003023	/NM_006506790				0.00718086	-1.00	-1.13	-1.45	<i>Avl9</i>	AVL9 homolog (S. cerevisiae)
NM_019503	/NM_052991	/NM_052992	/NM_1		0.00394801	-1.10	-1.15	-1.45	<i>Fxyd1</i>	FXYD domain-containing ion transport regulator 1
NM_001243064	/NM_007616	/NM_006504974			8.83E-04	-1.04	-1.20	-1.45	<i>Cav1</i>	caveolin 1, caveolin protein
NM_009978	/NM_006498658	/NM_00653252			1.01	-1.22	-1.45	-1.45	<i>Cst8</i>	castellan 8 (cystatin-related epididymal spermatogenic)
NM_027852	/NM_006506623	/NM_002332313			7.50E-04	-1.14	-1.33	-1.45	<i>Rarres2</i>	retinoic acid receptor responder (tazarotene induced) 2
NM_001097617	/NM_144938	/NM_006506365			0.00734369	-1.04	-1.22	-1.45	<i>C1s1</i>	complement component 1, s subcomponent
NM_181390		0.00511664	1.03	-1.17	-1.46	-1.17	-1.46	<i>Mu2t1</i>	musculoskeletal, embryonic nuclear core protein 1	
NM_001160319		0.002522	-1.13	-1.17	-1.46	-1.17	-1.46	<i>Ubr4</i>	ubiquitin protein ligase E3 component n-recogin 4	
NM_001161731	/NM_007447				0.00190745	-1.12	-1.45	-1.46	<i>Ang</i>	angiogenin, ribonuclease, RNase A family, 5
NM_020259	/NM_00013622	0.001779717			0.00291367	-1.27	-1.38	-1.46	<i>Hhip</i>	Hedgehog-interacting protein
NM_028127	/NM_006515977	/NM_006515978			0.0114941	-1.05	-1.13	-1.46	<i>Frmf6</i>	FERM domain containing 6
NM_001161775	/NM_013607	/NM_006521843			0.00784953	-1.01	-1.22	-1.46	<i>Mylh11</i>	myosin, heavy polypeptide 11, smooth muscle
NM_133187	/NM_006501984	/NM_006501985			0.00656879	-1.05	-1.15	-1.47	<i>Fom198b</i>	family with sequence similarity 198, member B
NM_011545		0.00454961			-1.50	-1.35	-1.47	<i>Tcf21</i>	transcription factor 21	
NM_025285		0.00552678	-1.21	-1.42	-1.47	-1.42	-1.47	<i>Srrm2</i>	srafin-like 2	
NM_011076	/NM_006503555	/NM_006503556			5.48E-04	-1.23	-1.10	-1.47	<i>Abcb1a</i>	ATP-binding cassette, sub-family B (MDR/TAP), member 1A
NM_001131054	/NM_013911	/NM_006533515			0.00309395	-1.01	-1.15	-1.47	<i>Ptgs1</i>	prostaglandin synthase 1
NM_001193666	/NM_001193667	/NM_00119366			0.00298848	-1.12	-1.16	-1.48	<i>Cd21a</i>	chemokine (C-C motif) ligand 21A [serine]//chemokine (C-C motif
NM_011125	/NM_006498952				0.0073195	-1.16	-1.18	-1.48	<i>Pltp</i>	phospholipid transfer protein
NM_010570		0.00392377	-1.08	-1.23	-1.48	-1.23	-1.48	<i>Irs1</i>	insulin receptor substrate 1	
NM_00110211	/NM_013472	0.006801735			-1.15	-1.18	-1.48	<i>Anxa6</i>	annexin A6	
NM_010681		0.004714686	6.19E-04	-1.11	-1.25	-1.48	-1.48	<i>Lama4</i>	laminin, alpha 4	
NM_00103208		5.25E-04	-1.16	-1.16	-1.48	-1.16	-1.48	<i>Mycopap</i>	myocardial zonula adherens protein	
NM_011784		0.00128085	0.005279274		-1.28	-1.65	-1.48	<i>Aplnr</i>	apelin receptor	
NM_009749		0.00369415	-1.09	-1.11	-1.49	-1.11	-1.49	<i>Bxnl2</i>	brain expressed X-linked 2	
NM_054077	/NM_006529083	/NM_007509701			-1.18	-1.39	-1.50	<i>Prplp</i>	proline arginine-rich end leucine-rich repeat	
NM_001077398	/NM_001286348	/NM_010698			3.89E-04	-1.10	-1.35	-1.50	<i>Lad2</i>	LIM domain binding 2
NM_001282000	/NM_00703129				0.00368084	-1.29	-1.36	-1.50	<i>Rbl2</i>	retinoblastoma-like 2
NM_008580	/NM_000785419				-1.19	-1.25	-1.51	<i>Mop3k5</i>	mitogen-activated protein kinase kinase kinase 5	
NM_009150		0.00485919	-1.02	1.13	-1.51	-1.51	<i>Selenbp1</i>	selenium binding protein 1		
NM_001004150	/NM_0045804	0.00477315			-1.22	-1.40	-1.51	<i>Adaglt</i>	alpha 1.4-galactosyltransferase	
NM_010370		0.0038162	0.007069772		-1.50	-1.64	-1.51	<i>Gzma</i>	granzyme A	
NM_053247		0.005769849	-1.00	-1.57	-1.56	-1.35	-1.51	<i>Lyme1</i>	lymphatic vessel endothelial hyaluronan receptor 1	
NM_001113325	/NM_001252403	/NM_008165			1.22E-04	-1.03	-1.10	-1.52	<i>Gria1</i>	glutamate receptor, ionotropic, AMPA1 (alpha 1)
NM_011693		0.00320531	-1.08	-1.43	-1.52	-1.43	-1.52	<i>Vcam1</i>	vascular cell adhesion molecule 1	
NM_001083312	/NM_00410791				-1.45	-1.47	-1.52	<i>Gbp7</i>	glyanlate binding protein 7	
NM_027045	/NM_028407	/NM_006519603	/NM_0027581		-1.03	-1.30	-1.52	<i>Csers2</i>	coiled-coil serine rich 2	
NM_173788	/NM_00033721	0.003112879	3.50E-04	-1.23	-1.28	-1.52	<i>Npr2</i>	natriuretic peptide receptor 2		



RefSeq	Transcript ID	p (24h n=460)	p (48h n=657)	p (72h n=805)	FC 24h	FC 48h	FC 72h	Gene Symbol	Gene Title	Gene Ontology Biological Process
NM_008306	/NM_006525667	9.89E-04	1.76E-04	-1.24	-1.54	-1.52	<b>Ndst1</b>	N-deacetylase/N-sulfotransferase (heparan glucosaminyl) 1	0000165 // MAPK cascade // inferred from mutant phenotype//0000271 // polysaccharide biosynthetic process // inferred from mutant phenotype//0003279 // cardiac septum dev	
NM_138741			0.00143162	-1.06	-1.17	-1.52	<b>Sdpr</b>	serum deprivation response	0045944 // positive regulation of transcription from RNA polymerase II promoter // not recorded	
NM_001290541	/NM_001290543	0.005963474	3.52E-04	-1.12	-1.59	-1.52	<b>Acer2</b>	alkaline ceramidase 2	0001953 // negative regulation of cell-matrix adhesion // not recorded//0006629 // lipid metabolic process // inferred from electronic annotation//0006672 // ceramide metabolic p	
NM_001302255	/NM_001302257	0.004129136		-1.02	-1.30	-1.52	<b>Pmp22</b>	peripheral myelin protein 22	0007049 // cell cycle // inferred from electronic annotation//0007050 // cell cycle arrest // inferred from electronic annotation//0008219 // cell death // not recorded//0008285 //	
NM_0021398	/NM_000951896		0.00471223	-1.25	-1.13	-1.53	<b>Slc33a3</b>	solute carrier family 34, member 3	0055083 // transmembrane transport // inferred from electronic annotation	
NM_026433	/NM_000711232	0.001134347	0.00514138	-1.38	-1.51	-1.53	<b>Tmem100</b>	transmembrane protein 100	0001525 // angiogenesis // inferred from mutant phenotype//0001570 // vasculogenesis // inferred from mutant phenotype//0001701 // in utero embryonic development // infer	
NM_019707	/NM_006530627	3.36E-04	3.62E-05	-1.13	-1.36	-1.53	<b>Cdh13</b>	cadherin 13	0000278 // mitotic cell cycle // inferred from electronic annotation//0001558 // regulation of cell growth // inferred from electronic annotation//0001938 // positive regulation of e	
NM_001081337	/NM_006531024	0.006770804	0.00196578	-1.08	-1.28	-1.53	<b>Sipa12</b>	signal-induced proliferation-associated 1 like 2	004354 // positive regulation of GTPase activity // inferred from electronic annotation//0051056 // regulation of small GTPase mediated signal transduction // inferred from electro	
NM_001109661	/NM_0075211	0.006537666	0.00289919	-1.15	-1.30	-1.54	<b>Bach2</b>	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	
NM_001029836	/NM_001287101	0.007688779	0.00403771	-1.22	-1.48	-1.54	<b>Npnt</b>	nephroctinin	0001657 // ureteric bud development // inferred from mutant phenotype//0001658 // branching involved in ureteric bud morphogenesis // inferred from mutant phenotype//0007	
NM_025809			0.00619041	-1.35	-1.12	-1.54	<b>Clec4A</b>	C-type lectin domain family 14, member a		
NM_001025613	/NM_000480264	0.004081433	1.98E-04	-1.35	-1.42	-1.54	<b>Otu4b</b>	OTU domain containing 7b	0000122 // negative regulation of transcription from RNA polymerase II promoter // inferred from direct assay//0000122 // negative regulation of transcription from RNA polymeras	
NM_019740	/NM_006512806	1.94E-04	1.02	-1.37	-1.54	<b>Foxo3</b>	forkhead box O3	0000122 // negative regulation of transcription from RNA polymerase II promoter // not recorded//0001542 // ovulation from ovarian follicle // inferred from mutant phenotype//C		
NM_001042634	/NM_009095	0.004129136	0.00685503	-1.05	-1.30	-1.54	<b>Cbl1</b>	CDC-like kinase 1	0006468 // protein phosphorylation // inferred from electronic annotation//0016310 // phosphorylation // inferred from electronic annotation//0018105 // peptidyl serine phosph	
NM_010680	/NM_000178259	3.29E-04	0.00205006	-1.33	-1.65	-1.54	<b>Lama3</b>	laminin, alpha 3	0007155 // cell adhesion // inferred from electronic annotation//0016337 // single organism cell-cell adhesion // not recorded//0030155 // regulation of cell adhesion // inferred f	
NM_010231	/NM_006496662	0.006496663	6.95E-04	-1.05	-1.16	-1.55	<b>Fmo1</b>	flavin containing monoxygenase 1	0006082 // organic acid metabolic process // not recorded//0006970 // response to osmotic stress // inferred from electronic annotation//0009404 // toxin metabolic process // nc	
NM_010612	/NM_011240817		0.00352878	-1.03	-1.24	-1.55	<b>Kdr</b>	kinase insert domain protein receptor	0001525 // angiogenesis // inferred from electronic annotation//0015451 // ovarian follicle development // inferred from mutant phenotype//0001570 // vasculogenesis // infer	
NM_001142916	/NM_0119161	0.002469924	5.45E-05	-1.08	-1.55	-1.55	<b>Plod2</b>	procollagen lysine, 2-oxoglutarate 5-dioxygenase 2	0001666 // response to hypoxia // inferred from electronic annotation//0032870 // cellular response to hormone stimulus // inferred from electronic annotation//0055114 // oxid	
NM_001285833	/NM_001285833	0.0015760	0.00468835	-1.28	-1.17	-1.56	<b>Nov4</b>	NADPH oxidase 4	0000902 // cell morphogenesis // inferred from mutant phenotype//0001666 // response to hypoxia // inferred from electronic annotation//0006801 // superoxide metabolic proc	
NM_024288	/NM_000249365		8.01E-05	-1.21	-1.34	-1.56	<b>Rmnd5a</b>	required for meiotic nuclear division 5 homolog A (S. cerevisiae)		
NM_181414	/XR_385	0.00975831	-1.30	-1.30	-1.57	<b>Pik3c3</b>	phosphoinositide-3-kinase, class 3	0000045 // autophagosome assembly // not recorded//0000910 // cytokinesis // not recorded//0006468 // protein phosphorylation // inferred from mutant phenotype//0006897		
NM_172479		6.31E-04	0.00349072	-1.04	-1.81	-1.57	<b>Slc38a5</b>	solute carrier family 38, member 5	0003333 // amino acid transmembrane transport // not recorded//0015804 // neutral amino acid transport // not recorded//0015816 // glycine transport // not recorded	
NM_018738		0.00516403	-1.66	-1.55	-1.58	<b>Igtp</b>	interferon gamma induced GTPase	0035458 // cellular response to interferon-beta // inferred from direct assay		
NM_133670	/NM_006507538	0.0011241719	0.0013462	-1.08	1.20	-1.59	<b>Sut1a1</b>	sulfotransferase family 1A, phenol-prefering, member 1	0006584 // catecholamine metabolic process // not recorded//0006629 // lipid metabolic process // inferred from electronic annotation//0006805 // xenobiotic metabolic process,	
NM_001122733	/NM_000951896	4.47E-04	0.003857236	-1.39	-1.49	-1.59	<b>Kit</b>	kit oncogene	0000187 // activation of MAPK activity // not recorded//0001541 // ovarian follicle development // inferred from mutant phenotype//0002318 // myeloid progenitor cell differentia	
NM_001081433	/NM_006496070	0.006496071	5.05E-04	-1.09	-1.24	-1.59	<b>Ankrd44</b>	ankyrin repeat domain 44	0001843 // neural tube closure // not recorded//0006606 // protein import into nucleus // not recorded//0031398 // positive regulation of protein ubiquitination // not recorded//	
NM_001033217	/NM_000991441	0.00991441	0.00119568	-1.38	-1.29	-1.60	<b>Prickle1</b>	prickle homolog 1 (Drosophila)	0007165 // signal transduction // inferred from electronic annotation//0010811 // positive regulation of cell-substrate adhesion // inferred from direct assay//0019800 // peptide cr	
NM_052994	/NM_006514347	0.006514347	4.21E-05	-1.16	-1.15	-1.60	<b>Spock2</b>	sparc/osteonectin, cvc and kazal-like domains proteoglycan 2	0001504 // neurotransmitter uptake // inferred from mutant phenotype//0002026 // regulation of the force of heart contraction // inferred from mutant phenotype//0002087 // re	
NM_178405			0.00288794	-1.22	-1.27	-1.60	<b>Atp1a2</b>	ATPase, Na <sup>+</sup> /K <sup>+</sup> -transporting, alpha 2 polypeptide	0031032 // actomyosin structure organization // inferred from electronic annotation	
NM_001001980	/NM_001256122	0.00650417	6.47E-04	-1.15	-1.32	-1.61	<b>Limch1</b>	LIM and calponin homology domains 1		
NM_001002900	/NM_000200764	0.00200764	0.00108225	-1.43	-1.32	-1.61	<b>Higd1c</b>	HIG1 domain family, member 1C//methyltransferase hypoxia indi	0000278 // methylation // not recorded	
NM_153145	/NM_006533061	0.005519043	0.00152682	-1.16	-1.42	-1.62	<b>Abca8a</b>	ATP-binding cassette, sub-family A (ABC1), member 8a	0006810 // transport // inferred from electronic annotation//0006869 // lipid transport // not recorded//0008152 // metabolic process // inferred from electronic annotation//000	
NM_001172424	/NM_000445186	0.00445186	1.41E-04	-1.22	-1.23	-1.63	<b>Dhrs3</b>	dehydrogenase/reductase (SDR family) member 3	0001523 // retinoid metabolic process // inferred from mutant phenotype//0003151 // outflow tract morphogenesis // inferred from mutant phenotype//0008152 // metabolic pro	
NM_010260		2.75E-04	0.005782543	-1.49	-1.65	-1.63	<b>Gbp2</b>	guanlylate binding protein 2	0008152 // metabolic process // inferred from electronic annotation//0035458 // cellular response to interferon-beta // inferred from direct assay//0042832 // defense response to	
NM_010358	/NM_006501017	0.006501017	0.00528406	-1.03	-1.22	-1.63	<b>Gstm1</b>	glutathione S-transferase, mu 1	0006749 // glutathione metabolic process // not recorded//0008152 // metabolic process // inferred from electronic annotation//0035690 // cellular response to drug // inferred fr	
NM_019440		0.00668344	-1.77	-1.51	-1.63	<b>Irgm2</b>	immunity-related GTPase family M member 2	0034341 // response to interferon-gamma // inferred from direct assay//0034341 // response to interferon-gamma // inferred from mutant phenotype//0042742 // defense respon		
NM_001143689	/NM_023124	0.007648	0.00373648	-1.46	-1.23	-1.64	<b>H2-Q4</b>	H2-Q4//H2-Q6//H2-Q8//LOC6	0002474 // antigen processing and presentation of peptide antigen via MHC class II // not recorded//0006955 // immune response // inferred from electronic annotation//0013882 //	
NM_001308489	/NM_010216	0.00528700	0.00197627	-1.04	-1.23	-1.64	<b>Fgf1</b>	c-fos induced growth factor	0001525 // angiogenesis // inferred from electronic annotation//0001666 // response to hypoxia // inferred from electronic annotation//0007275 // multicellular organismal develo	
NM_001316728	/NM_00180348	0.00225299	-1.28	-1.26	-1.64	<b>Rn167</b>	ring finger protein 167	0000209 // protein polyubiquitination // not recorded//001567 // protein ubiquitination // inferred from electronic annotation//0045786 // negative regulation of cell cycle // not		
NM_177231	/NM_178220	0.00531968	-1.21	-1.11	-1.65	<b>Arv1</b>	arrestin, beta 1	0000187 // activation of MAPK activity // not recorded//0001933 // negative regulation of protein phosphorylation // not recorded//0001934 // positive regulation of protein phosph		
NM_001284392	/NM_001284394	0.007575203	0.00727098	-1.13	-1.35	-1.66	<b>4-Sep</b>	sepin 4	0007049 // cell cycle // inferred from electronic annotation//0007286 // spermatid development // inferred from mutant phenotype//0007420 // brain development // inferred fr	
NM_001081346	/NM_133244	0.00513290	0.00125755	-1.15	-1.22	-1.67	<b>Rtkn2</b>	rosetin 2	0008284 // positive regulation of cell proliferation // inferred from direct assay//0030097 // hemopoiesis // inferred from direct assay	
NM_001312918	/NM_010145	1.21E-04	0.00408213	-1.13	-1.47	-1.67	<b>Ephx1</b>	epoxide hydrolase 1, microsomal	0006725 // cellular aromatic compound metabolic process // inferred from mutant phenotype//0009636 // response to toxic substance // inferred from electronic annotation//001	
NM_009421	/NM_000	8.30E-04	0.008350425	-1.56	-1.45	-1.68	<b>Traf1</b>	TNF receptor-associated factor 1	0006915 // apoptotic process // inferred from electronic annotation//0007165 // signal transduction // inferred from electronic annotation//0042981 // regulation of apoptotic pr	
NM_001161420	/NM_013703	0.004043921	0.00318838	-1.21	-1.36	-1.68	<b>Vldlr</b>	very low density lipoprotein receptor	0000122 // negative regulation of transcription from RNA polymerase II promoter // inferred from mutant phenotype//0001666 // response to hypoxia // inferred from electronic an	
NM_019919	/NM_206958	0.00524348	0.00751087	-1.13	-1.21	-1.68	<b>Ltbp1</b>	latency transforming growth factor beta binding protein 1	0003281 // ventricular septum development // inferred from mutant phenotype//0007179 // transforming growth factor beta receptor signaling pathway // traceable outer stater	
NM_001136059	/NM_009992	0.009992	1.94E-04	-1.02	-2.58	-1.70	<b>Cyp1a1</b>	cytochrome P450, family 1, subfamily a, polypeptide 1	0001666 // response to hypoxia // inferred from electronic annotation//0001889 // liver development // inferred from electronic annotation//0006778 // porphyrin-containing cor	
NM_023785		0.002648783	-1.10	-1.74	-1.70	<b>Ppbp</b>	pro-platelet basic protein	0002523 // leukocyte migration involved in inflammatory response // inferred from mutant phenotype//0002690 // positive regulation of leukocyte chemotaxis // not recorded//00		
NM_029568	/NM_006534422	0.00237378	-1.23	-1.53	-1.75	<b>Mjpa4</b>	microfibrillar-associated protein 4	0001955 // cell adhesion // inferred from electronic annotation//0009650 // UV protection // not recorded//0010712 // regulation of collagen metabolic process // not recorded//		
NM_029620		0.0048443	0.001332161	-1.35	-1.58	-1.75	<b>Pcolce2</b>	procollagen C-endopeptidase enhancer 2	001952 // positive regulation of peptidase activity // not recorded	
NM_007876		0.00390525	4.74E-05	-1.21	-1.06	-1.75	<b>Dpep1</b>	dipeptidase 1 (renal)	0006508 // proteolysis // inferred from electronic annotation//0016999 // antibiotic metabolic process // not recorded//0030336 // negative regulation of cell migration // not rec	
NM_019521			1.74E-04	-1.11	-1.29	-1.75	<b>Gas6</b>	growth arrest specific 6	0001764 // neuron migration // inferred from genetic interaction//0001934 // positive regulation of protein phosphorylation // not recorded//0001961 // positive regulation of cyt	
NM_008720		0.00173486	0.008053107	-1.49	-1.69	-1.75	<b>Npc1</b>	Niemann-Pick type C1	0006486 // protein glycosylation // inferred from direct assay//0006486 // protein glycosylation // not recorded//0006629 // lipid metabolic process // inferred from electronic an	
NM_008278			5.77E-04	1.05	-1.07	-1.78	<b>Hpgd</b>	hydroxyprostaglandin dehydrogenase 15 (NAD)	0006629 // lipid metabolic process // inferred from electronic annotation//0006631 // fatty acid metabolic process // inferred from electronic annotation//0006693 // prostaglandin	
NM_023755	/NM_000	4.04E-04	0.001339916	-1.33	-1.28	-1.79	<b>Tfcp2l1</b>	transcription factor CP2-like 1	0000122 // negative regulation of transcription from RNA polymerase II promoter // inferred from direct assay//0000902 // cell morphogenesis // inferred from mutant phenotype//	
NM_008986	/NM_011248817	0.006829428	-1.07	-1.32	-1.82	<b>Ptj1</b>	polymerase I and transcript release factor	0006351 // transcription, DNA-templated // inferred from electronic annotation//0006353 // DNA-templated transcription, termination // inferred from electronic annotation//000		
NM_011134	/NM_006505011	0.004530125	8.47E-05	-1.03	-1.30	-1.82	<b>Pon1</b>	paraoxonase 1	0006470 // protein dephosphorylation // inferred from electronic annotation//0006470 // protein dephosphorylation // inferred from electronic annotation//0006629 // lipid metabolic process // inferred from elec	
NM_001077364	/NM_010286	0.001384441	0.00122274	1.13	-1.35	-1.82	<b>Tsc2d3</b>	TSC22 domain family, member 3	0000122 // negative regulation of transcription from RNA polymerase II promoter // inferred from direct assay//0006355 // regulation of transcription, DNA-templated // inferred fr	
NM_013691	/NM_000	7.70E-05	8.99E-06	4.66E-05	-1.65	-2.19	<b>Thbs3</b>	thrombospondin 3	0003417 // growth plate cartilage development // inferred from genetic interaction//0003417 // growth plate cartilage development // inferred from mutant phenotype//0007155 //	
NM_008030			1.09E-04	-1.03	-1.16	-1.85	<b>Fmo3</b>	flavin containing monoxygenase 3	0017144 // drug metabolic process // not recorded//0055114 // oxidation-reduction process // not recorded	
NM_009654		0.00391393	0.002279399	-1.67	-1.83	-1.87	<b>Alb</b>	albumin	0001895 // retina homeostasis // inferred from electronic annotation//0006810 // transport // inferred from electronic annotation//0009267 // cellular response to starvation // nc	
NM_023617	/NM_000468122	0.00468122	1.80E-04	-1.25	-1.15	-1.88	<b>Aox3</b>	aldehyde oxidase 3	0055114 // oxidation-reduction process // inferred from electronic annotation	
NM_020052		0.00325367	1.90E-04	-1.33	-1.79	-1.92	<b>Scube2</b>	signal peptide, CUB domain, EGF-like 2		
NM_009245		0.00709003	0.007495557	0.00443722	-1.73	-1.82	-1.95	<b>Serpina1c</b>	serine (or cysteine) peptidase inhibitor, clade A, member 1C	0010466 // negative regulation of peptidase activity // inferred from electronic annotation//0010951 // negative regulation of endopeptidase activity // not recorded//0034097 // n
NM_001039181	/NM_00011588	1.43E-04	0.00108739	-1.93	-2.82	-2.10	<b>Npp3</b>	natriuretic peptide receptor 3	0001501 // skeletal system development // inferred from direct assay//0001501 // skeletal system development // inferred from mutant phenotype//0002158 // osteoclast prolifer	
NM_026481	/NM_006531324	0.003040487	0.00441058	-1.28	-1.59	-2.18	<b>Tpp3</b>	thymulin polymerization-promoting protein family member 3	0001578 // microtubule bundle formation // not recorded//0046785 // microtubule polymerization // inferred from electronic annotation	
NM_011458		0.00583808	0.003455335	-2.08	-2.18	-2.22	<b>Serpina3k</b>	serpin (or cysteine) peptidase inhibitor, clade A, member 3K	0010466 // negative regulation of peptidase activity // inferred from electronic annotation//0010951 // negative regulation of endopeptidase activity // not recorded//0034097 // n	
NM_008343	/NM_000	0.00213245	6.28E-08	1.21E-05	-1.68	-3.30	-3.86	<b>Igfhr3</b>	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
NM_001045550	/NM_000	8.88E-04	8.61E-05	-6.62	-11.08	-23.14	<b>Gm2083</b>	Gm2083//Gm21320//Mup1// major urinary protein LOC100048885//predicted gene, 21320//h	0006112 // energy reserve metabolic process // inferred from sequence or structural similarity//0006112 // energy reserve metabolic process // inferred from direct assay//000681	

Table S2. Top 50 chemical drugs among upstream modulators of O3-responsive transcriptome (24-72 hr) suggestive to be therapeutic targets for O3 toxicity.

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Upstream Regulator	Molecule Type	Predicted Activation State	Activation z-score	p-value of overlap	Target molecules in dataset
calcitriol	chemical drug	Inhibited	-4.214	1.60E-24	ABCB1,ACADS5,Acps,ADCY9,ALB,ANGPT2,ANLN,AREG,ARGHEF3,BCL2L1,BCL3,BIRC5,BUB1B,CCL20,CCNA2,CCNE1,CD14,CD20,CD36,CDCA5,CDK1,CDKN1A,CDT1,CEBPB,CEBPD,CENPA,CENPQ,CESE1,CHTF18,CTSK,CXCL10,CYP1A1,CYR61,DCTPP1,DUSP10,ECT2,EDN1,ERBB2,ERBB3,ETV5,F3,FASN,FDPS,FDX1,FIGLN1,FN1,GADD45G,GATA3,GLRX,GRK5,GRK6,HBEFG,HK2,Hmg2 (includes others),HPGD,JD2,IGFBP3,IL18,IL1L1R,IL1RN,IL6,INCEP,ITGAX,KIF20A,KIF23,KPNA2,KRT23,LCN2,LGALS1,LIG1,LPAR1,LTBP1,MAD2L1,MAL,MCM2,MCM3,MCM5,MCM7,MEK1,MYC,MYD88,NCAPD2,NDC1,NOX4,NRM,NUSAP1,PBK,PC,PCNA,PDE9A,POLE,POLE2,PRC1,PTGS2,PTRF,RAB32,RACGAP1,RAD51,RRM2,S100A8,S100A9,S100G,SDSL,SERPINA1,SLC16A1,SLC25A36,SOC35,SPP1,STMN1,TCF19,THBD,THBS1,TK1,TLR2,TMEM100,TPX2
dexamethasone	chemical drug		-1.744	1.65E-22	AACS,ABCB1,ACADM,ACOT7,Acps,ACTG1,ADAMTS1,ADRB3,Akr1c14,ALB,ANGPT4,ANXA1,APLN,AREG,ARL4C,ARRB1,ATF4,ATN1,AXIN2,B4GALT4,BCKDHA,BCL2L1,BHLHE40,BIRC3,BIRC5,C8orf4,CASP6,CAV1,CCL17,Ccl2,CCL20,CCNA2,CCND2,CCNE1,CCR1,CD74,CDKN1A,CEBPB,CEBPD,CESE1,CHI3L1,CLEC7A,CNN3,CP,CRYAB,CTGF,CTSK,CUL1,CXCL10,CXCL14,CYP1A1,CYP251,CYP3A5,CYP51A1,CYR61,DAPK1,DCNT6,DUSP10,DUSP16,DUT,ECT2,EDN1,EGR2,EIF1AX,ELOVL1,EPB41L4B,EREGL,ETV5,F3,FASN,FBN1,FOX1,FGF7,FMO1,FN1,FOSL1,FOXO3,FOXQ1,FST,GAB1,GAL,GAS6,GATA3,GBP2,GCLC,GIA1,GPX1,GRK5,GSTM5,GZMA,HBEFG,HERPUD1,HLA-A,HMMGR,HNRNPAB,HOMER2,HSD11B1,HSPH1,JD2,JFT1B1,JFRD1,IGFBP2,IGFBP3,IL18,IL1B,IL1RN,IL13,IL4R,IL6,ILF2,IRS1,IRS2,JVD,JUNB,KOR,KIF4A,KIT,KHLH24,KPNA2,KRT7,KRT8,LAMA2,LAMA3,LAMA4,LCN2,LDHA,LDLR,LGALS1,LGALS2,LPAR1,LRRC8A,LSS,LTB,LTBP2,LVVE1,MAP3K5,MARCO,MAT1A,MAT2A,MATN4,ME1,MFAP5,MFGE8,MIF,MXIP,MMP12,MMP14,MMP2,MMP9,MS4A1,Mt1,Mt2,MVK,M/C,N4BP2L1,NFIL3,NPR2,NPR3,NR3C1,NREP,NUF2,P2RY2,P4HA2,PC,PKD2,PER1,PHLDA1,PLDOD2,POU2AF1,PPA1,Ppdp,PRELP,PRSS8,PTGES,PTGS1,PTGS2,RACGAP1,RASD1,RBL2,RCAN1,RG52,ROSA,S100A8,S100A9,S100G,Saa3,SCD,SDPR,SELE,SELL,SERPINA1,SERPINA3,SERPINE1,SESN1,SLC25A5,SLC2A3,SLC40A1,SLC4A1,SMARCD2,SOC35,SOD2,SPARC,SPOCK2,SPP1,SRF,SRM,SULF2,Suit1a1,TFFI2,TFR2,TGFB1,THBD,THBS1,TIMP1,TIMP2,TK1,TLR2,TMPRSS4,TNC,TNFAIP2,TNFRSF19,Tnfrsf9,TP2A,TRAF1,TRRAP,TSC22D3,TSPAN2,TSPY14,UBE2C,VCAM1,VMPI1,XRCC5,ZFPM1,ZNF704
dextran sulfate	chemical drug		0.77	9.83E-19	ADAMTS1,ADORA2B,ANLN,AURKA,BIRC5,BUB1,BUB1B,Ccl2,CCNA2,CCNF,CD14,CD74,CD20,CDCA3,CDCA5,CDK1,CHTF18,CKS1B,CTGF,E2F8,ERCC6,FGF1,FIGLN1,GSTM5,JFT1B1,IL18,IL1B,IL6,MCM3,MC M5,MCM6,MKI67,MMP14,MMP2,MMP9,MNS1,MYC,MYLK,NCAPD2,NDS1,NUSAP1,OSMR,PCNA,PLK1,POLE,PRC1,PTGS2,RACGAP1,RAD51,RRM2,S100A8,S100A9,Saa3,SERPINE1,SOC35,SP2C5,STMN1,THBS1,TIMP2,TP2A,TPX2,UBE2C,UHRF1,VCAM1
PD98059	chemical - kinase inhibitor	Inhibited	-3.868	1.11E-17	ACOT7,ANGPT2,ANXA1,AREG,ARRB1,ATFS,ATF4,BCL2L1,BIRC5,CAV1,Ccl2,CCL20,CCNA2,CCND2,CCNE1,CCR1,CD14,CD74,CDKN1A,CEBPB,CEBPD,CLU,CTGF,CTSK,CXCL10,CYP1A1,DHRS3,DNMT1,EDN1,EGR2,ERBB2,F3,FBN1,FOXO3,GCLC,GPX2,GSR,H2AFX,HBEFG,JD2,IL1B,KIF20A,KRT18,KRT8,LCN2,LGALS1,MAD2L1,MAP4,MCM3,MFE2C,MMP2,MYC,NFE2L2,NOXA,PCNA,PID1,PLK1,PRC1,PTGS2,PTTG1,Pvr,RAC2,RAD51,RBL2,RRM2,SCN3B,SDCC,SESN1,SFN,SIRT3,SOD2,SPP1,STMN1,TIMP1,TK1,TNFRSF12A,TP2A,TUBB
doxorubicin	chemical drug		-0.398	5.60E-16	ABCB1,ADAMTS1,ADORA2B,ALB,ANXA1,AREG,ATF3,AURKA,AURKB,BCL2L1,BHLHE40,BIRC3,BIRC5,BMP4,BUB1B,Ccl2,CCNB2,CD14,CDK1,CDKN1A,CENPA,CKAP4,CLDN4,CLU,CP,CTGF,CYR61,DNMT1,EDN1,EIF5A,ELF3,ERBB2,F3,FBN1,FOXO3,GCLC,GPX2,GSR,H2AFX,HBEFG,JD2,IL1B,KIF20A,KRT18,KRT8,LCN2,LGALS1,MAD2L1,MAP4,MCM3,MFE2C,MMP2,MYC,NFE2L2,NOXA,PCNA,PID1,PLK1,PRC1,PTGS2,PTTG1,Pvr,RAC2,RAD51,RBL2,RRM2,SCN3B,SDCC,SESN1,SFN,SIRT3,SOD2,SPP1,STMN1,TIMP1,TK1,TNFRSF12A,TP2A,TUBB
LY294002	chemical - kinase inhibitor	Inhibited	-3.879	4.22E-15	ABCB1,ADAMTS1,ADH1C,ATF3,ATF4,AURKA,BCL2L1,BHLHE40,BIRC3,BIRC5,BUB1B,Ccl2,CCNA2,CCND2,CCNE1,CCR1,CD14,CD74,CDKN1A,CEBPB,CKS2,CLDN4,CP,CTGF,CXCL10,CYR61,EGR2,EIF1AX,ERBB3,EREG,F3,FASN,FGF7,FN1,FOSL1,GCLC,GIA1,GRB10,GSR,HBEFG,HERPUD1,HMG82,HMGCR,HMGCS1,IGFBP2,IGFBP3,IL1B,IL1RN,IL6,IRS1,IRS2,JUNB,KLF10,LCN2,MAT2A,ME1,MFE2C,MMP14,MMP2,MMP9,MPP2,MYC,MYH11,NFE2L2,NPTX1,PCNA,PGK1,PHLDA1,PTGS2,PTPN2,PTPRU,RBL2,RF4,SGS2,SCD,SERPINE1,SFN,SLCO1A2,SOC35,SPP1,SQLE,SRF,TFFI2,THBD,THBS1,TLR2,TP2A,TRB2,UBE2C,VCAM1,ZEB1
trichostatin A	chemical drug		-0.638	1.50E-14	ABCB1,ADAMTS1,ADAMTS5,ANXA6,ARL6IP1,AURKB,BCL2L1,BMP4,CAP2,Ccl2,CCNA2,CCNB2,CCND2,CD14,CD79B,CD36,CDK1,CDKN1A,CKS1B,CLU,CREBBP,CSF3R,CTPS1,CXCL10,CYP1A1,CYP3A5,CYP4B1,DLA1,DNMT1,DUSP16,ELF3,ERBB2,F3,FASN,FBN1,FOX2,FUT8,GADD45G,GATA3,GCLC,GSN,GSTA3,HLA-DRA,HMGR,HMGCS1,HMGCS2,JD2,IGFBP3,IL1B,IL6,KDR,KIF20A,KIT,LAMA2,LAMA3,LDLR,LEPR,MAP4,MAT1A,MAT2A,MCM3,MCM6,MGST3,MMP9,MVK,MYC,MYH14,NDRG2,NPC1,PCNA,PLCE1,PLK1,PTGRC1,PRDM1,PRSS23,PTGS1,PTGS2,RECK,Retna,SDC1,SDCC,SELE,SIAH2,SFR,STMN1,STMN2,TFFI2,TGM1,THBS1,TIMP1,TIMP2,TK1,TLR2,TNFAIP2,TP2A,VCAM1,ZEB1
bleomycin	chemical drug	Activated	4.062	4.07E-14	ANGPT2,BCL2L1,CCL17,Ccl2,CCL22,CCR1,CDKN1A,CTGF,CTSK,CTSS,CXCL10,FABP1,FN1,FOSL1,FZD6,H2AFX,HBEFG,IL18,IL1B,IL4R,IL6,LNMB1,MAP4,MIF,MMP12,MMP14,MMP2,MMP9,MYC,MYCT1,NDN1,CNA,PTTG1,Retna,S100A4,Saa3,SERPINE1,SPP1,TIMP1,TIMP2,TLR2,UBE2C,UBE2T,UHRF1,WISP1
paclitaxel	chemical drug		0.857	7.45E-13	ABCB1,ADORA2B,APLN,AREG,ATF3,ATF4,BCL2L1,BHLHE40,BIRC3,BIRC5,CAV1,CD20,CDKN1A,CLU,CRY2,CTGF,CXCL10,CYP1A1,CYP3A5,DNMT1,DUSP10,EEF1E1,EPHA2,EREG,ETV5,FMO3,FOSL1,FOXO3,H2AFX,HBEFG,HLA-A,IGFBP3,IL1B,IL6,ITGA6,KIF20A,MMP9,MYC,NREP,OSMR,PCNA,PHLDA1,PLAUR,PRELP,PTGS2,RAC2,S100A9,SLC2A3,SOD2,SPTLC2,SRF,STMN1,TFFI2,THBD,THBS1,TRAF1,TULP3,UHRF1
ritonavir	chemical drug		-1.114	2.17E-12	ABCB1,AXIN2,BCL2L1,BIRC5,CCND2,CRYAB,CYP1A1,CYP3A5,DHCR7,ECT2,FDPS,GBP2,HMGR,HMMR,IFRD1,IL1B,IL6,LAMA3,LDLR,ME1,MMP9,MSMO1,MVK,MYC,NUF2,RACGAP1,SCD,SELE,SQLE,TMEM140,TMPRSS4,TSC22D3,VCAM1,XRCC5
simvastatin	chemical drug		-1.964	3.19E-12	ADAMTS1,ANGPT2,Anp32a,ANXA1,ANXA3,BCL2L1,BIRC5,CCL20,CCND2,CD14,CDKN1A,CTGF,CYR61,EDN1,F3,FABP1,GIA1,HIST1H1C,HMGCR,HS3T1,IGFBP3,IL1B,IL6,ITGB2,KIT,LCN2,LDLR,MKI67,MMP2,MMP9,MPP6,MYC,PON1,PTGS2,RHOA,S100A6,SELE,SERPINE1,SOC35,SPP1,STAT6,THBD,TIMM10,TIMP1,TLR2,VCAM1
mibolerone	chemical drug	Activated	4.11	3.48E-12	ALDH3A1,CD74,CDK1,CLTB,CLU,CYP51A1,DHRS3,EIF2S1,ERP29,F3,FDPS,FN1,GADD45G,HMGCS1,IGFBP3,INCEP,ISYNA1,KLF10,LDLR,LRG1,LSS,MAL,MAT2A,MYC,NME1,NME2,PCNA,PGK1,PRELP,SERP1,SLC25A5,SQLE,SRM,STMN1,TGFB1,TK1,TP2A,UCLH5
gefitinib	chemical drug		0.715	3.78E-12	ADAMTS1,AREG,AURKA,AURKB,BCL2L1,BIRC5,BUB1,Ccl2,CCNE1,CCNF,CD36,CEBPB,CEBPD,CYP2F1,ECT2,FOSL1,FSCN1,GJA1,HSPB1,KIF23,KIT,KRT19,MCM3,MKI67,MMP11,MMP15,NOX4,OSMR,PCNA,PLAUR,PRC1,PTGS2,PTTG1,S100A14,S100A9,SLC2A3,Suit1a1,TIMP2,TLR2,TP2A,TRAF1,VILL
mifepristone	chemical drug		1.135	5.37E-12	ABCB1,ANXA1,AREG,ATF3,BCL2L1,CAV1,Ccl2,CD14,CD74,CDKN1A,CEBPB,CEBPD,CHI3L1,CLU,CTGF,CYP3A5,DKK3,DNAJC2,EGR2,EPCAM,F3,FST,GAL,GAS6,GJA1,HBEFG,HPGD,HSD11B1,IGFBP3,IL1B,IL4R,IL6,IRS2,JUNB,KIT,LAMA2,LDLR,MAD2L1,MMP9,Mt1,MYC,NDN,NFE2L2,NME2,NOX4,NR3C1,PC,PCNA,PTGS1,PTGS2,SGS2,S100A6,S100G,Saa3,SERPINE1,SERPINE1,SLCO1B3,SPP1,SRM,TK1
U0126	chemical - kinase inhibitor	Inhibited	-2.22	8.65E-12	ABCB1,ADAMTS4,ADORA2B,ANGPT4,APLN,AREG,ATF3,ATF4,AXIN2,BCL2L1,BHLHE40,BIRC3,BIRC5,CAV1,CCL17,Ccl2,CCND2,CCNE1,CDH5,CDKN1A,CEBPB,CEBPD,CLDN4,CRY2,CTGF,CXCL10,CYP1A1,DP P,DUSP10,EDN1,EEF1E1,EIF1AX,EPHA2,EREG,ETV5,F3,FMO3,FN1,FOSL1,GCLC,GIA1,GRIA1,GSN,HBEFG,HERPUD1,HPGD,IL1B,IL6,ITGA6,JUNB,KDR,KLF10,LDLR,MAT2A,MMP12,MMP2,MMP9,MYC,NREP,C SMR,PER1,PHLDA1,PLAUR,PRELP,PTGS2,RAC2,S100A9,SERPINE1,SLC2A3,SOC35,SPP1,SPRR1A,TFFI2,THBS1,TIMP2,TLR2,TRAF1,TSC22D3,TULP3,VCAM1,WISP1
decitabine	chemical drug		-0.508	1.25E-11	ABCB1,ANGPT4,BIRC3,BMP4,CAV1,Ccl2,CCNA2,CCND2,CD79B,CDH13,CDK1,CDKN1A,CHI3L1,CLU,CTGF,CXCL10,CYP1A1,CYP3A5,CYP4B1,DAPK1,DNMT1,FN1,FOXF2,GADD45G,GLRX,GPX1,GSN,HBEFG,HK2,HMGCS2,HMMR,HPGD,HSPA1A/HSPA1B,IGFBP2,IGFBP3,IL1B,IL6,JUNB,KRT18,KRT7,KRT8,LAMA2,LAMA3,LDLR,LEPR,LGALS3,MAT1A,MGST3,MKI67,MMP14,MMP2,MMP9,MYC,NME1,NPTX1,NR3C1,PCNA,PDE9A,PLCE1,PTGS2,RECK,RNASE4,RRAD,SELL,SERPINH1,SFN,SLC2A3,SLCO1B3,SMARCA2,SOC35,SPARC,SPP1,TFFI2,TFR2,TGFB1,THBD,THBS1,TIMP2,TP2A
dihydrotestosterone	chemical - endogenous mammalian		1.248	3.96E-11	Acps,ADAMTS1,ADH1C,ADRB3,AREG,AXIN2,BCL2L1,BUB1B,CCNA2,CCND2,CCNE1,CD74,CD20,CD36,CDKN1A,CHI3L1,CLU,CST8,CTGF,CYP4B1,DCTPP1,E2F8,EPB41L4B,ERBB2,FASN,FGF7,FN1,Foxp1,FOX Q1,FST,FZD6,GAS6,GPX3,GRWD1,GSN,HK2,HLA-A,HMGR,HOMER2,HOXA5,HPGD,HSPA1A/HSPA1B,HSPB1,JD2,IGFBP2,IGFBP3,IL6,IRS2,KRT19,LDHA,LDLR,LGALS1,LTBP1,MAFF,MCM5,ME1,MMP2,Mt1,MYC,MYLK,NR3C1,PC,PDE9A,PER1,PFN1,PHF21A,PHLDA1,PTGER4,PTGS2,RARRES2,RASSF9,SCD,SELENBP1,SLC1A3,SLC2A3,SPARC,SPP1,SQLE,STXBP1,TACC2,TALDO1,THBS1,TKT,VCAM1,VLDLR,ZEB1
3-deoxy-2-octulosonic acid(2)-PPARA	chemical - endogenous non-mammalian ligand-dependent nuclear receptor		1.387	4.09E-11	Ccl2,CH25H,CXCL10,DHCR7,HMGR,JFT1B1,IL1B,IL6,LSS,PTGES,PTGS1,PTGS2,SQLE
			-0.867	4.96E-11	ACADM,ADRB3,ANGPT4,AURKA,BCL2L1,C1R,C1S,Ccl2,CCNA2,CCNE1,CDK1,CDKN1A,CEBPB,CEBPD,CHKA,CSAD,CYP1A1,CYP51A1,CYP7B1,DHCR7,EDN1,FABP1,FASN,FDPS,H2AFX,HIST1H1C,HMGR,HMG CS1,HMGCS2,Hmg2 (includes others),IGFBP2,IGFBP3,IL1RN,IL6,KIF20A,KIF4A,KRT23,KRT8,LGALS4,LSS,MAD2L1,MAT2A,MGST3,MKI67,MMP9,MSMO1,MVD,MVK,MYC,NFE2L2,NR1D1,PC,PCNA,PHLDA1,PLA2G7,PLK1,PLTP,PMVK,PON 1,PPA1,PRC1,PTGS2,RETSAT,RNF186,SCD,SELENBP1,SORD,SQLE,SRM,TALDO1,TLR2,TP2A,UCLH5,UQCRC1,VCAM1

Upstream Regulator	Molecule Type	Predicted Activation State	Activation z-score	p-value of overlap	Target molecules in dataset
phorbol myristate acetate	chemical drug	Activated	2.671	5.28E-11	ABC1,ACOI,ADAMT51,ADAMT54,ADRB3,AKR1B10,ALB,ANGPT2,ANGPT4,ANXA1,AREG,AURKA,AURKB,BCL2L1,BIRC3,BIRC5,CAPG,CAV1,Ccl2,CCL20,CCNA2,CCND2,CCNE1,CCNH,CD14,CD68,CDK1,CDKN1A,CE51,CH25H,CMKP1,CREBBP,CTGF,CXCL10,CYP1A1,CYR61,DBGP,DDP,DNM1,ECM1,EGR2,EIF5A,EPHA2,ERBB2,ERCC6L,F3,FCER1G,FDX1,FGF7,FOSL1,FST,GAL,GATA3,GCLC,GJA1,GK5,HAS1,HBEFG,HLA-DRA,HXA5,HS011B1,ID2,IGFBP2,IGFBP3,IL18,IL1B,IL1RN,IL6,ITGAX,ITGB2,JUNB,KIT,LCN2,LDLR,LEPR,LTB,LVYE1,MMP11,MMP12,MMP14,MMP2,MMP9,MRP12,MYC,NF13,NFKBIE,NME2,NPR3,P2RY2,PCNA,PER1,PKM,PLAUR,PON1,POU2AF1,PRKE,PTGER4,PTGES,PTGS1,PTGS2,RANBP1,RCAN1,Retnla,SGS2,S100A8,S100A9,S100A9,SDC1,SELE,SELL,SERPINA1,SERPINA3,SERPINE1,SLC16A1,SOC3,SOD2,SPARC,SPP1,SPRR1A,TEF,TEKT1,TFPI2,TGM1,THBS1,TIMP1,TK1,TLR2,TNFRSF12A,TRAF1,TRPC1,TSC22D3,TSHB,VCAM1,VLDLR,ZEB1
fulvestrant	chemical drug	Inhibited	-2.716	6.31E-11	ADCY9,AREG,ATF4,AURKA,BIRC5,BMP4,CAV1,Ccl2,CCNA2,CCNE1,CD74,CDC20,CDK1,CDKN1A,CENPF,CHTF18,CXK1B,CLK1,CXCL10,CYR61,ERBB3,GAL,GJA1,H2AFX,ID2,IL1B,IRS1,KLF10,LDLR,LEPR,MCM2,MCM3,MCM5,MCM7,MYC,NME1,PCNA,POLE,PRSS23,PTGS2,PTTG1,RBL2,RFCS,S100G,SHH2,SLC25A5,STMN1,TFRC,TK1,TSC22D3,UBE2C,VCAM1,ZEB1,ZFX
indomethacin	chemical drug	Activated	0.906	7.59E-11	ADAMT51,ADAMT55,ANGPT2,ANXA1,BCL2L1,BIRC3,BIRC5,Ccl2,CD14,CDKN1A,CEBPB,CLDN4,CLU,CP,DDC,ELF3,FASN,FCGR2A,FGF7,GPX2,HAS1,IL1B,IL6,KRTR,LCN2,LDLR,LGALS3,MCM3,MMP12,MMP14,MMP2,MYC,PCNA,PLAUR,Ppbb,PTGER4,PTGES,PTGS1,PTGS2,Pvr,S100A8,SDC1,SELL,SPP1,TFPI2,TIMP1,TNFRSF12A,TUBB,XRCC5
nitrofurantoin	chemical drug	Activated	2.152	8.19E-11	ACADM,ACTG1,ADAMT51,ALB,BCL2L1,CASP6,CE51,CLU,CP,CTSS,CXCL10,ERBB2,FABP1,FETUB,FGF7,GPX2,GSR,HMGR,HMGC51,HMGC52,IFRD1,IGFBP3,IL1B,IL6,ITIH4,KRT19,LGALS3,MMP12,MMP14,Mt1,MYC,PCNA,SDC1,SELENBP1,SERPINA1,SPP1,STMN1,TIMP1,TNFRSF12A,TUBB,VCAM1
gentamicin	chemical drug	Activated	4.668	8.94E-11	ACADM,ACADS,ASNSD1,ATF3,Ccl2,CDC34,CEBPB,CHKA,CHORDC1,CIPC,CLU,CP,CQ,SPR2,CXCL10,CYP1A1,DDC,DDX39A,DMD,DPEP1,FMO1,GNL3,GSTM5,H2AFX,HSPA1A/HSPA1B,HSPB1,IFRD1,IGFBP3,IL1B,JUNB,KTI12,LCN2,MCM6,MYBBP1A,MYC,NCL,NME1,NOP58,NR1D1,PC,PLIP,PSAT1,Pvr,RPS27L,S100G,SPP1,ST6GALNAC3,Suit1a1,TFRC,TIMP1,TUBB,VCAM1
medroxyprogesterone acetate	chemical drug	Inhibited	-2.697	2.80E-10	ANGPT2,ANLN,ASPM,BCL2L1,BIRC5,Ccl2,CCNB2,CDK1,CENPF,CXCL10,CYP1A1,CYR61,ERBB2,F3,FASN,FN1,GCH1,HS011B1,HTRA1,IL1B,IL6,ITGB2,JUNB,MCM5,MYC,MYLK,NUSAP1,PKB,PRC1,SCD,SPC25,TFPI2,TNC
acetaminophen	chemical drug	Activated	2.716	4.16E-10	ABC1,ACADM,ACO1,ACTG1,ALB,BCKDHA,Ccl2,CCR1,CDKN1A,CE51,CXCL10,CYP3A5,FABP1,GPX1,GSR,HMGR,HMGC51,HMGC52,IFRD1,IGFBP3,IL18,IL1B,IL6,IRS1,KDR,ME1,Mt1,MYC,NDRG2,PCNA,PLAUR,PTGS2,Retnla,SOC3,TUBB,VCAM1
methylselenic acid	chemical reagent			5.73E-10	ADAMT51,ATF3,AURKA,BCL2L1,BIRC3,BIRC5,BMP4,BUB1B,CCNA2,CCNB2,CD20,CD6,CDK1,CDKN1A,CENPA,CENPF,CLU,CORO1A,DUSP10,ELF3,ENPP5,EPHX1,FN1,H1F0,HMMR,HNRNP3J,DI2,JUNB,MCM2,MCM3,MCM5,MCM6,MCM7,MKI67,MYC,NF13,NREP,PCNA,PEG3,PLK1,POLA1,POLE2,PTGES,RFCS,RRM2,SCD,SH3BP5,TLR2,TO2A,ZFX
raloxifene	chemical drug		-0.208	6.22E-10	ADCY9,ANXA3,AREG,BCL3,BMP4,CB6,CDKN1A,CLK1,CLU,CTSH,EDN3,ERBB2,ERBB3,FMO5,HSPA1A/HSPA1B,IFJ0,IL18,IL6,KRT7,LDLR,MFAPS5,MIF,MKI67,MMP2,PCNA,PPP1R3C,PRSS23,PTGS2,PTTG1,RF4,SELENBP1,SERPINE1,SHH2,SPP1,TFRC,THBD,TIMP1,TO2A,ZFX
cisplatin	chemical drug	Activated	2.839	7.27E-10	ACADM,ADAMT51,ALB,ANXA1,ASCC1,ATF3,ATF4,BCL2L1,BIRC3,BIRC5,BMP4,C8orf4,CASP6,CAV1,Ccl2,CCR1,CD14,CDK1,CDKN1A,CHKA,CLDN4,CLIP4,CLU,CP,CTGF,CXCL10,CXCL14,DHRS3,EDN1,ELF3,ERBB3,F3,FADS3,FASN,FBXW7,FCGR2A,FN1,FOSL1,FYN,GPX2,GRIA1,H2AFX,HEYL,HK2,HMGR,HMGC51,ID2,IGFBP3,IL18,IL1B,IL4R,IL6,ISYNA1,ITGA7,KRT19,LCN2,LGALS3,MAT1A,MCM3,MMP2,Mt1,MYC,NEO1,NOX4,NREP,PIDD1,PIK3C3,PLK1,PTGES,Pvr,RAD51,RPS27L,RRM2,SERPINE1,SESN1,SLC25A36,SLC2A3,SOC3,SPP1,STMN1,THBS1,TIMP1,TLA4,TNFRSF12A,TO2A,TUBB,UHRF1,USP3,VCAM1,XPC
AGN194204	chemical drug		1.306	8.40E-10	ARL4C,ATF3,AURKA,CCNA2,CDK1,CDKN1A,CHKA,CYP51A1,CYP7B1,DENND5A,DHCR7,FDP5,FDX1,Foxp1,GATA3,GBP2,GJA1,H2AFX,HIST1H1,HC2,Hmgn2 (includes others),Jgtp,IL4R,IRS2,ITGB2,KIF20A,KIF4A,LGALS1,LSS,MAD2L1,MKI67,MMP9,MYC,NNSAF,PHLDA1,PLK1,PRC1,SCD,SPP1,TIMP1,TO2A
tretinoin	chemical - endogenous mammalian	Inhibited	-3.136	8.88E-10	Acp5,ADAMT55,ALDH3A1,ANGPT4,ANXA1,ANXA6,APCCD1,APLN,APLN,AREG,ATF4,BCL2L1,BCL3,BHLHE40,BIRC3,BIRC5,BMP4,CALM13,CASP6,Ccl2,CCL20,CCL22,CCNA2,CCND2,CCNE1,CCR1,CD14,CD68,CD74,CDC20,CDH5,CDKN1A,CEBPB,CE51,CHKA,CHN2,CX52,CP,CSF3R,CTGF,CTSC,CTSK,CTSS,CXCL10,CYP1A1,CYP251,CYP4B1,CYR61,OHRS3,DMC1,EDN1,ELF3,EPACM,EPHX1,F3,FCER1G,FN1,FOSL1,FOXO3,FST,GJA1,GPX1,GPX2,GRB10,GRIA1,GZMA,HBEFG,HDFG,HLA-A,HMGC52,HXA5,HXB5,HS3T1,HS011B1,HSPB1,ID2,IF44,IGFBP2,IGFBP3,IL1B,IL6,INMT,IRS1,ITGA6,ITGAX,ITGB2,IVD,KCNE4,KDR,KIF23,KIT,KRT18,KRT19,KRT7,LAMA4,LEPR,LGALS1,LRP2,MAP3K5,M,EF2C,MERTK,MGST3,MMP11,MMP14,MMP9,MPP6,MS4A1,Mt1,MTHFD2,MYC,NCL,NCOA5,NFE2L2,NME2,NR3C1,P2RY2,P4HA2,PARP1A,PFN1,PGD,PHLDA1,PIK3C3,PLA2G7,PLAUR,PLCE1,PTGES,PTGS1,PTGS2,PTPRU,RRRES2,RBL2,RF4,RTKN2,S100A8,S100A9,SCD,SELL,SERPINE1,SERPING1,SLC16A1,SLC25A36,SLC38A2,SOX4,SPARC,SPP1,STAT6,TAL1,TB2,TFRC,TGFB1,TGM1,THBD,THBS1,TIMM8A,TIMP1,TK1,TLR2,TNC,TNFAIP2,TNFRSF19,Tnfsf9,TO2A,TSC22D3,TSHB,TYROBP,UBE2C,USP3,VCAM1,VMP1,XRCC5
sirolimus	chemical drug	Inhibited	-3.212	1.56E-09	ACADM,ADSS,ATF4,ATP6V1G1,BCKDHA,BCL2L1,BCL3,BEX1,BIRC5,Ccl2,CCND2,CCNE1,CD68,CDKN1A,CEBPB,DNAJC2,EIF1AX,EIF2S1,ERBB2,ERBB3,F3,FASN,FN1,FSCN1,GATA3,GCLC,GLA,GRIA1,HMGC52,ID2,IL1B,IL4R,IL6,IRS1,IRS2,JUNB,KDR,LCN2,LDHA,LEPR,LGALS3,MMP14,MMP2,MMP9,Mt1,MYC,MYH11,NCL,NR3C1,PCNA,PGK1,PKM,PLAUR,PSM3,S100A8,SCD,SELL,SERPINE1,SPN,SLC25A5,SLC3A3,SOC3,SQLE,STMN1,THBD,TIMP1,TMPD,TO2A,TRIM25,UCK2,VCAM1,VMP1
sulfurafan	chemical drug		-0.297	1.81E-09	ABC1,AKR1B10,AOX1,BCL2L1,BIRC5,CDKN1A,DDC,DNM1T1,EPHX1,GATA3,GCLC,GPX1,GPX2,GSR,GSTA3,GSTM5,IL1B,IL6,MMP9,Mt1,NFE2L2,PTGES,PTGS2,SELE,SOC3,TAALD01,TKT,TXNRND1,VCAM1,ZEB1
deferoxamine	chemical drug		1.559	1.84E-09	ANGPT2,ANGPT4,APLN,BHLHE40,CCL20,CCND2,CCNE1,CD14,CDKN1A,CP,CYP3A5,DUSP10,DUSP16,ECM1,F3,FASN,HK2,HSPA1A/HSPA1B,IGFBP2,IGFBP3,IL6,ITGB2,KIT,LAMA3,LCN2,LDHA,ME1,MMP2,M546A,MYC,NF13,PGK1,PKM,PLAUR,SELE,SERPINE1,SLC2A3,SPP1,SULF2,TFRC,VCAM1
epigallocatechin-gallate	chemical drug		-0.646	1.98E-09	ANGPT2,BCL2L1,BIRC5,CASP6,CCL17,CCL22,CDKN1A,CEBPB,CTGF,CTSK,CXCL10,CYR61,DNM1T1,EDN1,ERBB2,F3,FN1,FOSL1,FOXO3,GCLC,GJA1,GSR,IL18,IL1B,IL6,JUNB,KDR,LDLR,MAP3K5,MKI67,MMP2,MMP9,MYC,NFE2L2,PCNA,PRKE,PTGS2,SERPINE1,SLC16A1,TACSTD2,TFRC,TIMP1,TRAF1,VCAM1
SB203580	chemical - kinase inhibitor	Inhibited	-2.391	2.83E-09	Acp5,ADAMT54,ADAMT58,ANXA1,ANXA3,ATF3,BDKRB1,BIRC5,BMP4,CCL17,Ccl2,CCL20,CDK1,CDKN1A,CEBPB,CTGF,CTSK,CXCL10,CYP1A1,ERP29,F3,FN1,FPR2,GBP2,GJA1,GLRX,HAS1,IGFBP3,IL18,IL1B,IL1RN,IL6,JUNB,KDR,KRT23,MAT2A,MMP12,MMP9,MYC,MYH11,PLAUR,PTGES,PTGS2,SELE,SERPINE1,SERPING1,SOC3,SOD2,SPARC,SPP1,TGM1,THBS1,TIMP1,TIMP2,TLR2,TRAF1,VCAM1,ZFYVE26
lovastatin	chemical drug		0.868	3.94E-09	ADAMT51,ALB,ATF3,ATF4,BCL2L1,BIRC5,CCNA2,CDKN1A,CTGF,DHCR7,FASN,FDP5,GATA3,GPX3,HMGR,HMGC51,IL1B,IL6,LDLR,MKI67,MPP6,MVD,MVK,MYC,NOX4,PMVK,PTGS2,RRRES2,RHOV,SERPINE1
cyclosporin A	biologic drug		1.069	4.23E-09	ADORA2B,ANG,ANXA1,ATF3,BCL2L1,BIRC3,CAV1,CD14,CD68,CDKN1A,CLDN4,CLU,CP,CTGF,CYP3A5,EDN1,EGR2,ELF3,F3,FASN,FCGR2A,FN1,FST,FYN,GJA1,GPX2,GZMA,H2AFX,HERPUD1,HMGR,IL1B,IL6,KDR,LAMA3,LCN2,LDLR,LGALS3,LVYE1,MCM3,MDH2,MIF,MMP14,MMP2,MMP9,MYC,MYH11,NDUF86,NFE2NME1,NR3C1,PCNA,PKM,PRKACB,PTGS2,RCAN1,S100A9,SCD,SELE,SELL,SERPINE1,SERPINH1,SHH2,SMPDL3B,SPP1,TFEC,TIMP1,TNFRSF12A,TUBB,VCAM1
methylprednisolone	chemical drug	Activated	2.046	4.41E-09	Anp32a,ANXA1,ANXA3,C1QBP,Ccl2,CD74,CDH13,CDKN1A,CNN3,CTGF,CTSC,CTSH,CTSS,CYCL1,DGK2,DMD,EPHX1,F3,FBNS5,FBXW7,FCGR2A,FGF7,FN1,GBP2,GCH1,GCLC,GBL3,GNL3,HSPA1A/HSPA1B,HSPH1,IL1B,IL1RN,IL6,JRGM,ITGA7,IVD,KRT19,LAMA3,LDLR,LVYE1,ME1,MMP11,MMP9,Mt1,MVK,MYBBP1A,MYC,NCL,NFE2L2,NME1,NR3C1,PCNA,PGAM1,PIGR,PLAUR,PLIP,PRSS8,PSAT1,RBL2,RG52,SELE,SDC1,SERPINA1,SERPINA3,SERPINE1,SLC16A1,SLC25A10,SLC2A3,SLC40A1,SORD,SPARC,Suit1a1,TACSTD2,TFRC,TLR2,TMEM53,TOMM20,TO2A,TUBA1C,VCAM1,VMP1
atorvastatin	chemical drug		1.525	4.69E-09	ABC1,BCL2L1,C8orf4,CAV1,Ccl2,CTGF,CYP51A1,CYR61,DHCR7,DMC1,EDN1,ELF3,F3,FDP5,GJA1,GSR,HMGR,HMGC51,IL6,ITGB2,JUNB,LDLR,LSS,MMP2,MMP9,MSMO1,MVD,MVK,NOX4,PMVK,PTGS2,RH,EB,SELE,SERPINE1,SLC10B3,SPP1,SQLE,TLR2,VCAM1
allopurinol	chemical drug	Activated	2.488	5.45E-09	ADAMT51,ANXA1,BIRC3,CD14,CLDN4,CLU,CP,CXCL10,ELF3,FABP1,FCGR2A,GPX2,IL1B,LCN2,LGALS3,MCM3,MYC,PTGS2,Pvr,SPP1,TIMP1,TMEM173,TNFRSF12A,TUBB
tamoxifen	chemical drug		0.336	9.79E-09	ANG,BCL2L1,BIRC5,BMP4,CAV1,CCNA2,CDKN1A,CLU,CSAD,CYP2F1,CYP3A5,CYR61,EPHX1,ERBB2,ERBB3,ETV5,FABP1,FASN,HMGR,HMGC51,IGFBP3,IL1RN,IL6,IRS1,JUNB,KHLH2A,LDLR,LSS,LTBP2,MAFF,MIF,MKI67,MYC,PCNA,PFN1,PRSS23,PTGS2,RBL2,S100G,SCD,SCUBE2,SELE,SERPINA3,SLC2A3,SOD2,SPP1,USP1,YPEL3
fluticasone propionate	chemical drug		-1.907	9.84E-09	ANGPT4,CCL20,CCL22,CD74,CE51,CH1L1,CXCL10,FBNS5,FSCN1,GAL,HALA-HRA,HPGD,HS011B1,HTRA1,IL1B,IL1RN,IRS2,MERTK,MFGE8,MMP9,PCOLCE2,PHLDA1,PTGS1,RCAN1,S100A8,SERPINA1,SERPINE1,SESN1,SLC1A3,SPP1,THBS1,TIMP1,TSC22D3,ZCCHC6
bee venom	chemical - endogenous non-mammalian		-0.557	1.17E-08	AREG,Ccl2,CDC42EP4,CREBBP,DNAJB1,HAS1,HSPA4A,HSPB1,IFRD1,IL1B,IPO5,JUNB,KIF23,MKI67,NF13,NUSAP1,PRC1,PTGS2,RCAN1,SGS2,Saa3,SOC3,THBD,TNFAIP2,Tnfsf9,TO2A,TRAF1
rosiglitazone	chemical drug	Inhibited	-2.783	1.72E-08	ACADM,ADAMT51,ADRB3,ANGPT4,C1QP,CAV1,CCL17,Ccl2,CD68,CDKN1A,CLEC7A,CTGF,CXCL10,CYP1A1,DHRS3,F3,FABP1,FASN,FDX1,FGF1,FN1,FOSL1,GATA3,GBP2,GRIA1,HAS1,HLA-DRA,HPGD,HS011B1,IGFBP2,IL18,IL1B,IL1RN,IL6,IRS1,IRS2,KRT18,LCN2,LRG1,MAT2A,MCM6,MCM7,MDH2,MMP9,NOX4,NR1D1,PCNA,PLTP,PTGES,PTGS2,RRRES2,Retnla,SGS2,RORA,S100A8,S100A9,Saa3,SCD,SERPINE1,SOC3,SOD2,THBS1,TIMP1,TNC,VLDLR,WISP1
chlorpromazine	chemical drug		0.41	1.81E-08	DHCR7,FABP1,FDP5,HMGR,HMGC51,IL1B,IL1B,LDLR,LSS,MSMO1,MVK,SCD,SERPINA3,SLC2A3,SQLE,TMEM140,TSC22D3

Upstream Regulator	Molecule Type	Predicted Activation State	Activation z-score	p-value of overlap	Target molecules in dataset
N-acetyl-L-cysteine	chemical drug		-1.839	1.90E-08	ABCB1,ADORA2B,ATF4,BCL2L1,BIRC5,CAV1,Cd2,CCL20,CCND2,CDKN1A,CTGF,CXCL10,CYR61,EDN1,FASN,FOXO3,GCLC,GNL3,HBEGF,HLA-DRA,IL1B,IL6,MMP2,MMP9,MYC,MYH11,NFE2L2,PCNA,PLAUR,PPRC1,PTGS2,SELE,SERPINE1,SLC16A1,SOD2,SPP1,TNC,VCAM1

**Table S3. Tumor necrosis factor receptor (TNFR)-dependent basal lung genes.**  
Affymetrix\_GeneChip\_MOE430A. Moderated t-test (p<0.05). Order by fold difference (FD).  
Selected genes varied  $\geq 1.2$ -fold between C57BL/6J and Tnfr-KO mice (positive-higher in KO, negative-lower in KO).

p (WT:KO)	RefSeq Tran:	FD	Air	Gene Symbol	Gene Title	Gene Ontology Biological Process					
0.001472	NM_001045	-2.23	<b>Mup1</b>	<b>Mup10</b>	<b>Mup12</b>	<b>Mup13</b>	<b>Mup14</b>	<b>Mup15</b>	<b>Mup17</b>	major urinary protein LOC100048885//predicted gene, 21320//major urinary protein	0006112 // energy reserve metabolic process // inferred from sequence or structural similarity//0006112, 0001558 // regulation of cell growth // not recorded//0006281 // DNA repair // inferred from electronic annotation//0006810 // transport // inferred from electronic annotation//0006886 // intracellular protein transport // inferred from electronic annotation//0006112 // energy reserve metabolic process // inferred from sequence or structural similarity//0006112, 0002376 // immune system process // inferred from electronic annotation//0002523 // leukocyte migration // immune system process // inferred from electronic annotation//0002523 // leukocyte migration // response to hypoxia // inferred from electronic annotation//0003085 // negative regulation of peptidase activity // inferred from electronic annotation//00010951 // negative regulation of proteolysis // inferred from electronic annotation//0006915 // apoptotic process // inferred from electronic annotation//0001501 // skeletal system development // inferred from direct assay//0001501 // skeletal system development // inferred from electronic annotation//0006810 // transport // inferred from electronic annotation//0006810 // transport // inferred from electronic annotation//00010951 // negative regulation of peptidase activity // inferred from electronic annotation//00010951 // negative regulation of response to unfolded protein // traceable author statement//0043524 // negative regulation of MAPK cascade // not recorded//0002230 // positive regulation of defense response to virus by protein import into nucleus, translocation // inferred from direct assay//0006351 // transcript // response to hypoxia // inferred from electronic annotation//0001889 // liver development // inferred from electronic annotation//00018401 // peptidyl-proline hydroxylation to 4-hydroxy-L-proline // inferred from direct assay//0030199 // osteoblast differentiation // not recorded//0007155 // cell adhesion // inferred from electronic annotation//0001701 // in utero embryonic development // inferred from mutant phenotype//0006487 // protein N-glycosylation // neutrophil homeostasis // inferred from mutant phenotype//0006198 // cAMP catabolic process // inferred from mutant phenotype//0006508 // proteolysis // not recorded//00010243 // response to organonitrogen compound // inferred from electronic annotation//0031100 // response to hypoxia // inferred from direct assay//0006810 // transport // inferred from electronic annotation//000122 // negative regulation of transcription from RNA polymerase II promoter // not recorded//00063006457 // protein folding // not recorded//0006986 // response to unfolded protein // not recorded // phosphocreatine metabolic process // traceable author statement//0016310 // phosphorylation // regulation of cell growth // inferred from genetic interaction//0001649 // osteoblast differentiation // acute inflammatory response // inferred from electronic annotation//0002740 // negative regulation of gene expression // inferred from sequence or structural similarity//00090002376 // immune system process // inferred from electronic annotation//0002448 // mast cell mediator // osteoblast differentiation // not recorded//0006457 // protein folding // inferred from electronic annotation//0001974 // blood vessel remodeling // inferred from electronic annotation//0002026 // regulation of adaptive immune response // inferred from electronic annotation//0002376 // immune system process // retina layer formation // inferred from mutant phenotype//0045494 // photoreceptor cell maturation // negative regulation of transcription from RNA polymerase II promoter // inferred from mutant phenotype//0055114 // oxidation-reduction process // inferred from electronic annotation
2.26E-08	NM_001131	-4.27	<b>Pttg1</b>							pituitary tumor-transforming gene 1	
1.93E-07	NM_173781	-3.10	<b>Rabb6</b>							RAM6B, member RAS oncogene family	
0.0191618	NM_001039	-2.66	<b>Mup1</b>	<b>Mup10</b>	<b>Mup11</b>	<b>Mup12</b>	<b>Mup14</b>	<b>Mup16</b>	<b>Mup18</b>	major urinary protein 1//major urinary protein 10//major urinary protein 11	
0.0027583	NM_013650	-2.46	<b>S100a8</b>							S100 calcium binding protein A8 (calgranulin A)	
2.47E-04	NM_001281	-2.40	<b>S100a9</b>							S100 calcium binding protein A9 (calgranulin B)	
0.0174304	NM_008725	-2.34	<b>Nppa</b>							natriuretic peptide type A	
0.0081202	NM_011458	-2.22	<b>Serpina3k</b>							serine (or cysteine) peptidase inhibitor, clade A, member 3K	
3.42E-05	NM_010370	-2.10	<b>Gzma</b>							granzyme A	
0.0332464	NM_001039	-2.08	<b>Npr3</b>							natriuretic peptide receptor 3	
0.0016276	NM_009654	-1.99	<b>Alb</b>							albumin	
0.0055523	NM_009245	-1.96	<b>Serpina1c</b>							serine (or cysteine) peptidase inhibitor, clade A, member 1C	
0.0053431	NM_013559	-1.89	<b>Hsph1</b>							heat shock 105kDa/110kDa protein 1	
1.40E-04	NM_013653	-1.79	<b>Ccl5</b>							chemokine (C-C motif) ligand 5	
7.16E-05	NM_001243	-1.73	<b>Arntl</b>							aryl hydrocarbon receptor nuclear translocator-like	
0.0031658	NM_001136	-1.67	<b>Cyp11a1</b>							cytochrome P450, family 1, subfamily a, polypeptide 1	
0.0069887	NM_001316	-1.66	<b>P4ha1</b>							procollagen-proline, 2-oxoglutarate 4-dioxygenase (proline 4-hydroxylase), alpha 1	
0.0040327	NM_011607	-1.65	<b>Tnc</b>							tenascin C	
0.0166123	NM_009244	-1.60	<b>Serpina1b</b>							serine (or cysteine) peptidase inhibitor, clade A, member 1B	
0.0010145	NM_001177	-1.58	<b>Pde4b</b>							phosphodiesterase 4B, cAMP specific	
3.57E-05	NM_010809	-1.56	<b>Mmp3</b>							matrix metalloproteinase 3	
5.40E-05	NM_001311	-1.55	<b>Nnmt</b>							nicotinamide N-methyltransferase	
0.0328579	NM_016737	-1.54	<b>Stip1</b>							stress-induced phosphoprotein 1	
0.0201377	NM_053247	-1.54	<b>Lyve1</b>							lymphatic vessel endothelial hyaluronan receptor 1	
6.37E-04	NM_017373	-1.53	<b>Nfil3</b>							nuclear factor, interleukin 3, regulated	
0.0312099	NM_011020	-1.52	<b>Hspa4l</b>							heat shock protein 4 like	
0.0370396	NM_198415	-1.52	<b>Ckmt2</b>							creatine kinase, mitochondrial 2	
7.06E-04	NM_008343	-1.52	<b>Igf1bp3</b>							insulin-like growth factor binding protein 3	
0.0321213	NM_001305	-1.51	<b>Apoa2</b>							apolipoprotein A-II	
0.0256944	NM_009610	-1.50	<b>Actg2</b>							actin, gamma 2, smooth muscle, enteric	
0.0017118	NM_133903	-1.50	<b>Spon2</b>							spondin 2, extracellular matrix protein	
0.0273517	NM_008303	-1.47	<b>Hspe1</b>							heat shock protein 1 (chaperonin 10)	
0.0456736	NM_001198	-1.46	<b>Csrp3</b>							cysteine and glycine-rich protein 3	
0.030649	NM_001317	-1.45	<b>Fgg</b>							fibronogen gamma chain	
9.35E-04	NM_001163	-1.45	<b>Prom1</b>							prominin 1	
0.006453	NM_007771	-1.45	<b>Cry1</b>							cryptochrome 1 (photolyase-like)	
0.0039426	NM_007818	-1.44	<b>Cyp3a11</b>							cytochrome P450, family 3, subfamily a, polypeptide 11	
0.0058147	NM_020509	-1.44	<b>Retnla</b>							resistin like alpha	
2.80E-04	NM_008719	-1.44	<b>Npas2</b>							neuronal PAS domain protein 2	
0.0022047	NM_022324	-1.43	<b>Sdf2l1</b>							stromal cell-derived factor 2-like 1	
0.0085954	NM_001111	-1.42	<b>Serpinh1</b>							serine (or cysteine) peptidase inhibitor, clade H, member 1	
6.48E-04	NM_017399	-1.41	<b>Fabp1</b>							fatty acid binding protein 1, liver	
0.0016451	NM_018775	-1.41	<b>Tbc1d8</b>							TBC1 domain family, member 8	
0.0141223	NM_010477	-1.41	<b>Hspd1</b>							heat shock protein 1 (chaperonin)	
0.0013471	NM_019696	-1.40	<b>Cpxm1</b>							carboxypeptidase X 1 (M14 family)	
0.0453166	NM_146036	-1.40	<b>Ahsa1</b>							AHA1, activator of heat shock protein ATPase 1	
5.12E-04	NM_024253	-1.39	<b>Nkg7</b>							natural killer cell group 7 sequence	
2.92E-05	NM_009498	-1.39	<b>Vamp3</b>							vesicle-associated membrane protein 3	
0.0010585	NM_019738	-1.39	<b>Nupr1</b>							nuclear protein transcription regulator 1	
0.0288408	NM_010480	-1.39	<b>Hsp90aa1</b>							heat shock protein 90, alpha (cytosolic), class A member 1	
0.0213734	NM_008096	-1.39	<b>Gc</b>							group specific component	
0.0416337	NM_001097	-1.38	<b>Hist1h2bc</b>	<b>Hist1h2be</b>	<b>Hist1h2bl</b>	<b>Hist1h2bm</b>	<b>Hist1h2bp</b>	<b>Hist1h2b</b>	<b>Hist1h2b</b>	histone cluster 1, H2bc//histone cluster 1, H2be//histone cluster 1, H2bl//histone cluster 1, H2b//histone cluster 1, H2b	
0.0135876	NM_009692	-1.37	<b>Apoa1</b>							apolipoprotein A-I	
6.81E-04	NM_011332	-1.37	<b>Ccl17</b>							chemokine (C-C motif) ligand 17	
0.0028375	NM_009786	-1.37	<b>Cacybp</b>							calyculin binding protein	
0.0026462	NM_026785	-1.37	<b>Ube2c</b>							ubiquitin-conjugating enzyme E2C	
0.0031939	NM_001290	-1.37	<b>Ahsa2</b>							AHA1, activator of heat shock protein ATPase 2	
8.97E-05	NM_146063	-1.36	<b>Krt79</b>							keratin 79	
0.0047312	NM_011817	-1.34	<b>Gadd45g</b>							growth arrest and DNA-damage-inducible 45 gamma	
5.69E-05	NM_026174	-1.34	<b>Entpd4</b>	<b>Gm21685</b>						ectonucleoside triphosphate diphosphohydrolase 4//predicted gene, 21685	
2.19E-04	NM_001270	-1.33	<b>Plac9a</b>	<b>Plac9b</b>						placenta specific 9a//placenta specific 9b	
0.0069225	NM_016668	-1.33	<b>Bhmt</b>							betaine-homocysteine methyltransferase	
0.0120883	NM_001285	-1.33	<b>Tmem33</b>							transmembrane protein 33	

p (WT:KO)	RefSeq Tran: FD Air	Gene Symbol	Gene Title	Gene Ontology Biological Process
0.015553	NM_001111	-1.33 <i>Cdkn1a</i>	cyclin-dependent kinase inhibitor 1A (P21)	0000079 // regulation of cyclin-dependent protein serine/threonine kinase activity // inferred from mutant
0.0111063	NM_134110	-1.33 <i>Kcne2</i>	potassium voltage-gated channel, Isk-related subfamily, gene 2	0006810 // transport // inferred from electronic annotation//0006811 // ion transport // inferred from el
0.0097235	NM_007638	-1.33 <i>Cac7</i>	chaperonin containing Tcp1, subunit 7 (eta)	0006457 // protein folding // inferred from electronic annotation//0007339 // binding of sperm to zona p
0.0036645	NM_013697	-1.32 <i>Ttr</i>	transthyretin	0006810 // transport // inferred from electronic annotation//0042572 // retinol metabolic process // not
0.0049989	NM_001111	-1.32 <i>Igf1</i>	insulin-like growth factor 1	0001649 // osteoblast differentiation // inferred from expression pattern//0001775 // cell activation // nc
0.028701	NM_010219	-1.32 <i>Fkbp4</i> // <i>LOC102642559</i>	FK506 binding protein 4//uncharacterized LOC102642559	0000413 // protein peptidyl-prolyl isomerization // not recorded//0006457 // protein folding // inferred f
0.0193119	NM_001281	-1.32 <i>Ifi2712a</i>	interferon, alpha-inducible protein 27 like 2A	0007568 // aging // inferred from direct assay//0009615 // response to virus // inferred from direct assay
0.003145	NM_011403	-1.32 <i>Slc4a1</i>	solute carrier family 4 (anion exchanger), member 1	0006810 // transport // inferred from electronic annotation//0006811 // ion transport // inferred from el
0.0022191	NM_001081	-1.31 <i>Mki67</i>	antigen identified by monoclonal antibody Ki 67	0006259 // DNA metabolic process // inferred from electronic annotation//0007126 // meiotic nuclear di
1.61E-04	NM_010391	-1.31 <i>H2-Q10</i>	histocompatibility 2, Q region locus 10	0002376 // immune system process // inferred from electronic annotation//0002474 // antigen processin
0.0242281	NM_021384	-1.31 <i>Rsad2</i>	radical S-adenosyl methionine domain containing 2	0001503 // ossification // not recorded//0002376 // immune system process // inferred from electronic a
6.87E-04	NM_009978	-1.30 <i>Cst8</i>	cystatin 8 (cystatin-related epididymal spermatogenic)	0010466 // negative regulation of peptidase activity // inferred from electronic annotation//0010951 // n
0.0100065	NM_009912	-1.30 <i>Ccr1</i>	chemokine (C-C motif) receptor 1	0006816 // calcium ion transport // not recorded//0006874 // cellular calcium ion homeostasis // not rec
0.009008	NM_027959	-1.30 <i>Pdia6</i>	protein disulfide isomerase associated 6	0006457 // protein folding // not recorded//0008152 // metabolic process // inferred from electronic ann
0.0062015	NM_001110	-1.30 <i>Apoc1</i>	apolipoprotein C-1	0006641 // triglyceride metabolic process // inferred from mutant phenotype//0006810 // transport // ini
0.0108044	NM_0011631	-1.29 <i>Hsp90b1</i>	heat shock protein 90, beta (Grp94), member 1	0001666 // response to hypoxia // not recorded//0006457 // protein folding // inferred from electronic ar
0.0015525	NM_145562	-1.29 <i>Parm1</i>	prostate androgen-regulated mucin-like protein 1	0051973 // positive regulation of telomerase activity // not recorded
0.0062092	NM_133981	-1.29 <i>Alg9</i>	asparagine-linked glycosylation 9 (alpha 1,2 mannosyltransferase)	0006486 // protein glycosylation // inferred from electronic annotation//0008152 // metabolic process //
0.0070554	NM_012006	-1.29 <i>Acot1</i> // <i>Acot2</i>	acyl-CoA thioesterase 1//acyl-CoA thioesterase 2	0001676 // long-chain fatty acid metabolic process // inferred from direct assay//0006637 // acyl-CoA me
0.0324248	NM_011082	-1.29 <i>Pigr</i>	polymeric immunoglobulin receptor	0001580 // detection of chemical stimulus involved in sensory perception of bitter taste // not recorded//
0.0099119	NM_010495	-1.28 <i>Id1</i>	inhibitor of DNA binding 1	0000122 // negative regulation of transcription from RNA polymerase II promoter // inferred from direct a
0.0085936	NM_011568	-1.28 <i>Alyref</i> // <i>Alyref2</i>	Aly/REF export factor//Aly/REF export factor 2	0006397 // mRNA processing // inferred from electronic annotation//0006406 // mRNA export from nucle
0.0053837	NM_001290	-1.28 <i>Acer2</i>	alkaline ceramidase 2	0001953 // negative regulation of cell-matrix adhesion // not recorded//0006629 // lipid metabolic proces
0.0050811	NM_001077	-1.28 <i>Ldb2</i>	LIM domain binding 2	0001942 // hair follicle development // inferred from genetic interaction//0006357 // regulation of transc
0.0482885	NM_133726	-1.28 <i>St13</i>	suppression of tumorigenicity 13	0006457 // protein folding // not recorded//0051260 // protein homooligomerization // not recorded//0
0.00238	NM_013599	-1.28 <i>Mmp9</i>	matrix metalloproteinase 9	0001501 // skeletal system development // inferred from genetic interaction//0001501 // skeletal system
0.0304962	NM_008877	-1.27 <i>Plg</i>	plasminogen	0006508 // proteolysis // inferred from electronic annotation//0007596 // blood coagulation // not recor
0.0026767	NM_176848	-1.27 <i>Fbxo2</i>	F-box protein 2	0006511 // ubiquitin-dependent protein catabolic process // inferred from direct assay//0006516 // glyco
0.020154	NM_010104	-1.27 <i>Edn1</i>	endothelin 1	0000122 // negative regulation of transcription from RNA polymerase II promoter // not recorded//00015
0.0148855	NM_177301	-1.27 <i>Hnrnp1</i>	heterogeneous nuclear ribonucleoprotein L	0006397 // mRNA processing // inferred from electronic annotation//0034198 // cellular response to amii
0.0318101	NM_001110	-1.27 <i>Atp2a2</i>	ATPase, Ca++ transporting, cardiac muscle, slow twitch 2	0002026 // regulation of the force of heart contraction // inferred from genetic interaction//0006810 // tr
0.0079441	NM_030599	-1.27 <i>Klrb1b</i>	killer cell lectin-like receptor subfamily B member 1B	0045953 // negative regulation of natural killer cell mediated cytotoxicity // inferred from direct assay//0C
3.66E-04	NM_010180	-1.27 <i>Fbln1</i>	fibulin 1	0001933 // negative regulation of protein phosphorylation // not recorded//0007162 // negative regulati
0.0053302	NM_001163	-1.27 <i>Clec4d</i>	C-type lectin domain family 4, member d	0002250 // adaptive immune response // inferred from mutant phenotype//0002292 // T cell differentiati
0.0069436	NM_031165	-1.27 <i>Hspa8</i>	heat shock protein 8	0001916 // positive regulation of T cell mediated cytotoxicity // not recorded//0006351 // transcription, T
0.0062382	NM_029620	-1.27 <i>Pcolce2</i>	procollagen C-endopeptidase enhancer 2	0010952 // positive regulation of peptidase activity // not recorded
0.0100064	NM_001190	-1.26 <i>Clec4n</i>	C-type lectin domain family 4, member n	0002250 // adaptive immune response // inferred from electronic annotation//0002376 // immune system
0.0332937	NM_007743	-1.26 <i>Col1a2</i>	collagen, type I, alpha 2	0001501 // skeletal system development // not recorded//0001568 // blood vessel development // not re
1.33E-04	NM_145923	-1.26 <i>Rel1</i>	REL1-like 1	
4.32E-04	NM_021789	-1.26 <i>Trappc4</i>	trafficking protein particle complex 4	0006810 // transport // inferred from electronic annotation//0006888 // ER to Golgi vesicle-mediated tra
0.0035458	NM_011545	-1.26 <i>Tcf21</i>	transcription factor 21	0000122 // negative regulation of transcription from RNA polymerase II promoter // inferred from direct a
3.99E-04	NM_001289	-1.26 <i>Cryab</i>	crystallin, alpha B	0001666 // response to hypoxia // inferred from mutant phenotype//0002088 // lens development in can
0.0049088	NM_008083	-1.26 <i>Gap43</i>	growth associated protein 43	0007275 // multicellular organismal development // inferred from electronic annotation//0007399 // ner
0.0074224	NM_001271	-1.26 <i>Ackr3</i>	atypical chemokine receptor 3	0001525 // angiogenesis // inferred from electronic annotation//0001570 // vasculogenesis // inferred fro
0.0291845	NM_001163	-1.26 <i>Tcf19</i>	transcription factor 19	
0.0014895	NM_010511	-1.26 <i>Ifng1</i>	interferon gamma receptor 1	0019221 // cytokine-mediated signaling pathway // not recorded
0.0090109	NM_009850	-1.25 <i>Cd3g</i>	CD3 antigen, gamma polypeptide	0007163 // establishment or maintenance of cell polarity // not recorded//0007166 // cell surface recept
0.0149551	NM_001145	-1.25 <i>Zkscan3</i>	zinc finger with KRAB and SCAN domains 3	0000122 // negative regulation of transcription from RNA polymerase II promoter // not recorded//00063
0.0480251	NM_008039	-1.25 <i>Fpr2</i>	formyl peptide receptor 2	0006935 // chemotaxis // inferred from electronic annotation//0007165 // signal transduction // inferre
0.0227478	NM_001190	-1.25 <i>Dnajb11</i>	Dnaj (Hsp40) homolog, subfamily B, member 11	0006457 // protein folding // inferred from electronic annotation//0016556 // mRNA modification // infer
0.0030634	NM_027411	-1.25 <i>Spd1</i>	spindle apparatus coiled-coil protein 1	0000132 // establishment of mitotic spindle orientation // not recorded//0007049 // cell cycle // inferre
0.0459714	NM_138953	-1.24 <i>Elf2</i>	elongation factor RNA polymerase II 2	0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 // regulation o
0.0111285	NM_001285	-1.24 <i>Dapk1</i>	death associated protein kinase 1	0006417 // regulation of translation // inferred from electronic annotation//0006468 // protein phosphor
0.0080922	NM_024263	-1.24 <i>Mxra8</i>	matrix-remodelling associated 8	0006857 // establishment of glial blood-brain barrier // inferred from expression pattern
3.25E-04	NM_007875	-1.24 <i>Dpagt1</i>	dolichyl-phosphate (UDP-N-acetylglucosamine) acetylglucosaminophosphotransferase 1	0000271 // polysaccharide biosynthetic process // --//0006047 // UDP-N-acetylglucosamine metabolic pr
0.0014476	NM_011609	-1.24 <i>Tnfrsf1a</i>	tumor necrosis factor receptor superfamily, member 1a	0006693 // prostaglandin metabolic process // traceable author statement//0006915 // apoptotic proces
0.0010342	NM_026347	-1.24 <i>Iah1</i>	isoamyl acetate-hydrolyzing esterase 1 homolog (S. cerevisiae)	0006629 // lipid metabolic process // inferred from electronic annotation//0016042 // lipid catabolic proc
0.0031938	NM_015814	-1.24 <i>Dkk3</i>	dickkopf homolog 3 (Xenopus laevis)	0007275 // multicellular organismal development // inferred from electronic annotation//0016055 // Wn
0.0154652	NM_009943	-1.24 <i>Cox6a2</i>	cytochrome c oxidase subunit VIa polypeptide 2	1902600 // hydrogen ion transmembrane transport // inferred from electronic annotation
7.62E-04	NM_011280	-1.24 <i>Trim10</i>	tripartite motif-containing 10	0030218 // erythrocyte differentiation // inferred from direct assay//0045087 // innate immune response
9.96E-04	NM_011610	-1.23 <i>Tnfrsf1b</i>	tumor necrosis factor receptor superfamily, member 1b	0006954 // inflammatory response // inferred from mutant phenotype//0006955 // immune response // i
0.0017916	NM_001243	-1.23 <i>Tspan2</i>	tetraspanin 2	0006954 // inflammatory response // inferred from genetic interaction//0007166 // cell surface receptor :
0.0033299	NM_133238	-1.23 <i>Cd209a</i>	CD209a antigen	0006897 // endocytosis // inferred from electronic annotation//0010468 // regulation of gene expression
0.0230947	NM_012042	-1.23 <i>Cul1</i>	cullin 1	0006511 // ubiquitin-dependent protein catabolic process // inferred by curator//0006513 // protein mor
0.0039434	NM_013691	-1.23 <i>Thbs3</i>	thrombospondin 3	0003417 // growth plate cartilage development // inferred from genetic interaction//0003417 // growth p
9.48E-04	NM_001034	-1.23 <i>Ppp2r1b</i>	protein phosphatase 2, regulatory subunit A, beta	0006461 // protein complex assembly // inferred from electronic annotation//0034047 // regulation of pr

p (WT:KO)	RefSeq Tran: FD Air	Gene Symbol	Gene Title	Gene Ontology Biological Process
0.0048828	NM_0010181	-1.22 <i>Palld</i>	palladin, cytoskeletal associated protein	0003334 // keratinocyte development // inferred from mutant phenotype//0003382 // epithelial cell mor
0.00257	NM_019707	-1.22 <i>Cdh13</i>	cadherin 13	0000278 // mitotic cell cycle // inferred from electronic annotation//0001558 // regulation of cell growth
0.0406531	NM_007865	-1.22 <i>Dll1</i>	delta-like 1 (Drosophila)	0001701 // in utero embryonic development // non-traceable author statement//0001756 // somitogeny
7.90E-04	NM_007825	-1.22 <i>Cyp7b1</i>	cytochrome P450, family 7, subfamily b, polypeptide 1	0006629 // lipid metabolic process // inferred from electronic annotation//0006699 // bile acid biosynthe
0.038422	NM_008720	-1.22 <i>Npc1</i>	Niemann-Pick type C1	0006486 // protein glycosylation // inferred from direct assay//0006486 // protein glycosylation // not rec
0.0085297	NM_025348	-1.22 <i>Ndufa3</i>	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 3	0006810 // transport // inferred from electronic annotation//0005514 // oxidation-reduction process // ir
0.0079752	NM_021288	-1.22 <i>Tyms//Tyms-ps</i>	thymidylate synthase//thymidylate synthase, pseudogene	0006206 // pyrimidine nucleobase metabolic process // inferred from electronic annotation//0006231 // r
0.0424505	NM_013542	-1.22 <i>Gzmb</i>	granzyme B	0001913 // T cell mediated cytotoxicity // inferred from mutant phenotype//0006508 // proteolysis // inf
0.0278048	NM_008929	-1.22 <i>Dnajc3</i>	Dnaj (Hsp40) homolog, subfamily C, member 3	0006469 // negative regulation of protein kinase activity // inferred from sequence or structural similarity//
0.0167853	NM_009131	-1.22 <i>Clec11a</i>	C-type lectin domain family 11, member a	0008284 // positive regulation of cell proliferation // not recorded
0.0069927	NM_009763	-1.22 <i>Bst1</i>	bone marrow stromal cell antigen 1	0008152 // metabolic process // not recorded//0030890 // positive regulation of B cell proliferation // no
0.0065881	NM_028394	-1.22 <i>Hspb11</i>	heat shock protein family B (small), member 11	0001501 // skeletal system development // inferred from mutant phenotype//0006810 // transport // inf
0.0022784	NM_012033	-1.22 <i>Tinag</i>	tubulointerstitial nephritis antigen	0006508 // proteolysis // inferred from electronic annotation//0006898 // receptor-mediated endocytosis
0.0043699	NM_011794	-1.21 <i>Bpnt1</i>	bisphosphate 3'-nucleotidase 1	0006139 // nucleobase-containing compound metabolic process // not recorded//0006470 // protein dep
0.0057984	NM_009829	-1.21 <i>Ccnd2</i>	cyclin D2	0000082 // G1/S transition of mitotic cell cycle // not recorded//0001934 // positive regulation of protein
0.011662	NM_010369	-1.21 <i>Gypa</i>	glycophorin A	0007016 // cytoskeletal anchoring at plasma membrane // inferred from mutant phenotype//0047484 //
0.0352691	NM_001166	-1.21 <i>Fkbp2</i>	FK506 binding protein 2	0000413 // protein peptidyl-prolyl isomerization // not recorded//0006457 // protein folding // inferred f
0.031296	NM_009627	-1.21 <i>Adm</i>	adrenomedullin	0001570 // vasculogenesis // not recorded//0001666 // response to hypoxia // inferred from electronic ar
0.0118508	NM_026602	-1.21 <i>Bcas2</i>	breast carcinoma amplified sequence 2	0000398 // mRNA splicing, via spliceosome // not recorded//0006397 // mRNA processing // inferred from
0.0019934	NM_025319	-1.21 <i>0610009B22Rik</i>	RIKEN cDNA 0610009B22 gene	0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 // regulation o
0.0385818	NM_016752	-1.21 <i>Slc35b1</i>	solute carrier family 35, member B1	0006810 // transport // inferred from electronic annotation//0008643 // carbohydrate transport // infer
0.0061123	NM_001252	-1.21 <i>Csf3r</i>	colony stimulating factor 3 receptor (granulocyte)	0007155 // cell adhesion // inferred from electronic annotation//0019221 // cytokine-mediated signaling
0.032887	NM_001305	-1.21 <i>Apoe</i>	apolipoprotein E	0001937 // negative regulation of endothelial cell proliferation // not recorded//0002021 // response to d
0.0259667	NM_177564	-1.21 <i>Dhrs11</i>	dehydrogenase/reductase (SDR family) member 11	0008152 // metabolic process // inferred from electronic annotation//0005514 // oxidation-reduction pro
0.0101478	NM_028176	-1.21 <i>Cda</i>	cytidine deaminase	0009972 // cytidine deamination // not recorded//0030308 // negative regulation of cell growth // not re
0.0017991	NM_001135	-1.20 <i>Gm38718//Gm39869//Ptpri</i>	predicted gene, 38718//predicted gene, 39869//protein tyrosine phosphatase	0001570 // vasculogenesis // inferred from mutant phenotype//0001954 // positive regulation of cell-mat
0.0176624	NM_133198	-1.20 <i>Pygl</i>	liver glycogen phosphorylase	0005975 // carbohydrate metabolic process // inferred from electronic annotation//0005977 // glycogen m
0.0018152	NM_001113	-1.20 <i>Isg20</i>	interferon-stimulated protein	0000738 // DNA catabolic process, exonucleolytic // not recorded//0002376 // immune system process //
0.0045163	NM_016696	-1.20 <i>Gpc1</i>	glypican 1	0014037 // Schwann cell differentiation // not recorded//0030200 // heparan sulfate proteoglycan catab
0.0300747	NM_134188	-1.20 <i>Acot2//Acot1</i>	acyl-CoA thioesterase 2//acyl-CoA thioesterase 1	0000038 // very long-chain fatty acid metabolic process // not recorded//0001666 // response to hypoxia
0.0155165	NM_010006	-1.20 <i>Cyp2d9</i>	cytochrome P450, family 2, subfamily d, polypeptide 9	0006805 // xenobiotic metabolic process // not recorded//0019369 // arachidonic acid metabolic process
0.0349869	NM_018870	-1.20 <i>Pgam2</i>	phosphoglycerate mutase 2	0006094 // gluconeogenesis // not recorded//0006096 // glycolytic process // inferred from direct assay//
0.0253425	NM_008611	-1.20 <i>Mmp8</i>	matrix metalloproteinase 8	0006508 // proteolysis // not recorded//0030574 // collagen catabolic process // inferred from electronic
0.0043765	NM_001033	-1.20 <i>Dnah1</i>	dynein, axonemal, heavy chain 1	0003341 // cilium movement // inferred from electronic annotation//0003351 // epithelial cilium movem
0.0235566	NM_019474	-1.20 <i>Olfir156</i>	olfactory receptor 156	0007165 // signal transduction // inferred from electronic annotation//0007186 // G-protein coupled rec
0.0323284	NM_146167	-1.20 <i>Gimap7</i>	GPase, IMAP family member 7	0008152 // metabolic process // inferred from electronic annotation
0.0397775	NM_001004	-1.20 <i>Grasp1</i>	G protein-coupled receptor associated sorting protein 1	0008333 // endosome to lysosome transport // not recorded//1990172 // G-protein coupled receptor cat
0.0145098	NM_025569	-1.20 <i>Mgst3</i>	microsomal glutathione S-transferase 3	0010243 // response to organonitrogen compound // inferred from electronic annotation//0005514 // ox
0.0043618	NM_019791	-1.20 <i>Maged1</i>	melanoma antigen, family D, 1	0006357 // regulation of transcription from RNA polymerase II promoter // inferred from direct assay//00
0.0215543	NM_029614	-1.20 <i>Prss23</i>	protease, serine 23	0006508 // proteolysis // inferred from electronic annotation
0.0342132	NM_001308	-1.20 <i>Alox5ap</i>	arachidonate 5-lipoxygenase activating protein	0002540 // leukotriene production involved in inflammatory response // inferred from mutant phenotype//
0.0384087	NM_010942	-1.20 <i>Nsg1</i>	neuron specific gene family member 1	0001921 // positive regulation of receptor recycling // not recorded//0007212 // dopamine receptor sign
0.0061579	NM_001002	-1.20 <i>Hspa2</i>	heat shock protein 2	0001934 // positive regulation of protein phosphorylation // inferred from mutant phenotype//0007140 //
0.0094518	NM_001169	1.20 <i>B3gnt2</i>	UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 2	0006486 // protein glycosylation // inferred from mutant phenotype//0007411 // axon guidance // infer
0.002047	NM_012017	1.20 <i>Zfp346</i>	zinc finger protein 346	0043065 // positive regulation of apoptotic process // inferred from mutant phenotype//0072332 // intrin
0.0225771	NM_144796	1.20 <i>Susd4</i>	sushi domain containing 4	0030449 // regulation of complement activation // not recorded//0045957 // negative regulation of comp
0.022997	NM_001110	1.20 <i>Lsm2</i>	LSM2 homolog, U6 small nuclear RNA associated (S. cerevisiae)	0000244 // spliceosomal tri-snRNP complex assembly // not recorded//0000398 // mRNA splicing, via spli
0.0328204	NM_175309	1.20 <i>Upk3b</i>	uroplakin 3B	0010629 // negative regulation of gene expression // not recorded//0046325 // negative regulation of glu
0.0172706	NM_172645	1.20 <i>Suco</i>	SUN domain containing ossification factor	0001503 // ossification // inferred from electronic annotation//0007275 // multicellular organismal devel
0.0197225	NM_010361	1.20 <i>Gstt2</i>	glutathione S-transferase, theta 2	0006749 // glutathione metabolic process // not recorded//0005514 // oxidation-reduction process // not
0.0120097	NM_001005	1.20 <i>Syne2</i>	spectrin repeat containing, nuclear envelope 2	0006998 // nuclear envelope organization // inferred from mutant phenotype//0007097 // nuclear migrat
0.0027919	NM_001079	1.20 <i>Srsf5</i>	serine/arginine-rich splicing factor 5	0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 // regulation o
0.0019571	NM_001098	1.20 <i>Hic1</i>	hypermethylated in cancer 1	0000122 // negative regulation of transcription from RNA polymerase II promoter // inferred from direct a
0.0101649	NM_007426	1.20 <i>Angpt2</i>	angiotensin 2	0001525 // angiogenesis // inferred from genetic interaction//0001666 // response to hypoxia // inferred
9.43E-04	NM_133677	1.20 <i>Zbtb11os1</i>	zinc finger and BTB domain containing 11, opposite strand 1	
0.0123404	NM_153533	1.20 <i>Tns2</i>	tensin 2	0001822 // kidney development // inferred from mutant phenotype//0006470 // protein dephosphorylati
6.32E-04	NM_010593	1.20 <i>Jup</i>	junction plakoglobin	0002159 // desmosome assembly // inferred from mutant phenotype//0002159 // desmosome assembly,
0.013172	NM_001164	1.20 <i>Hspb2</i>	heat shock protein 2	0007525 // somatic muscle development // inferred from genetic interaction//0009408 // response to he
0.0280921	NM_001164	1.21 <i>Sptsb</i>	serine palmitoyltransferase, small subunit B	0006629 // lipid metabolic process // inferred from electronic annotation//0006665 // sphingolipid metat
0.0086943	NM_133710	1.21 <i>Ctdsp1</i>	CTD (carboxy-terminal domain, RNA polymerase II, polypeptide A) small phospho	0001933 // negative regulation of protein phosphorylation // inferred from direct assay//0006470 // prot
0.0100975	NM_010798	1.21 <i>Mif</i>	macrophage migration inhibitory factor	0001516 // prostaglandin biosynthetic process // not recorded//0001934 // positive regulation of protein
0.0072266	NM_138683	1.21 <i>Rspo1</i>	R-spondin 1	0001934 // positive regulation of protein phosphorylation // not recorded//0002090 // regulation of rece
0.0197331	NM_153459	1.21 <i>Dusp7</i>	dual specificity phosphatase 7	0000188 // inactivation of MAPK activity // not recorded//0006470 // protein dephosphorylation // not rec
0.028392	NM_001308	1.21 <i>Porcn</i>	porcupine homolog (Drosophila)	0006497 // protein lipidation // inferred from direct assay//0009100 // glycoprotein metabolic process //
8.86E-04	NM_008027	1.21 <i>Flot1</i>	flotillin 1	0001765 // membrane raft assembly // not recorded//0001819 // positive regulation of cytokine product
0.0051718	NM_001284	1.21 <i>Bcl2l11</i>	BCL2-like 11 (apoptosis facilitator)	0001701 // in utero embryonic development // inferred from genetic interaction//0001776 // leukocyte h

p (WT:KO)	RefSeq Tran: FD Air	Gene Symbol	Gene Title	Gene Ontology Biological Process
0.0040917	NM_001163	1.21 <i>Fbxo6</i>	F-box protein 6	0006281 // DNA repair // inferred from electronic annotation///0006516 // glycoprotein catabolic process
0.0011939	NM_173440	1.21 <i>Nrip1</i>	nuclear receptor interacting protein 1	0000122 // negative regulation of transcription from RNA polymerase II promoter // inferred from direct a
0.0103284	NM_001164	1.21 <i>Pias2</i>	protein inhibitor of activated STAT 2	0006351 // transcription, DNA-templated // inferred from direct assay///0006355 // regulation of transcrip
0.0066668	NM_001111	1.21 <i>Ngef</i>	neuronal guanine nucleotide exchange factor	0007275 // multicellular organismal development // inferred from electronic annotation///0007399 // ner
7.45E-04	NM_001272	1.22 <i>Trim24</i>	tripartite motif-containing 24	0006351 // transcription, DNA-templated // inferred from electronic annotation///0006355 // regulation o
0.0022797	NM_027198	1.21 <i>Zswim7</i>	zinc finger SWIM-type containing 7	0000724 // double-strand break repair via homologous recombination // not recorded///0006281 // DNA r
0.0293327	NM_001083	1.21 <i>Scn3b</i>	sodium channel, voltage-gated, type III, beta	0006810 // transport // inferred from electronic annotation///0006811 // ion transport // inferred from el
0.0227504	NM_153789	1.22 <i>Myliip</i>	myosin regulatory light chain interacting protein	0006928 // movement of cell or subcellular component // not recorded///0007399 // nervous system deve
0.0162668	NM_138951	1.22 <i>Ttc36</i>	tetratricopeptide repeat domain 36	
0.0072588	NM_009759	1.22 <i>Bmx</i>	BMX non-receptor tyrosine kinase	0002250 // adaptive immune response // not recorded///0006468 // protein phosphorylation // inferred f
0.0370463	NM_007974	1.22 <i>F2r1l</i>	coagulation factor II (thrombin) receptor-like 1	0002286 // T cell activation involved in immune response // inferred from direct assay///0002376 // immu
0.0153785	NM_008012	1.22 <i>Akr1b8</i>	aldo-keto reductase family 1, member B8	0016488 // farnesol catabolic process // not recorded///0044597 // daunorubicin metabolic process // not
0.0082785	NM_145403	1.22 <i>Tmprss4</i>	transmembrane protease, serine 4	0006508 // proteolysis // inferred from electronic annotation///0006898 // receptor-mediated endocytosis
0.0197822	NM_027168	1.22 <i>Hddc2</i>	HD domain containing 2	
0.0085118	NM_026058	1.22 <i>Cers4</i>	ceramide synthase 4	0006629 // lipid metabolic process // inferred from electronic annotation///0030148 // sphingolipid biosyr
6.43E-04	NM_030206	1.22 <i>Cygb</i>	cytoglobin	0001666 // response to hypoxia // inferred from electronic annotation///0006810 // transport // inferred f
0.0020733	NM_001199	1.22 <i>Prrc2a</i>	proline-rich coiled-coil 2A	
0.0011858	NM_172736	1.22 <i>Leng8</i>	leukocyte receptor cluster (LRC) member 8	
0.0173041	NM_027356	1.22 <i>Ufsp1</i>	UFM1-specific peptidase 1	0006508 // proteolysis // inferred from mutant phenotype
0.0067067	NM_001025	1.23 <i>Brd2</i>	bromodomain containing 2	0006334 // nucleosome assembly // not recorded///0006351 // transcription, DNA-templated // inferred f
0.0075527	NM_001122	1.23 <i>Nab2</i>	Ngfi-A binding protein 2	0001958 // endochondral ossification // inferred from genetic interaction///0006351 // transcription, DNA
0.0410965	NM_009344	1.23 <i>Phlda1</i>	pleckstrin homology-like domain, family A, member 1	0006915 // apoptotic process // inferred from electronic annotation///0021879 // forebrain neuron differe
0.0465258	NM_001110	1.23 <i>Prg4</i>	proteoglycan 4 (megakaryocyte stimulating factor, articular superficial zone p	0006898 // receptor-mediated endocytosis // inferred from electronic annotation///0006955 // immune re
0.0021794	NM_033314	1.23 <i>Slco2a1</i>	solute carrier organic anion transporter family, member 2a1	0006810 // transport // inferred from electronic annotation///0006811 // ion transport // inferred from el
0.0165178	NM_153175	1.23 <i>Gimap6</i>	GTase, IMAP family member 6	
0.0078029	NM_001289	1.23 <i>Per3</i>	period circadian clock 3	0000122 // negative regulation of transcription from RNA polymerase II promoter // inferred from direct a
0.0044302	NM_018856	1.23 <i>Ccnl2</i>	cyclin L2	0000079 // regulation of cyclin-dependent protein serine/threonine kinase activity // inferred from electri
0.0029783	NM_019518	1.23 <i>Grasp</i>	GRP1 (general receptor for phosphoinositides 1)-associated scaffold protein	0006886 // intracellular protein transport // not recorded///0007165 // signal transduction // inferred fr
0.0027706	NM_001038	1.23 <i>Sertad2</i>	SERTA domain containing 2	0006351 // transcription, DNA-templated // inferred from electronic annotation///0006355 // regulation o
0.0058051	NM_145478	1.23 <i>Pim3</i>	proviral integration site 3	0006468 // protein phosphorylation // not recorded///0006915 // apoptotic process // inferred from elect
0.001162	NM_009201	1.24 <i>Slc1a5</i>	solute carrier family 1 (neutral amino acid transporter), member 5	0003333 // amino acid transmembrane transport // not recorded///0006810 // transport // inferred from i
0.0014692	NM_001013	1.24 <i>Prkg1</i>	protein kinase, cGMP-dependent, type I	0001764 // neuron migration // inferred from mutant phenotype///0006468 // protein phosphorylation //
0.0149314	NM_001161	1.24 <i>Tnfrsf12a</i>	tumor necrosis factor receptor superfamily, member 12a	0001525 // angiogenesis // inferred from electronic annotation///0006915 // apoptotic process // inferred
0.0016175	NM_023831	1.24 <i>Ifi46</i>	intraflagellar transport 46	0007224 // smoothed signaling pathway // inferred from mutant phenotype///0015031 // protein trans
0.0088693	NM_008256	1.24 <i>Hmgcs2</i>	3-hydroxy-3-methylglutaryl-Coenzyme A synthase 2	0001822 // kidney development // inferred from electronic annotation///0001889 // liver development //
0.0361806	NM_001289	1.24 <i>Zeb2</i>	zinc finger E-box binding homeobox 2	0000122 // negative regulation of transcription from RNA polymerase II promoter // inferred from mutant
0.0309031	NM_026573	1.24 <i>Upf3b</i>	UPF3 regulator of nonsense transcripts homolog B (yeast)	0000184 // nuclear-transcribed mRNA catabolic process, nonsense-mediated decay // not recorded///0006
0.0055189	NM_001289	1.24 <i>Tns1</i>	tensin 1	0007044 // cell-substrate junction assembly // inferred from mutant phenotype///0010761 // fibroblast mi
0.0014352	NM_001114	1.24 <i>Slc16a11</i>	solute carrier family 16 (monocarboxylic acid transporters), member 11	0006629 // lipid metabolic process // not recorded///0006810 // transport // inferred from electronic ann
0.0078167	NM_172563	1.24 <i>Hif</i>	hepatic leukemia factor	0006351 // transcription, DNA-templated // inferred from electronic annotation///0006355 // regulation o
0.0049926	NM_175030	1.24 <i>Tctex1d4</i>	Tctex1 domain containing 4	
0.0017945	NM_178931	1.24 <i>Tnfrsf14</i>	tumor necrosis factor receptor superfamily, member 14 (herpesvirus entry me	0002741 // positive regulation of cytokine secretion involved in immune response // inferred from mutant
4.30E-04	NM_007885	1.24 <i>Slc26a2</i>	solute carrier family 26 (sulfate transporter), member 2	0001503 // ossification // not recorded///0006810 // transport // inferred from electronic annotation///00
0.0016893	NM_007964	1.25 <i>Evi5</i>	ecotropic viral integration site 5	0007049 // cell cycle // inferred from electronic annotation///0042147 // retrograde transport, endosome
9.56E-04	NM_145828	1.25 <i>Xylt2</i>	xylosyltransferase II	0006024 // glycosaminoglycan biosynthetic process // inferred from mutant phenotype///0015012 // hepa
0.0114493	NM_145549	1.25 <i>Efcab7</i>	EF-hand calcium binding domain 7	
0.0028765	NM_001290	1.25 <i>Eps8l1</i>	EPS8-like 1	0007266 // Rho protein signal transduction // not recorded///0016601 // Rac protein signal transduction /
0.03092	NM_028136	1.25 <i>Dhx36</i>	DEAH (Asp-Glu-Ala-His) box polypeptide 36	0001503 // ossification // inferred from mutant phenotype///0006351 // transcription, DNA-templated // i
0.0276244	NM_145220	1.25 <i>App12</i>	adaptor protein, phosphotyrosine interaction, PH domain and leucine zipper	0007049 // cell cycle // inferred from electronic annotation///0008283 // cell proliferation // not recorded
3.30E-04	NM_024472	1.25 <i>Cptp</i>	ceramide-1-phosphate transfer protein	0006810 // transport // inferred from electronic annotation///0006869 // lipid transport // inferred from e
0.0017087	NM_018874	1.25 <i>Pnliprp1</i>	pancreatic lipase related protein 1	0006629 // lipid metabolic process // inferred from electronic annotation
6.80E-04	NM_001161	1.25 <i>Gucy1b3</i>	guanylate cyclase 1, soluble, beta 3	0006182 // cGMP biosynthetic process // not recorded///0007165 // signal transduction // not recorded//
7.54E-04	NM_001302	1.26 <i>Impdh1</i>	inosine 5'-phosphate dehydrogenase 1	0006164 // purine nucleotide biosynthetic process // inferred from mutant phenotype///0006177 // GMP I
0.0092268	NM_001277	1.26 <i>Acrv1l</i>	activin A receptor, type II-like 1	0001525 // angiogenesis // inferred from mutant phenotype///0001525 // angiogenesis // not recorded///
0.0150706	NM_019864	1.26 <i>Atr</i>	ataxia telangiectasia and Rad3 related	0000077 // DNA damage checkpoint // inferred from mutant phenotype///0000077 // DNA damage checkp
0.0017954	NM_133772	1.26 <i>Ssbp4</i>	single stranded DNA binding protein 4	
0.0015706	NM_013770	1.26 <i>Slc25a10</i>	solute carrier family 25 (mitochondrial carrier, dicarboxylate transporter), me	0006810 // transport // inferred from electronic annotation///0006817 // phosphate ion transport // not r
0.0040538	NM_017398	1.26 <i>Diaph2</i>	diaphanous related formin 2	0007015 // actin filament organization // inferred from electronic annotation///0007275 // multicellular o
0.0012928	NM_008344	1.26 <i>Igfbp6</i>	insulin-like growth factor binding protein 6	0001558 // regulation of cell growth // inferred from electronic annotation///0043567 // regulation of insu
0.0052937	NM_001174	1.26 <i>Camk2b</i>	calcium/calmodulin-dependent protein kinase II, beta	0000082 // G1/S transition of mitotic cell cycle // inferred from mutant phenotype///0002030 // inhibitory
0.0011485	NM_011066	1.26 <i>Per2</i>	period circadian clock 2	0000122 // negative regulation of transcription from RNA polymerase II promoter // inferred from direct a
0.0015635	NM_008197	1.26 <i>H1fo</i>	H1 histone family, member 0	0006334 // nucleosome assembly // inferred from electronic annotation
0.0084722	NM_010518	1.26 <i>Igfbp5</i>	insulin-like growth factor binding protein 5	0001558 // regulation of cell growth // inferred from genetic interaction///0001649 // osteoblast different
0.0033936	NM_008416	1.26 <i>Junb</i>	jun B proto-oncogene	0000122 // negative regulation of transcription from RNA polymerase II promoter // not recorded///00015
5.01E-04	NM_001130	1.26 <i>Arhgef1</i>	Rho guanine nucleotide exchange factor (GEF) 1	0035023 // regulation of Rho protein signal transduction // inferred from electronic annotation///0038032
0.0042069	NM_010415	1.27 <i>Hbegf</i>	heparin-binding EGF-like growth factor	0001525 // angiogenesis // non-traceable author statement///0001832 // blastocyst growth // traceable a



p (WT:KO)	RefSeq Tran: FD Air	Gene Symbol	Gene Title	Gene Ontology Biological Process
0.0391272	NM_008655	<b>1.27</b> <i>Gadd45b</i>	growth arrest and DNA-damage-inducible 45 beta	0000185 // activation of MAPKK activity // not recorded//0000186 // activation of MAPKK activity // infe
0.0014458	NM_025476	<b>1.27</b> <i>Rmdn1</i>	regulator of microtubule dynamics 1	
0.0033835	NM_008055	<b>1.27</b> <i>Fzd4</i>	frizzled homolog 4 (Drosophila)	0001553 // luteinization // inferred from mutant phenotype//0001568 // blood vessel development // inf
0.0177529	NM_025436	<b>1.27</b> <i>Msmo1</i>	methylsterol monooxygenase 1	0006629 // lipid metabolic process // inferred from electronic annotation//0006633 // fatty acid biosynth
0.0255131	NM_001111	<b>1.28</b> <i>Zfp322a</i>	zinc finger protein 322A	0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 // regulation o
0.0097232	NM_013833	<b>1.28</b> <i>Grip//Rax</i>	gastrin releasing peptide//retina and anterior neural fold homeobox	0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 // regulation o
0.0027466	NM_001146	<b>1.28</b> <i>Nkx2-1</i>	NK2 homeobox 1	0000122 // negative regulation of transcription from RNA polymerase II promoter // inferred from direct a
0.0160011	NM_001290	<b>1.28</b> <i>Cwc22//Xdh</i>	CWC22 spliceosome-associated protein homolog (S. cerevisiae)//xanthine de	0000398 // mRNA splicing, via spliceosome // not recorded//0001933 // negative regulation of protein ph
0.004408	NM_001168	<b>1.28</b> <i>Tmc3</i>	transmembrane and coiled coil domains 3	
0.044719	NM_001145	<b>1.29</b> <i>Slc15a2</i>	solute carrier family 15 (H+/peptide transporter), member 2	0006810 // transport // inferred from electronic annotation//0006857 // oligopeptide transport // inferre
0.0067158	NM_011436	<b>1.29</b> <i>Sor11</i>	sortilin-related receptor, LDLR class A repeats-containing	0000042 // protein targeting to Golgi // not recorded//0006605 // protein targeting // not recorded//000
0.001724	NM_001163	<b>1.29</b> <i>Bri3</i>	brain protein I3	
2.21E-04	NM_172505	<b>1.29</b> <i>A730008H23Rik//Hjurp//6430706D22Rik</i>	RIKEN cDNA A730008H23 gene//Holliday junction recognition protein//RIKE	0007049 // cell cycle // inferred from electronic annotation//0007059 // chromosome segregation // not i
0.0089814	NM_009135	<b>1.29</b> <i>Scn7a</i>	sodium channel, voltage-gated, type VII, alpha	0006810 // transport // inferred from electronic annotation//0006811 // ion transport // inferred from el
0.0189613	NM_019568	<b>1.29</b> <i>Cxcl14</i>	chemokine (C-X-C motif) ligand 14	0006955 // immune response // inferred from electronic annotation//0045662 // negative regulation of r
0.0351907	NM_009438	<b>1.29</b> <i>Fhl3//Rpl13a</i>	FMS-like tyrosine kinase 3 ligand//ribosomal protein L13A	0001934 // positive regulation of protein phosphorylation // inferred from genetic interaction//0006412 //
0.0029986	NM_026428	<b>1.29</b> <i>Dcxr</i>	dicarbonyl L-xylulose reductase	0005975 // carbohydrate metabolic process // inferred from electronic annotation//0005997 // xylulose n
0.0049446	NM_001146	<b>1.29</b> <i>Pdgfrb</i>	platelet derived growth factor receptor, beta polypeptide	0001568 // blood vessel development // inferred from expression pattern//0001701 // in utero embryoni
0.0110091	NM_021395	<b>1.29</b> <i>Hyou1</i>	hypoxia up-regulated 1	0001666 // response to hypoxia // not recorded//0002931 // response to ischemia // inferred from direct
0.0010226	NM_007419	<b>1.30</b> <i>Adrb1</i>	adrenergic receptor, beta 1	0001996 // positive regulation of heart rate by epinephrine-norepinephrine // inferred from mutant pheno
3.50E-04	NM_023133	<b>1.30</b> <i>Rps19//Rps19-ps1//Rps19-ps2//Rps19-ps3//Rps19-ps6//Rps19-p</i>	ribosomal protein S19//ribosomal protein S19, pseudogene 1//ribosomal pr	0000028 // ribosomal small subunit assembly // not recorded//0000462 // maturation of SSU-rRNA from i
9.47E-04	NM_001036	<b>1.30</b> <i>Atp2b2</i>	ATPase, Ca++ transporting, plasma membrane 2	0000902 // cell morphogenesis // inferred from mutant phenotype//0006810 // transport // inferred from
0.0222483	NM_015800	<b>1.30</b> <i>Crim1</i>	cysteine rich transmembrane BMP regulator 1 (chordin like)	0001558 // regulation of cell growth // inferred from electronic annotation//0010951 // negative regulati
0.0013962	NM_008898	<b>1.30</b> <i>Por</i>	P450 (cytochrome) oxidoreductase	0003420 // regulation of growth plate cartilage chondrocyte proliferation // not recorded//0007584 // res
1.55E-04	NM_172505	<b>1.30</b> <i>6430706D22Rik//A730008H23Rik//Hjurp</i>	Holliday junction recognition protein	0007049 // cell cycle // inferred from electronic annotation//0007059 // chromosome segregation // not i
0.0020454	NM_001109	<b>1.31</b> <i>Kazn</i>	kazrin, periplakin interacting protein	0031424 // keratinization // inferred from electronic annotation
0.0054159	NM_009196	<b>1.31</b> <i>Slc16a1</i>	solute carrier family 16 (monocarboxylic acid transporters), member 1	0006629 // lipid metabolic process // inferred from mutant phenotype//0006810 // transport // inferred f
9.29E-04	NM_001289	<b>1.32</b> <i>Pira1//Pira2//Pira6//Gm10693//Gm14548//Lira6//Pira11//Pi</i>	paired-ig-like receptor A1//paired-ig-like receptor A2//paired-ig-like recepto	0001782 // B cell homeostasis // inferred from mutant phenotype//0002250 // adaptive immune respons
0.0156341	NM_021349	<b>1.32</b> <i>Tnfrsf13b</i>	tumor necrosis factor receptor superfamily, member 13b	0001782 // B cell homeostasis // inferred from direct assay//0001782 // B cell homeostasis // inferre
0.0061959	NM_001081	<b>1.32</b> <i>Irs2</i>	insulin receptor substrate 2	0002053 // positive regulation of mesenchymal cell proliferation // inferred from genetic interaction//000
0.0036453	NM_009911	<b>1.32</b> <i>Cxcr4</i>	chemokine (C-X-C motif) receptor 4	0001569 // patterning of blood vessels // inferred from mutant phenotype//0001666 // response to hypoxi
0.0237046	NM_001035	<b>1.32</b> <i>Akap2//Pakap</i>	A kinase (PRKA) anchor protein 2//paralemmin A kinase anchor protein	0007015 // actin filament organization // inferred from direct assay//0007178 // transmembrane recepto
0.0390949	NM_001290	<b>1.33</b> <i>Ttc14</i>	tetratricopeptide repeat domain 14	0001947 // heart looping // ---//0003341 // cilium movement // ---//0003356 // regulation of cilium beat
0.0101252	NM_001142	<b>1.33</b> <i>Lmo2</i>	LIM domain only 2	0035162 // embryonic hemopoiesis // inferred from genetic interaction//0042789 // mRNA transcription i
0.0025517	NR_002847	<b>1.34</b> <i>Malat1</i>	metastasis associated lung adenocarcinoma transcript 1 (non-coding RNA)	0000381 // regulation of alternative mRNA splicing, via spliceosome // inferred from mutant phenotype//
0.0015302	NM_001113	<b>1.34</b> <i>Ldb1</i>	LIM domain binding 1	0000972 // transcription-dependent tethering of RNA polymerase II gene DNA at nuclear periphery // infer
0.0208486	NM_001077	<b>1.35</b> <i>Hnrnpd</i>	heterogeneous nuclear ribonucleoprotein D	0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 // regulation o
0.0067467	NM_001164	<b>1.35</b> <i>Ankrd33b</i>	ankyrin repeat domain 33B	
0.0090709	NM_018820	<b>1.35</b> <i>Sertad1</i>	SERTA domain containing 1	0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 // regulation o
1.95E-04	NM_027873	<b>1.35</b> <i>Ubiad1</i>	UbiA prenyltransferase domain containing 1	0001885 // endothelial cell development // inferred from sequence or structural similarity//0006744 // ut
0.0055772	NM_001111	<b>1.36</b> <i>Cd59a</i>	CD59a antigen	0001775 // cell activation // ---//0001971 // negative regulation of activation of membrane attack comple
0.0028429	NM_001177	<b>1.36</b> <i>Pfkfb3</i>	6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 3	0006000 // fructose metabolic process // inferred from electronic annotation//0006003 // fructose 2,6-bi
0.0195851	NM_009052	<b>1.36</b> <i>Bex1</i>	brain expressed gene 1	0002052 // positive regulation of neuroblast proliferation // not recorded//0007275 // multicellular organ
6.30E-04	NM_001289	<b>1.37</b> <i>Sox17</i>	SRV (sex determining region Y)-box 17	0000122 // negative regulation of transcription from RNA polymerase II promoter // inferred from mutant
2.78E-04	NM_021332	<b>1.38</b> <i>Glip1r</i>	glucagon-like peptide 1 receptor	0006950 // response to stress // inferred from mutant phenotype//0007165 // signal transduction // infer
0.0017829	NM_001163	<b>1.39</b> <i>Emcn</i>	endomucin	0001525 // angiogenesis // inferred from sequence or structural similarity//0016337 // single organismal i
0.0020934	NM_008360	<b>1.39</b> <i>Il18</i>	interleukin 18	0000165 // MAPK cascade // not recorded//0001525 // angiogenesis // not recorded//0001525 // angiog
0.0069613	NM_013672	<b>1.39</b> <i>Sp1</i>	trans-acting transcription factor 1	0001503 // ossification // inferred from genetic interaction//0001701 // in utero embryonic development
1.71E-04	NM_001083	<b>1.40</b> <i>Gm13139</i>	predicted gene 13139	0002244 // hematopoietic progenitor cell differentiation // inferred from mutant phenotype//0006355 //
1.03E-04	NM_029357	<b>1.40</b> <i>Pcdh1</i>	protocadherin 1	0007155 // cell adhesion // inferred from electronic annotation//0007156 // homophilic cell adhesion via
0.0440882	NM_007705	<b>1.41</b> <i>Cirbp</i>	cold inducible RNA binding protein	0009409 // response to cold // inferred from electronic annotation//0009411 // response to UV // not rec
2.70E-04	NM_001289	<b>1.41</b> <i>Pira1//Pira2//Pira6//Gm10693//Gm14548//Lira6//Pira11//Pi</i>	paired-ig-like receptor A1//paired-ig-like receptor A2//paired-ig-like recepto	0001782 // B cell homeostasis // inferred from mutant phenotype//0002250 // adaptive immune respons
1.92E-04	NM_001111	<b>1.41</b> <i>Comt</i>	catechol-O-methyltransferase	0006584 // catecholamine metabolic process // inferred from electronic annotation//0007565 // female p
1.31E-04	NM_011057	<b>1.42</b> <i>Pdgfb</i>	platelet derived growth factor, B polypeptide	0001568 // blood vessel development // inferred from expression pattern//0001666 // response to hypoxi
0.0452824	NM_022983	<b>1.45</b> <i>Lpar3</i>	lysophosphatidic acid receptor 3	0000187 // activation of MAPK activity // inferred from direct assay//0007165 // signal transduction // inf
0.0026965	NR_045032	<b>1.45</b> <i>Gdap10</i>	ganglioside-induced differentiation-associated-protein 10	
2.59E-04	NM_001003	<b>1.47</b> <i>Pcdha1//Pcdha10//Pcdha11//Pcdha12//Pcdha2//Pcdha3//Pcdh</i>	protocadherin alpha 1//protocadherin alpha 10//protocadherin alpha 11//	0007155 // cell adhesion // inferred from electronic annotation//0007155 // cell adhesion // traceable au
1.47E-04	NM_001252	<b>1.49</b> <i>Tspan4</i>	tetraspanin 4	0006461 // protein complex assembly // not recorded//0007166 // cell surface receptor signaling pathwa
4.55E-05	NM_153068	<b>1.51</b> <i>Ehd2</i>	EH-domain containing 2	0006897 // endocytosis // inferred from direct assay//0008152 // metabolic process // inferred from elect
1.07E-05	NM_009003	<b>1.53</b> <i>Rab4a</i>	RAB4A, member RAS oncogene family	0006810 // transport // inferred from electronic annotation//0006886 // intracellular protein transport //
0.0335806	NM_001166	<b>1.54</b> <i>Gm15453//Rbm3</i>	predicted gene 15453//RNA binding motif protein 3	0006412 // translation // inferred from direct assay//0006417 // regulation of translation // inferred from
0.0038689	NM_139149	<b>1.55</b> <i>Fus</i>	fused in sarcoma	0071277 // cellular response to calcium ion // not recorded//1903506 // regulation of nucleic acid-templa
2.21E-04	NM_017376	<b>1.55</b> <i>Tef</i>	thyrotroph embryonic factor	0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 // regulation o
0.0062066	NR_002840/	<b>1.56</b> <i>Gass5//Snord47</i>	growth arrest specific 5//small nucleolar RNA, C/D box 47	
1.76E-05	NM_001160	<b>1.57</b> <i>Gnb1</i>	guanine nucleotide binding protein (G protein), beta 1	0007165 // signal transduction // inferred from electronic annotation//0007186 // G-protein coupled rece
1.70E-06	NM_001111	<b>1.60</b> <i>Wdfy1</i>	WD repeat and FYVE domain containing 1	0034141 // positive regulation of toll-like receptor 3 signaling pathway // inferred from mutant phenotype

p (WT:KO)	RefSeq Tran: FD Air	Gene Symbol	Gene Title	Gene Ontology Biological Process
3.15E-04	NM_001165	1.60 <i>Tshb</i>	thyroid stimulating hormone, beta subunit	0033189 // response to vitamin A // inferred from electronic annotation///0043627 // response to estrog
7.45E-04	NM_145434	1.64 <i>Nr1d1</i>	nuclear receptor subfamily 1, group D, member 1	0000122 // negative regulation of transcription from RNA polymerase II promoter // not recorded///00059
3.92E-04	NM_011122	1.65 <i>Plod1</i>	procollagen-lysine, 2-oxoglutarate 5-dioxygenase 1	0001666 // response to hypoxia // inferred from electronic annotation///0008544 // epidermis developme
0.0171234		1.67 <i>Ighd</i>	immunoglobulin heavy constant delta	0016064 // immunoglobulin mediated immune response // inferred from mutant phenotype///0016446 //
3.30E-04	NM_001003	1.68 <i>Pcdha1///Pcdha10///Pcdha11///Pcdha12///Pcdha2///Pcdha3///Pcdh</i>	protocadherin alpha 1///protocadherin alpha 10///protocadherin alpha 11///	0007155 // cell adhesion // inferred from electronic annotation///0007155 // cell adhesion // traceable au
0.0221363	NM_011584	1.79 <i>Nr1d2</i>	nuclear receptor subfamily 1, group D, member 2	0006351 // transcription, DNA-templated // inferred from electronic annotation///0006355 // regulation o
1.05E-04	XM_011238!	1.88 <i>Gm3579///Gm40514///Gm40814///Gm40991///Gm42035///Gm4210</i>	predicted gene 3579///predicted gene, 40514///predicted gene, 40814///pre	0015074 // DNA integration // inferred from electronic annotation///0090502 // RNA phosphodiester bonc
2.41E-05	NM_001308	1.92 <i>Nnt</i>	nicotinamide nucleotide transhydrogenase	0006740 // NADPH regeneration // not recorded///0015992 // proton transport // not recorded///004545-
1.37E-07	NM_177673	1.92 <i>Cep104</i>	centrosomal protein 104	
4.55E-05	XM_011238!	2.30 <i>Gm3579///Gm40514///Gm40814///Gm40991///Gm42035///Gm4210</i>	predicted gene 3579///predicted gene, 40514///predicted gene, 40814///pre	0015074 // DNA integration // inferred from electronic annotation///0090502 // RNA phosphodiester bonc
1.15E-06	XM_011238!	2.54 <i>Gm37416///Gm39743///Gm40611///Gm40814///Gm41035///Gm414</i>	predicted gene, 37416///predicted gene, 39743///predicted gene, 40611///pr	0006278 // RNA-dependent DNA replication // inferred from electronic annotation///0008152 // metabol
4.98E-06	NM_016974	3.66 <i>Dbp</i>	D site albumin promoter binding protein	0001889 // liver development // inferred from electronic annotation///0006351 // transcription, DNA-tem

**Table S4. Tumor necrosis factor receptor (TNFR)-dependently changed lung genes by 0.3-parts per million (ppm) ozone (O<sub>3</sub>).**

Affymatrix\_GeneChip\_MOE430A. 2 Way ANOVA (p<0.05). Order by fold difference (FD) at 48 hr O<sub>3</sub>.

Selected genes varied at least one time point between C57BL/6J and Tnfr-KO mice (positive-higher in KO, negative-lower in KO).

RefSeq	Tri	p 24h	p 48h	p 72h	FD Air	FD 24h	FD 48h	FD 72h	Gene Symbol	Gene Title	Gene Ontology Biological Process
NM_173781	///XM	0.027			-3.10	-3.96	-4.12	-2.90	<b>Rab6b</b>	RAB6B, member RAS oncogene family	0006810 // transport // inferred from electronic annotation//0006886 // intracellular pr
NM_001131054	///	0.014	2E-04	-4.27	-4.12	-3.09	-1.84		<b>Pttg1</b>	pituitary tumor-transforming gene 1	0001558 // regulation of cell growth // not recorded//0006281 // DNA repair // inferred
NM_001045550	///	0.046	0.019	-18.72	-4.81	-2.82	1.33		<b>Mup1</b> /// <b>Mup10</b> /// <b>Mup12</b> /// <b>Mup13</b> /// <b>Mup14</b> /// <b>Mup15</b> /// <b>Mup16</b> /// <b>Mup17</b> /// <b>Mup18</b> /// <b>Mup19</b> /// <b>Mup20</b> /// <b>Mup21</b> /// <b>Mup22</b> /// <b>Mup23</b> /// <b>Mup24</b> /// <b>Mup25</b> /// <b>Mup26</b> /// <b>Mup27</b> /// <b>Mup28</b> /// <b>Mup29</b> /// <b>Mup30</b> /// <b>Mup31</b> /// <b>Mup32</b> /// <b>Mup33</b> /// <b>Mup34</b> /// <b>Mup35</b> /// <b>Mup36</b> /// <b>Mup37</b> /// <b>Mup38</b> /// <b>Mup39</b> /// <b>Mup40</b> /// <b>Mup41</b> /// <b>Mup42</b> /// <b>Mup43</b> /// <b>Mup44</b> /// <b>Mup45</b> /// <b>Mup46</b> /// <b>Mup47</b> /// <b>Mup48</b> /// <b>Mup49</b> /// <b>Mup50</b> /// <b>Mup51</b> /// <b>Mup52</b> /// <b>Mup53</b> /// <b>Mup54</b> /// <b>Mup55</b> /// <b>Mup56</b> /// <b>Mup57</b> /// <b>Mup58</b> /// <b>Mup59</b> /// <b>Mup60</b> /// <b>Mup61</b> /// <b>Mup62</b> /// <b>Mup63</b> /// <b>Mup64</b> /// <b>Mup65</b> /// <b>Mup66</b> /// <b>Mup67</b> /// <b>Mup68</b> /// <b>Mup69</b> /// <b>Mup70</b> /// <b>Mup71</b> /// <b>Mup72</b> /// <b>Mup73</b> /// <b>Mup74</b> /// <b>Mup75</b> /// <b>Mup76</b> /// <b>Mup77</b> /// <b>Mup78</b> /// <b>Mup79</b> /// <b>Mup80</b> /// <b>Mup81</b> /// <b>Mup82</b> /// <b>Mup83</b> /// <b>Mup84</b> /// <b>Mup85</b> /// <b>Mup86</b> /// <b>Mup87</b> /// <b>Mup88</b> /// <b>Mup89</b> /// <b>Mup90</b> /// <b>Mup91</b> /// <b>Mup92</b> /// <b>Mup93</b> /// <b>Mup94</b> /// <b>Mup95</b> /// <b>Mup96</b> /// <b>Mup97</b> /// <b>Mup98</b> /// <b>Mup99</b> /// <b>Mup100</b> /// <b>Mup101</b> /// <b>Mup102</b> /// <b>Mup103</b> /// <b>Mup104</b> /// <b>Mup105</b> /// <b>Mup106</b> /// <b>Mup107</b> /// <b>Mup108</b> /// <b>Mup109</b> /// <b>Mup110</b> /// <b>Mup111</b> /// <b>Mup112</b> /// <b>Mup113</b> /// <b>Mup114</b> /// <b>Mup115</b> /// <b>Mup116</b> /// <b>Mup117</b> /// <b>Mup118</b> /// <b>Mup119</b> /// <b>Mup120</b> /// <b>Mup121</b> /// <b>Mup122</b> /// 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<b>Mup178</b> /// <b>Mup179</b> /// <b>Mup180</b> /// <b>Mup181</b> /// <b>Mup182</b> /// <b>Mup183</b> /// <b>Mup184</b> /// <b>Mup185</b> /// <b>Mup186</b> /// <b>Mup187</b> /// <b>Mup188</b> /// <b>Mup189</b> /// <b>Mup190</b> /// <b>Mup191</b> /// <b>Mup192</b> /// <b>Mup193</b> /// <b>Mup194</b> /// <b>Mup195</b> /// <b>Mup196</b> /// <b>Mup197</b> /// <b>Mup198</b> /// <b>Mup199</b> /// <b>Mup200</b> /// <b>Mup201</b> /// <b>Mup202</b> /// <b>Mup203</b> /// <b>Mup204</b> /// <b>Mup205</b> /// <b>Mup206</b> /// <b>Mup207</b> /// <b>Mup208</b> /// <b>Mup209</b> /// <b>Mup210</b> /// <b>Mup211</b> /// <b>Mup212</b> /// <b>Mup213</b> /// <b>Mup214</b> /// <b>Mup215</b> /// <b>Mup216</b> /// <b>Mup217</b> /// <b>Mup218</b> /// <b>Mup219</b> /// <b>Mup220</b> /// <b>Mup221</b> /// <b>Mup222</b> /// <b>Mup223</b> /// <b>Mup224</b> /// <b>Mup225</b> /// <b>Mup226</b> /// <b>Mup227</b> /// <b>Mup228</b> /// <b>Mup229</b> /// <b>Mup230</b> /// <b>Mup231</b> /// <b>Mup232</b> /// <b>Mup233</b> /// <b>Mup234</b> /// <b>Mup235</b> /// <b>Mup236</b> /// <b>Mup237</b> /// <b>Mup238</b> /// <b>Mup239</b> /// <b>Mup240</b> /// <b>Mup241</b> /// <b>Mup242</b> /// <b>Mup243</b> /// <b>Mup244</b> /// <b>Mup245</b> /// <b>Mup246</b> /// <b>Mup247</b> /// <b>Mup248</b> /// <b>Mup249</b> /// <b>Mup250</b> /// <b>Mup251</b> /// <b>Mup252</b> /// <b>Mup253</b> /// <b>Mup254</b> /// <b>Mup255</b> /// <b>Mup256</b> /// <b>Mup257</b> /// <b>Mup258</b> /// <b>Mup259</b> /// <b>Mup260</b> /// <b>Mup261</b> /// <b>Mup262</b> /// <b>Mup263</b> /// <b>Mup264</b> /// <b>Mup265</b> /// <b>Mup266</b> /// <b>Mup267</b> /// <b>Mup268</b> /// <b>Mup269</b> /// <b>Mup270</b> /// <b>Mup271</b> /// <b>Mup272</b> /// <b>Mup273</b> /// <b>Mup274</b> /// <b>Mup275</b> /// <b>Mup276</b> /// <b>Mup277</b> /// <b>Mup278</b> /// <b>Mup279</b> /// <b>Mup280</b> /// <b>Mup281</b> /// <b>Mup282</b> /// <b>Mup283</b> /// <b>Mup284</b> /// <b>Mup285</b> /// <b>Mup286</b> /// <b>Mup287</b> /// 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<b>Mup398</b> /// <b>Mup399</b> /// <b>Mup400</b> /// <b>Mup401</b> /// <b>Mup402</b> /// <b>Mup403</b> /// <b>Mup404</b> /// <b>Mup405</b> /// <b>Mup406</b> /// <b>Mup407</b> /// <b>Mup408</b> /// <b>Mup409</b> /// <b>Mup410</b> /// <b>Mup411</b> /// <b>Mup412</b> /// <b>Mup413</b> /// <b>Mup414</b> /// <b>Mup415</b> /// <b>Mup416</b> /// <b>Mup417</b> /// <b>Mup418</b> /// <b>Mup419</b> /// <b>Mup420</b> /// <b>Mup421</b> /// <b>Mup422</b> /// <b>Mup423</b> /// <b>Mup424</b> /// <b>Mup425</b> /// <b>Mup426</b> /// <b>Mup427</b> /// <b>Mup428</b> /// <b>Mup429</b> /// <b>Mup430</b> /// <b>Mup431</b> /// <b>Mup432</b> /// <b>Mup433</b> /// <b>Mup434</b> /// <b>Mup435</b> /// <b>Mup436</b> /// <b>Mup437</b> /// <b>Mup438</b> /// <b>Mup439</b> /// <b>Mup440</b> /// <b>Mup441</b> /// <b>Mup442</b> /// <b>Mup443</b> /// <b>Mup444</b> /// <b>Mup445</b> /// <b>Mup446</b> /// <b>Mup447</b> /// <b>Mup448</b> /// <b>Mup449</b> /// <b>Mup450</b> /// <b>Mup451</b> /// <b>Mup452</b> /// <b>Mup453</b> /// <b>Mup454</b> /// <b>Mup455</b> /// <b>Mup456</b> /// <b>Mup457</b> /// <b>Mup458</b> /// <b>Mup459</b> /// <b>Mup460</b> /// <b>Mup461</b> /// <b>Mup462</b> /// <b>Mup463</b> /// <b>Mup464</b> /// <b>Mup465</b> /// <b>Mup466</b> /// <b>Mup467</b> /// <b>Mup468</b> /// <b>Mup469</b> /// <b>Mup470</b> /// <b>Mup471</b> /// <b>Mup472</b> /// <b>Mup473</b> /// <b>Mup474</b> /// <b>Mup475</b> /// <b>Mup476</b> /// <b>Mup477</b> /// <b>Mup478</b> /// <b>Mup479</b> /// <b>Mup480</b> /// <b>Mup481</b> /// <b>Mup482</b> /// <b>Mup483</b> /// <b>Mup484</b> /// <b>Mup485</b> /// <b>Mup486</b> /// <b>Mup487</b> /// <b>Mup488</b> /// <b>Mup489</b> /// <b>Mup490</b> /// <b>Mup491</b> /// <b>Mup492</b> /// <b>Mup493</b> /// <b>Mup494</b> /// <b>Mup495</b> /// <b>Mup496</b> /// <b>Mup497</b> /// <b>Mup498</b> /// <b>Mup499</b> /// <b>Mup500</b> /// <b>Mup501</b> /// <b>Mup502</b> /// <b>Mup503</b> /// <b>Mup504</b> /// <b>Mup505</b> /// <b>Mup506</b> /// <b>Mup507</b> /// <b>Mup508</b> /// <b>Mup509</b> /// <b>Mup510</b> /// <b>Mup511</b> /// <b>Mup512</b> /// <b>Mup513</b> /// <b>Mup514</b> /// <b>Mup515</b> /// <b>Mup516</b> /// <b>Mup517</b> /// <b>Mup518</b> /// <b>Mup519</b> /// <b>Mup520</b> /// <b>Mup521</b> /// <b>Mup522</b> /// <b>Mup523</b> /// <b>Mup524</b> /// <b>Mup525</b> /// <b>Mup526</b> /// <b>Mup527</b> /// <b>Mup528</b> /// <b>Mup529</b> /// <b>Mup530</b> /// <b>Mup531</b> /// <b>Mup532</b> /// <b>Mup533</b> /// <b>Mup534</b> /// <b>Mup535</b> /// <b>Mup536</b> /// <b>Mup537</b> /// <b>Mup538</b> /// <b>Mup539</b> /// <b>Mup540</b> /// <b>Mup541</b> /// <b>Mup542</b> /// <b>Mup543</b> /// <b>Mup544</b> /// <b>Mup545</b> /// <b>Mup546</b> /// <b>Mup547</b> /// <b>Mup548</b> /// <b>Mup549</b> /// <b>Mup550</b> /// <b>Mup551</b> /// <b>Mup552</b> /// <b>Mup553</b> /// <b>Mup554</b> /// <b>Mup555</b> /// <b>Mup556</b> /// <b>Mup557</b> /// <b>Mup558</b> /// <b>Mup559</b> /// <b>Mup560</b> /// <b>Mup561</b> /// <b>Mup562</b> /// <b>Mup563</b> /// <b>Mup564</b> /// <b>Mup565</b> /// <b>Mup566</b> /// <b>Mup567</b> /// <b>Mup568</b> /// <b>Mup569</b> /// <b>Mup570</b> /// <b>Mup571</b> /// <b>Mup572</b> /// <b>Mup573</b> /// <b>Mup574</b> /// <b>Mup575</b> /// <b>Mup576</b> /// <b>Mup577</b> /// <b>Mup578</b> /// <b>Mup579</b> /// <b>Mup580</b> /// <b>Mup581</b> /// <b>Mup582</b> /// <b>Mup583</b> /// <b>Mup584</b> /// <b>Mup585</b> /// <b>Mup586</b> /// <b>Mup587</b> /// <b>Mup588</b> /// <b>Mup589</b> /// <b>Mup590</b> /// <b>Mup591</b> /// <b>Mup592</b> /// <b>Mup593</b> /// <b>Mup594</b> /// <b>Mup595</b> /// <b>Mup596</b> /// <b>Mup597</b> /// <b>Mup598</b> /// <b>Mup599</b> /// <b>Mup600</b> /// <b>Mup601</b> /// <b>Mup602</b> /// <b>Mup603</b> /// <b>Mup604</b> /// <b>Mup605</b> /// <b>Mup606</b> /// <b>Mup607</b> /// <b>Mup608</b> /// <b>Mup609</b> /// <b>Mup610</b> /// <b>Mup611</b> /// <b>Mup612</b> /// <b>Mup613</b> /// <b>Mup614</b> /// <b>Mup615</b> /// <b>Mup616</b> /// <b>Mup617</b> /// <b>Mup618</b> /// <b>Mup619</b> /// <b>Mup620</b> /// <b>Mup621</b> /// <b>Mup622</b> /// <b>Mup623</b> /// <b>Mup624</b> /// <b>Mup625</b> /// <b>Mup626</b> /// <b>Mup627</b> /// <b>Mup628</b> /// <b>Mup629</b> /// <b>Mup630</b> /// <b>Mup631</b> /// <b>Mup632</b> /// <b>Mup633</b> /// <b>Mup634</b> /// <b>Mup635</b> /// <b>Mup636</b> /// <b>Mup637</b> /// <b>Mup638</b> /// <b>Mup639</b> /// <b>Mup640</b> /// <b>Mup641</b> /// <b>Mup642</b> /// <b>Mup643</b> /// <b>Mup644</b> /// <b>Mup645</b> /// <b>Mup646</b> /// <b>Mup647</b> /// <b>Mup648</b> /// <b>Mup649</b> /// <b>Mup650</b> /// <b>Mup651</b> /// <b>Mup652</b> /// <b>Mup653</b> /// <b>Mup654</b> /// <b>Mup655</b> /// <b>Mup656</b> /// <b>Mup657</b> /// <b>Mup658</b> /// <b>Mup659</b> /// <b>Mup660</b> /// <b>Mup661</b> /// <b>Mup662</b> /// <b>Mup663</b> /// <b>Mup664</b> /// <b>Mup665</b> /// <b>Mup666</b> /// <b>Mup667</b> /// <b>Mup668</b> /// <b>Mup669</b> /// <b>Mup670</b> /// <b>Mup671</b> /// <b>Mup672</b> /// <b>Mup673</b> /// <b>Mup674</b> /// <b>Mup675</b> /// <b>Mup676</b> /// <b>Mup677</b> /// <b>Mup678</b> /// <b>Mup679</b> /// <b>Mup680</b> /// <b>Mup681</b> /// <b>Mup682</b> /// <b>Mup683</b> /// <b>Mup684</b> /// <b>Mup685</b> /// <b>Mup686</b> /// <b>Mup687</b> /// <b>Mup688</b> /// <b>Mup689</b> /// <b>Mup690</b> /// <b>Mup691</b> /// <b>Mup692</b> /// <b>Mup693</b> /// <b>Mup694</b> /// <b>Mup695</b> /// <b>Mup696</b> /// <b>Mup697</b> /// <b>Mup698</b> /// <b>Mup699</b> /// <b>Mup700</b> /// <b>Mup701</b> /// <b>Mup702</b> /// <b>Mup703</b> /// <b>Mup704</b> /// <b>Mup705</b> /// <b>Mup706</b> /// <b>Mup707</b> /// <b>Mup708</b> /// <b>Mup709</b> /// <b>Mup710</b> /// <b>Mup711</b> /// <b>Mup712</b> /// <b>Mup713</b> /// <b>Mup714</b> /// <b>Mup715</b> /// <b>Mup716</b> /// <b>Mup717</b> /// <b>Mup718</b> /// <b>Mup719</b> /// <b>Mup720</b> /// <b>Mup721</b> /// <b>Mup722</b> /// <b>Mup723</b> /// <b>Mup724</b> /// <b>Mup725</b> /// <b>Mup726</b> /// <b>Mup727</b> /// <b>Mup728</b> /// <b>Mup729</b> /// <b>Mup730</b> /// <b>Mup731</b> /// <b>Mup732</b> /// <b>Mup733</b> /// <b>Mup734</b> /// <b>Mup735</b> /// <b>Mup736</b> /// <b>Mup737</b> /// <b>Mup738</b> /// <b>Mup739</b> /// <b>Mup740</b> /// <b>Mup741</b> /// <b>Mup742</b> /// <b>Mup743</b> /// <b>Mup744</b> /// <b>Mup745</b> /// <b>Mup746</b> /// <b>Mup747</b> /// <b>Mup748</b> /// <b>Mup749</b> /// <b>Mup750</b> /// <b>Mup751</b> /// <b>Mup752</b> /// <b>Mup753</b> /// <b>Mup754</b> /// <b>Mup755</b> /// <b>Mup756</b> /// <b>Mup757</b> /// <b>Mup758</b> /// <b>Mup759</b> /// <b>Mup760</b> /// <b>Mup761</b> /// <b>Mup762</b> /// <b>Mup763</b> /// <b>Mup764</b> /// <b>Mup765</b> /// <b>Mup766</b> /// <b>Mup767</b> /// <b>Mup768</b> /// <b>Mup769</b> /// <b>Mup770</b> /// <b>Mup771</b> /// <b>Mup772</b> /// <b>Mup773</b> /// <b>Mup774</b> /// <b>Mup775</b> /// <b>Mup776</b> /// <b>Mup777</b> /// <b>Mup778</b> /// <b>Mup779</b> /// <b>Mup780</b> /// <b>Mup781</b> /// <b>Mup782</b> /// <b>Mup783</b> /// <b>Mup784</b> /// <b>Mup785</b> /// <b>Mup786</b> /// <b>Mup787</b> /// <b>Mup788</b> /// <b>Mup789</b> /// <b>Mup790</b> /// <b>Mup791</b> /// <b>Mup792</b> /// <b>Mup793</b> /// <b>Mup794</b> /// <b>Mup795</b> /// <b>Mup796</b> /// <b>Mup797</b> /// <b>Mup798</b> /// <b>Mup799</b> /// <b>Mup800</b> /// <b>Mup801</b> /// <b>Mup802</b> /// <b>Mup803</b> /// <b>Mup804</b> /// <b>Mup805</b> /// <b>Mup806</b> /// <b>Mup807</b> /// <b>Mup808</b> /// <b>Mup809</b> /// <b>Mup810</b> /// <b>Mup811</b> /// <b>Mup812</b> /// <b>Mup813</b> /// <b>Mup814</b> /// <b>Mup815</b> /// <b>Mup816</b> /// <b>Mup817</b> /// <b>Mup818</b> /// <b>Mup819</b> /// <b>Mup820</b> /// <b>Mup821</b> /// <b>Mup822</b> /// <b>Mup823</b> /// <b>Mup824</b> /// <b>Mup825</b> /// <b>Mup826</b> /// <b>Mup827</b> /// <b>Mup828</b> /// <b>Mup829</b> /// <b>Mup830</b> /// <b>Mup831</b> /// <b>Mup832</b> /// <b>Mup833</b> /// <b>Mup834</b> /// <b>Mup835</b> /// <b>Mup836</b> /// <b>Mup837</b> /// <b>Mup838</b> /// <b>Mup839</b> /// <b>Mup840</b> /// <b>Mup841</b> /// <b>Mup842</b> /// <b>Mup843</b> /// <b>Mup844</b> /// <b>Mup845</b> /// <b>Mup846</b> /// <b>Mup847</b> /// <b>Mup848</b> /// <b>Mup849</b> /// <b>Mup850</b> /// <b>Mup851</b> /// <b>Mup852</b> /// <b>Mup853</b> /// <b>Mup854</b> /// <b>Mup855</b> /// <b>Mup856</b> /// <b>Mup857</b> /// <b>Mup858</b> /// <b>Mup859</b> /// <b>Mup860</b> /// <b>Mup861</b> /// <b>Mup862</b> /// <b>Mup863</b> /// <b>Mup864</b> /// <b>Mup865</b> /// <b>Mup866</b> /// <b>Mup867</b> /// <b>Mup868</b> /// <b>Mup869</b> /// <b>Mup870</b> /// <b>Mup871</b> /// <b>Mup872</b> /// <b>Mup873</b> /// <b>Mup874</b> /// <b>Mup875</b> /// <b>Mup876</b> /// <b>Mup877</b> /// <b>Mup878</b> /// <b>Mup879</b> /// <b>Mup880</b> /// <b>Mup881</b> /// <b>Mup882</b> /// <b>Mup883</b> /// <b>Mup884</b> /// <b>Mup885</b> /// <b>Mup886</b> /// <b>Mup887</b> /// <b>Mup888</b> /// <b>Mup889</b> /// <b>Mup890</b> /// <b>Mup891</b> /// <b>Mup892</b> /// <b>Mup893</b> /// <b>Mup894</b> /// <b>Mup895</b> /// <b>Mup896</b> /// <b>Mup897</b> /// <b>Mup898</b> /// <b>Mup899</b> /// <b>Mup900</b> /// <b>Mup901</b> /// <b>Mup902</b> /// <b>Mup903</b> /// <b>Mup904</b> /// <b>Mup905</b> /// <b>Mup906</b> /// <b>Mup907</b> /// <b>Mup908</b> /// <b>Mup909</b> /// <b>Mup910</b> /// <b>Mup911</b> /// <b>Mup912</b> /// <b>Mup913</b> /// <b>Mup914</b> /// <b>Mup915</b> /// <b>Mup916</b> /// <b>Mup917</b> /// <b>Mup918</b> /// <b>Mup919</b> /// <b>Mup920</b> /// <b>Mup921</b> /// <b>Mup922</b> /// <b>Mup923</b> /// <b>Mup924</b> /// <b>Mup925</b> /// <b>Mup926</b> /// <b>Mup927</b> /// <b>Mup928</b> /// <b>Mup929</b> /// <b>Mup930</b> /// <b>Mup931</b> /// <b>Mup932</b> /// <b>Mup933</b> /// <b>Mup934</b> /// <b>Mup935</b> /// <b>Mup936</b> /// <b>Mup937</b> /// <b>Mup938</b> /// <b>Mup939</b> /// <b>Mup940</b> /// <b>Mup941</b> /// <b>Mup942</b> /// <b>Mup943</b> /// <b>Mup944</b> /// <b>Mup945</b> /// <b>Mup946</b> /// <b>Mup947</b> /// <b>Mup948</b> /// <b>Mup949</b> /// <b>Mup950</b> /// <b>Mup951</b> /// <b>Mup952</b> /// <b>Mup953</b> /// <b>Mup954</b> /// <b>Mup955</b> /// <b>Mup956</b> /// <b>Mup957</b> /// <b>Mup958</b> /// <b>Mup959</b> /// <b>Mup960</b> /// <b>Mup961</b> /// <b>Mup962</b> /// <b>Mup963</b> /// <b>Mup964</b> /// <b>Mup965</b> /// <b>Mup966</b> /// <b>Mup967</b> /// <b>Mup968</b> /// <b>Mup969</b> /// <b>Mup970</b> /// <b>Mup971</b> /// <b>Mup972</b> /// <b>Mup973</b> /// <b>Mup974</b> /// <b>Mup975</b> /// <b>Mup976</b> /// <b>Mup977</b> /// <b>Mup978</b> /// <b>Mup979</b> /// <b>Mup980</b> /// <b>Mup981</b> /// <b>Mup982</b> /// <b>Mup983</b> /// <b>Mup984</b> /// <b>Mup985</b> /// <b>Mup986</b> /// <b>Mup987</b> /// <b>Mup988</b> /// <b>Mup989</b> /// <b>Mup990</b> /// <b>Mup991</b> /// <b>Mup992</b> /// <b>Mup993</b> /// <b>Mup994</b> /// <b>Mup995</b> /// <b>Mup996</b> /// <b>Mup997</b> /// <b>Mup998</b> /// <b>Mup999</b> /// <b>Mup1000</b> /// <b>Mup1001</b> /// <b>Mup1002</b> /// <b>Mup1003</b> /// <b>Mup1004</b> /// <b>Mup1005</b> /// <b>Mup1006</b> /// <b>Mup1007</b> /// <b>Mup1008</b> /// <b>Mup1009</b> /// <b>Mup1010</b> /// <b>Mup1011</b> /// <b>Mup1012</b> /// <b>Mup1013</b> /// <b>Mup1014</b> /// <b>Mup1015</b> /// <b>Mup1016</b> /// <b>Mup1017</b> /// <b>Mup1018</b> /// <b>Mup1019</b> /// <b>Mup1020</b> /// <b>Mup1021</b> /// <b>Mup1022</b> /// <b>Mup1023</b> /// <b>Mup1024</b> /// <b>Mup1025</b> /// <b>Mup1026</b> /// <b>Mup1027</b> /// <b>Mup1028</b> /// <b>Mup1029</b> /// <b>Mup1030</b> /// <b>Mup1031</b> /// <b>Mup1032</b> /// <b>Mup1033</b> /// <b>Mup1034</b> /// <b>Mup1035</b> /// <b>Mup1036</b> /// <b>Mup1037</b> /// <b>Mup1038</b> /// <b>Mup1039</b> /// <b>Mup1040</b> /// <b>Mup1041</b> /// <b>Mup1042</b> /// <b>Mup1043</b> /// <b>Mup1044</b> /// <b>Mup1045</b> /// <b>Mup1046</b> /// <b>Mup1047</b> /// <b>Mup1048</b> /// <b>Mup1049</b> /// <b>Mup1050</b> /// <b>Mup1051</b> /// <b>Mup1052</b> /// <b>Mup1053</b> /// <b>Mup1054</b> /// <b>Mup1055</b> /// <b>Mup1056</b> /// <b>Mup1057</b> /// <b>Mup1058</b> /// <b>Mup1059</b> /// <b>Mup1060</b> /// <b>Mup1061</b> /// <b>Mup1062</b> /// <b>Mup1063</b> /// <b>Mup1064</b>		

RefSeq	Tri	p 24h	p 48h	p 72h	FD Air	FD 24h	FD 48h	FD 72h	Gene Symbol	Gene Title	Gene Ontology Biological Process
NM_011345	///XM	0.045			-1.10	1.05	-1.25	-1.04	<i>Sele</i>	selectin, endothelial cell	0002092 // positive regulation of receptor internalization // not recorded///0002687 // p
NM_0010454540	///	0.025			-1.05	-1.02	-1.25	1.07	<i>Gm12185</i>	predicted gene 12185	
NM_0098	0.0232				-1.25	1.18	-1.25	-1.25	<i>Cd3g</i>	CD3 antigen, gamma polypeptide	0007163 // establishment or maintenance of cell polarity // not recorded///0007166 // c
NM_0085	0.0209				-1.17	-1.04	-1.25	-1.29	<i>Cxcl9</i>	chemokine (C-X-C motif) ligand 9	0002690 // positive regulation of leukocyte chemotaxis // not recorded///0006935 // che
NM_013585	///XM	0.043			1.08	1.16	-1.25	1.14	<i>Psmb9</i>	proteasome (prosome, macropain) subunit, beta type 9 (large multifunctional peptida	0002376 // immune system process // inferred from electronic annotation///0006508 //
NM_001033484	///XM_000	0.021		0.021	-1.09	-1.09	-1.25	1.09	<i>Iqgap3</i>	IQ motif containing GTPase activating protein 3	0000082 // G1/S transition of mitotic cell cycle // inferred from mutant phenotype///000
NM_0532	0.0052	0.003			-1.00	-1.20	-1.25	1.18	<i>Ces1d</i>	carboxylesterase 1D	0006629 // lipid metabolic process // inferred from electronic annotation///0006637 // a
NM_172378	///XM	0.043			1.03	-1.14	-1.25	-1.14	<i>Slc22a22</i>	solute carrier family 22 (organic cation transporter), member 22	0007186 // G-protein coupled receptor signaling pathway // inferred from direct assay///
NM_0089	0.0357				1.03	-1.31	-1.24	-1.18	<i>Prkg2</i>	protein kinase, cGMP-dependent, type II	0006468 // protein phosphorylation // inferred from electronic annotation///0007623 //
NM_053266	///XM	0.026			1.05	-1.07	-1.24	-1.06	<i>Gtf2ird2</i>	GTf2I repeat domain containing 2	0006351 // transcription, DNA-templated // inferred from electronic annotation///00063
NM_023850	///XM	0.005			1.13	-1.03	-1.24	-1.06	<i>Chst1</i>	carbohydrate (keratan sulfate Gal-6) sulfotransferase 1	0005975 // carbohydrate metabolic process // inferred from electronic annotation///000
NM_0078	0.0342				-1.08	1.30	-1.24	1.10	<i>Ear1</i> /// <i>Ear-ps2</i> /// <i>Ear12</i> /// <i>Ear2</i> /// <i>Ear3</i>	eosinophil-associated, ribonuclease A family, member 1///eosinophil-associated, ribor	0008152 // metabolic process // inferred from electronic annotation///0090305 // nuclei
XM_9773	0.0287				-1.03	1.47	-1.24	-1.17	<i>LOC665506</i> /// <i>Trcb-J</i> /// <i>Trbc1</i> /// <i>Trbc2</i>	T-cell receptor beta-2 chain C region-like///T cell receptor beta, joining region///T cell	receptor beta, constant region 1///T cell receptor beta, constant 2
NM_010326	///XM	0.029			-1.04	-1.11	-1.24	-1.11	<i>Gp1ba</i>	glycoprotein 1b, alpha polypeptide	0000902 // cell morphogenesis // inferred from mutant phenotype///0007155 // cell adh
NM_009999	0.04				1.02	-1.22	-1.24	1.26	<i>Cyp2b10</i>	cytochrome P450, family 2, subfamily b, polypeptide 10	0006805 // xenobiotic metabolic process // not recorded///0008202 // steroid metaboli
NR_131197	///NR_	0.032			1.05	-1.03	-1.24	-1.03	<i>Ggnbp2os</i>	gametogenin binding protein 2, opposite strand	
NM_026514	///XM	0.003			1.03	-1.08	-1.24	-1.08	<i>Cdc42ep3</i>	CDC42 effector protein (Rho GTPase binding) 3	0007266 // Rho protein signal transduction // not recorded///0008360 // regulation of ce
NM_134110	///XM_00652	0.024		0.024	-1.33	-1.34	-1.24	1.14	<i>Kcne2</i>	potassium voltage-gated channel, Isk-related subfamily, gene 2	0006810 // transport // inferred from electronic annotation///0006811 // ion transport /
NM_009994	///XM	0.037			1.04	-1.00	-1.23	-1.09	<i>Cyp1b1</i>	cytochrome P450, family 1, subfamily b, polypeptide 1	0001525 // angiogenesis // inferred from mutant phenotype///0002930 // trabecular me
NR_028574	0.034	0.034			1.03	1.04	-1.23	-1.09	<i>Snhg8</i>	small nucleolar RNA host gene 8	
NM_023168	///XM	0.008			1.00	1.03	-1.23	1.05	<i>Grina</i>	glutamate receptor, ionotropic, N-methyl D-aspartate-associated protein 1 (glutamate	0032469 // endoplasmic reticulum calcium ion homeostasis // inferred from direct assay/
NM_0011	0.0132				-1.06	1.02	-1.23	-1.07	<i>Tshr</i>	thyroid stimulating hormone receptor	0007165 // signal transduction // inferred from electronic annotation///0007186 // G-pr
NM_019431	0.003				1.04	-1.01	-1.23	-1.03	<i>Cacng4</i>	calcium channel, voltage-dependent, gamma subunit 4	0006810 // transport // inferred from electronic annotation///0006811 // ion transport /
NM_0010	0.0456	0.007			1.03	-1.14	-1.23	-1.05	<i>Calca</i>	calcitonin/calcitonin-related polypeptide, alpha	0001976 // neurological system process involved in regulation of systemic arterial blood p
NM_031377	///XM	0.008			1.04	-1.04	-1.23	-1.08	<i>Pramel1</i>	preferentially expressed antigen in melanoma-like 1	0008284 // positive regulation of cell proliferation // inferred from electronic annotation,
XM_9773	0.0133				-1.05	1.45	-1.23	-1.17	<i>LOC665506</i> /// <i>Trbc2</i> /// <i>Trcb-J</i> /// <i>Trbc1</i>	T-cell receptor beta-2 chain C region-like///T cell receptor beta, constant 2///T cell	receptor beta, joining region///T cell receptor beta, constant region 1
NM_0280	0.0151	0.007	#####		1.12	-1.09	-1.23	-1.24	<i>Cyp2c55</i>	cytochrome P450, family 2, subfamily c, polypeptide 55	0006805 // xenobiotic metabolic process // not recorded///0019369 // arachidonic acid i
NM_001253692	///	0.002			-1.03	-1.01	-1.23	1.06	<i>Elmod3</i>	ELMO/CEB-12 domain containing 3	
NM_0010	0.041				1.01	-1.24	-1.23	-1.18	<i>Sepp1</i>	selenoprotein P, plasma, 1	0001887 // selenium compound metabolic process // inferred from direct assay///00018
NM_172584	0.007				1.04	-1.04	-1.23	-1.04	<i>Itpk1</i>	inositol 1,3,4-triphosphate 5/6 kinase	0016310 // phosphorylation // inferred from electronic annotation///0032957 // inositol
NM_001160163	///	0.034			1.13	-1.02	-1.23	-1.05	<i>Neu2</i>	neuraminidase 2	0005975 // carbohydrate metabolic process // inferred from electronic annotation///000
NM_0012	0.0127				-1.21	1.24	-1.23	-1.21	<i>Csf3r</i>	colony stimulating factor 3 receptor (granulocyte)	0007155 // cell adhesion // inferred from electronic annotation///0019221 // cytokine-m
NM_001083959	///	0.028	0.018		1.07	-1.06	-1.23	-1.16	<i>Spo11</i>	SPO11 meiotic protein covalently bound to DSB	0000237 // leptotene // inferred from mutant phenotype///0000737 // DNA catalytic pr
NM_0010	0.0157				-1.12	-1.57	-1.22	1.01	<i>Otud7b</i>	OTU domain containing 7B	0000122 // negative regulation of transcription from RNA polymerase II promoter // infer
NM_0011	0.0043	0.004	0.032		1.03	-1.11	-1.22	-1.13	<i>Smoc1</i>	SPARC related modular calcium binding 1	0001654 // eye development // inferred from mutant phenotype///0001654 // eye devel
NM_008256	0.009	0.012			1.24	1.05	-1.22	-1.09	<i>Hmgcs2</i>	3-hydroxy-3-methylglutaryl-Coenzyme A synthase 2	0001822 // kidney development // inferred from electronic annotation///0001889 // live
NM_0268	0.0175	0.011			1.01	1.24	-1.22	-1.22	<i>Cd177</i>	CD177 antigen	
NM_0097	0.0184				-1.04	-1.32	-1.22	1.12	<i>Aspm</i>	asp (abnormal spindle)-like, microcephaly associated (Drosophila)	0001764 // neuron migration // inferred from genetic interaction///0001764 // neuron m
XM_9773	0.0143	0.0049			-1.05	1.39	-1.22	-1.16	<i>LOC665506</i> /// <i>Trbc2</i> /// <i>Trcb-J</i> /// <i>Trbc1</i> /// <i>Trt</i>	T-cell receptor beta-2 chain C region-like///T cell receptor beta, constant 2///T cell	receptor beta, joining region///T cell receptor beta, constant region 1///T cell receptor beta,
					-1.15	1.71	-1.22	-1.15	<i>Iglv1</i> /// <i>Igllc1</i>	immunoglobulin lambda variable 1///immunoglobulin lambda constant 1	
NR_003964	0.006				1.03	-1.06	-1.22	-1.14	<i>Tubb2a-ps2</i>	tubulin, beta 2a, pseudogene 2	
NM_1460	0.0038	0.008			1.06	-1.16	-1.22	-1.07	<i>Zdhhc14</i>	zinc finger, DHHC domain containing 14	0006612 // protein targeting to membrane // ---///0018230 // peptidyl-L-cysteine S-palm
NM_153067	0.049				1.01	-1.23	-1.22	-1.11	<i>Mrgpra3</i>	MAS-related GPR, member A3	0006953 // acute-phase response // inferred from electronic annotation///0007165 // si
NM_001308501	///	0.023			1.11	-1.04	-1.21	-1.22	<i>Gpr50</i>	G-protein-coupled receptor 50	0007165 // signal transduction // inferred from electronic annotation///0007166 // cell s
NM_0011	0.0485				-1.10	1.12	-1.21	-1.08	<i>Ccr6</i>	chemokine (C-C motif) receptor 6	0006955 // chemotaxis // inferred from electronic annotation///0006955 // immune res
NM_0012	0.0408	0.015			1.07	-1.13	-1.21	-1.04	<i>Ebf2</i>	early B cell factor 2	0001709 // cell fate determination // inferred from direct assay///0006351 // transcripti
NM_0013	0.0309	0.005	0.03		1.11	-1.04	-1.21	-1.11	<i>Stmn4</i>	stathmin-like 4	0007019 // microtubule depolymerization // not recorded///0031110 // regulation of mi
NM_001082531	///	0.048			1.01	-1.07	-1.21	-1.09	<i>Pla2g2a</i>	phospholipase A2, group IIA (platelets, synovial fluid)	0006629 // lipid metabolic process // inferred from electronic annotation///0006644 // p
NM_138683	///XM	0.004			1.21	-1.05	-1.21	-1.09	<i>Rspo1</i>	R-spondin 1	0001934 // positive regulation of protein phosphorylation // not recorded///0002090 //
NM_030720	///XM	0.017			1.03	1.12	-1.21	-1.08	<i>Gpr84</i>	G-protein-coupled receptor 84	0007165 // signal transduction // inferred from electronic annotation///0007186 // G-pr
NM_1336	0.0271				1.13	-1.45	-1.21	1.06	<i>Sult1a1</i>	sulfotransferase family 1A, phenol-preferring, member 1	0006584 // catecholamine metabolic process // not recorded///0006629 // lipid metabol
NM_001013373	///	0.031			-1.04	-1.12	-1.21	-1.18	<i>Tmprss13</i>	transmembrane protease, serine 13	0006508 // proteolysis // inferred from electronic annotation///0006898 // receptor-mec
NM_0010	0.0433	0.04			1.03	-1.07	-1.21	-1.12	<i>Arsi</i>	arylsulfatase i	0008152 // metabolic process // inferred from electronic annotation
NM_178086	0.009	0.002			1.03	-1.10	-1.21	-1.23	<i>Fa2h</i>	fatty acid 2-hydroxylase	0001949 // sebaceous gland cell differentiation // inferred from mutant phenotype///000
NM_007574	0.02				-1.00	-1.05	-1.21	-1.05	<i>C1qc</i>	complement component 1, q subcomponent, C chain	0002376 // immune system process // inferred from electronic annotation///0006958 //
NM_0011	0.0159				1.15	-1.40	-1.21	1.01	<i>Sphk1</i>	sphingosine kinase 1	0001568 // blood vessel development // inferred from genetic interaction///0001934 // s
NM_133667	///XM	0.008			1.14	-1.00	-1.21	1.11	<i>Pdk2</i>	pyruvate dehydrogenase kinase, isoenzyme 2	0005975 // carbohydrate metabolic process // inferred from electronic annotation///000
NM_183171	///XM	0.042	0.04		1.07	-1.04	-1.21	-1.14	<i>Fez1</i>	fasciculation and elongation protein zeta 1 (zygin I)	0006810 // transport // inferred from electronic annotation///0010976 // positive regula
NM_0012	0.03				-1.09	-1.21	-1.21	-1.01	<i>Gsn</i>	gelsolin	0006911 // phagocytosis, engulfment // inferred from mutant phenotype///0006915 // a
NM_013751	///XM	0.041			-1.05	1.01	-1.21	-1.13	<i>Hrasls</i>	HRAS-like suppressor	0001558 // regulation of cell growth // traceable author statement///0006629 // lipid me
NM_145364	///XM	0.049			-1.05	1.01	-1.21	-1.14	<i>Akr1d1</i>	aldo-keto reductase family 1, member D1	0006629 // lipid metabolic process // inferred from electronic annotation///0006699 // b
NM_010180	///XM_00652	0.003		0.003	-1.27	-1.22	-1.21	-1.03	<i>Fbln1</i>	fibulin 1	0001933 // negative regulation of protein phosphorylation // not recorded///0007162 //
NM_001165256	///	0.003	0.046		1.16	1.07	-1.20	-1.06	<i>Dcaf4</i>	DDb1 and CUL4 associated factor 4	
NM_0012	0.0324				1.01	-1.19	-1.20	1.07	<i>Myh14</i>	myosin, heavy polypeptide 14	0003009 // skeletal muscle contraction // not recorded///0007519 // skeletal muscle tiss

RefSeq	Tr	p	24h	p	48h	p	72h	FD Air	FD 24h	FD 48h	FD 72h	Gene Symbol	Gene Title	Gene Ontology Biological Process
					0.004			-1.04	-1.05	-1.20	-1.20	<i>Tcrg-C4</i>	T cell receptor gamma, constant 4	
NM_001033263	///				0.032			1.09	-1.01	-1.20	-1.12	<i>Agap2</i>	ArfGAP with GTPase domain, ankyrin repeat and PH domain 2	0007264 // small GTPase mediated signal transduction // inferred from electronic annota
NM_00131	0.0134	0.01						1.12	-1.19	-1.20	-1.17	<i>Ctj1</i>	cardiotrophin 1	0007166 // cell surface receptor signaling pathway // not recorded///0007399 // nervou
NM_013638		0.025						1.02	1.02	-1.20	-1.05	<i>Ptm3</i>	protamine 3	0007275 // multicellular organismal development // inferred from electronic annotation/
NM_00131	0.0364							-1.01	1.22	-1.20	-1.16	<i>Irf8</i>	interferon regulatory factor 8	0006351 // transcription, DNA-templated // inferred from electronic annotation///00063
NM_001286015	///				0.033			1.04	-1.10	-1.20	-1.03	<i>Csn1s1</i>	casein alpha s1	0006810 // transport // inferred from electronic annotation
NM_001170638	///				0.017			1.10	-1.02	-1.20	-1.02	<i>Slc17a1</i>	solute carrier family 17 (sodium phosphate), member 1	0006810 // transport // inferred from electronic annotation///0006811 // ion transport /
NM_029901		0.025						1.01	-1.05	-1.20	-1.13	<i>Akr1c21</i>	aldo-keto reductase family 1, member C21	0006629 // lipid metabolic process // inferred from electronic annotation///0006694 // s
NM_148940	///XM				0.019	0.016		-1.03	-1.08	-1.20	-1.18	<i>Prss44</i>	protease, serine 44	0006508 // proteolysis // inferred from electronic annotation///0007281 // germ cell dev
NM_0137	0.0242	0.005						1.08	-1.17	-1.20	-1.04	<i>Slco1a1</i>	solute carrier organic anion transporter family, member 1a1	0006810 // transport // inferred from electronic annotation///0006811 // ion transport /
NM_0010	0.0498							-1.20	-1.47	-1.20	-1.10	<i>Hspa2</i>	heat shock protein 2	0001934 // positive regulation of protein phosphorylation // inferred from mutant phen
NM_0097	0.0019							1.09	-1.32	-1.20	1.06	<i>Bnip3</i>	BCL2/adenovirus E1B interacting protein 3	0001666 // response to hypoxia // not recorded///0006915 // apoptotic process // not r
NM_008993	///XM				0.032			-1.06	-1.12	-1.20	-1.15	<i>Pxmp2</i>	peroxisomal membrane protein 2	
NM_145077		0.011				0.019		1.10	-1.04	-1.20	-1.21	<i>Ucn2</i>	urocortin 2	0006171 // cAMP biosynthetic process // inferred from sequence or structural similarity,/
NM_009396	///XM				0.005			1.03	1.09	-1.20	1.02	<i>Tnfaip2</i>	tumor necrosis factor, alpha-induced protein 2	0001525 // angiogenesis // inferred from electronic annotation///0006887 // exocytosis,
NM_139197	///XM				0.032			1.03	1.00	-1.20	-1.14	<i>Gbgt1</i>	glucosyltransferase 1, 3-N-acetylgalactosaminyltransferase 1	0005975 // carbohydrate metabolic process // inferred from electronic annotation///000
NM_010781	///XM				0.008	0.015		1.05	1.02	-1.20	-1.17	<i>Tpsb2</i>	trypsin beta 2	0006508 // proteolysis // inferred from electronic annotation///0006954 // inflammatory
NM_019485		0.045						1.05	-1.10	-1.19	-1.08	<i>Olfir70</i>	olfactory receptor 70	0007165 // signal transduction // inferred from electronic annotation///0007186 // G-pr
NM_0134	#####	0.01						1.04	-1.20	-1.19	1.03	<i>C2</i>	complement component 2 (within H-2S)	0002376 // immune system process // inferred from electronic annotation///0006508 //
NM_023617	///XM				0.002			1.11	1.04	-1.19	1.23	<i>Aox3</i>	aldehyde oxidase 3	0005114 // oxidation-reduction process // inferred from electronic annotation
NM_008780	///XM				0.04			-1.01	-1.05	-1.19	-1.11	<i>Pax1</i>	paired box 1	0001501 // skeletal system development // inferred from genetic interaction///0001501,
NM_025777		0.017						1.03	1.00	-1.19	-1.13	<i>Duoxa2</i>	dual oxidase maturation factor 2	0006810 // transport // inferred from electronic annotation///0015031 // protein transp
NM_1461	0.0226							-1.20	1.07	-1.19	-1.02	<i>Gimap7</i>	GTPase, IMAP family member 7	0008152 // metabolic process // inferred from electronic annotation
NM_145827	///XM				0.021			1.01	1.01	-1.19	-1.04	<i>Nlrp3</i>	NLR family, pyrin domain containing 3	0002376 // immune system process // inferred from electronic annotation///0002674 //
NM_010951	///XM				0.004			1.00	-1.11	-1.19	-1.09	<i>Gpr143</i>	G protein-coupled receptor 143	0007165 // signal transduction // inferred from electronic annotation///0007186 // G-pr
NM_032465		0.045						1.04	-1.00	-1.19	-1.15	<i>Cd96</i>	CD96 antigen	0007155 // cell adhesion // inferred from electronic annotation
NM_001310464	///				0.033			1.12	-1.12	-1.19	1.01	<i>Reln</i>	reelin	0000904 // cell morphogenesis involved in differentiation // inferred from mutant pheno
NM_145229		0.011						-1.01	1.01	-1.19	-1.16	<i>AY074887</i>	cDNA sequence AY074887	0007050 // cell cycle arrest // inferred from direct assay///0008285 // negative regulati
NM_053224						0.018		-1.07	-1.14	-1.19	-1.33	<i>Vmn1r54</i>	vomeronal 1 receptor 54	0007165 // signal transduction // inferred from electronic annotation///0007186 // G-pr
NM_0134	0.0425							1.00	-1.14	-1.19	-1.11	<i>Bcl2l10</i>	Bcl2-like 10	0006915 // apoptotic process // inferred from electronic annotation///0008625 // extrin:
NM_001080809	///				0.042			1.00	-1.18	-1.19	-1.15	<i>Cps1</i>	carbamoyl-phosphate synthetase 1	0000050 // urea cycle // not recorded///0000050 // urea cycle // inferred by curator///0
NM_008344		0.026						1.26	1.09	-1.19	-1.07	<i>Igfbp6</i>	insulin-like growth factor binding protein 6	0001558 // regulation of cell growth // inferred from electronic annotation///0043567 //
NM_0083	0.0207							1.26	1.09	-1.19	-1.07	<i>Igfbp6</i>	insulin-like growth factor binding protein 6	0001558 // regulation of cell growth // inferred from electronic annotation///0043567 //
NM_0010	0.0227							-1.10	1.39	-1.19	1.12	<i>Ear-ps2///Ear1///Ear12///Ear2///Ear3</i>	eosinophil-associated, ribonuclease A family, pseudogene 2//eosinophil-associated, r	0006935 // chemotaxis // inferred from direct assay///0008152 // metabolic process // tr
NM_013666	///NM				0.012			-1.00	-1.02	-1.19	-1.13	<i>St8sia5</i>	ST8 alpha-N-acetylneuraminidase alpha-2,8-sialyltransferase 5	0006486 // protein glycosylation // inferred from electronic annotation///0097503 // sial
NM_0082	0.0078							-1.06	1.34	-1.19	-1.18	<i>H2-Oa</i>	histocompatibility 2, O region alpha locus	0002376 // immune system process // inferred from electronic annotation///0002504 //
NM_001160406	///				0.039			-1.04	-1.02	-1.19	-1.12	<i>Gfi1b</i>	growth factor independent 1B	0000122 // negative regulation of transcription from RNA polymerase II promoter // not r
NM_013616		#####						-1.03	1.04	-1.19	-1.27	<i>Olfir65</i>	olfactory receptor 65	0007165 // signal transduction // not recorded///0007186 // G-protein coupled receptor
NM_010468		0.035						1.01	1.06	-1.19	-1.10	<i>Hoxd3</i>	homeobox D3	0006351 // transcription, DNA-templated // not recorded///0006355 // regulation of tra
NM_001282040	///NM_00				0.041			1.08	1.06	-1.18	1.17	<i>Pmm1</i>	phosphomannomutase 1	0006013 // mannose metabolic process // not recorded///0008152 // metabolic process
NM_001163270	///				0.027			1.06	-1.00	-1.18	-1.12	<i>Baiap3</i>	BAI1-associated protein 3	0007186 // G-protein coupled receptor signaling pathway // not recorded
NM_2015	0.0434							-1.07	-1.27	-1.18	1.05	<i>Lmo7</i>	LIM domain only 7	0016337 // single organismal cell-cell adhesion // not recorded///0023051 // regulatio
NM_1530	0.0434							1.04	-1.12	-1.18	-1.10	<i>Hrh4</i>	histamine receptor H4	0006954 // inflammatory response // not recorded///0006954 // inflammatory response
NM_0107	0.0034	0.008						1.10	-1.09	-1.18	-1.10	<i>Lgals4</i>	lectin, galactose binding, soluble 4	
NM_133922	///XM				0.045			1.01	1.06	-1.18	-1.08	<i>Krba1</i>	KRAB-A domain containing 1	
NM_015732	///XM				0.049			1.01	-1.09	-1.18	-1.09	<i>Axin2</i>	axin2	0001756 // somitogenesis // inferred from direct assay///0001934 // positive regulatio
NM_0011	0.0021	0.014				0.009		1.04	-1.33	-1.18	-1.22	<i>Ccl20</i>	chemokine (C-C motif) ligand 20	0002548 // monocyte chemotaxis // --//0006935 // chemotaxis // not recorded///0006
NM_026410						0.037		-1.14	1.05	-1.18	1.04	<i>Cdca5</i>	cell division cycle associated 5	0000082 // G1/S transition of mitotic cell cycle // not recorded///0006302 // double-str
NM_0196	0.0329							-1.01	1.40	-1.18	-1.21	<i>Rrad</i>	Ras-related associated with diabetes	0007165 // signal transduction // inferred from electronic annotation///0007264 // small
NM_001277847	///				0.045			1.09	-1.05	-1.18	-1.10	<i>Treh</i>	trehalase (brush-border membrane glycoprotein)	0005991 // trehalose metabolic process // inferred from electronic annotation///000599
NM_0011	0.0226							-1.01	-1.36	-1.18	-1.02	<i>Vldlr</i>	very low density lipoprotein receptor	0000122 // negative regulation of transcription from RNA polymerase II promoter // infer
NM_001199971	///				0.017			1.04	-1.02	-1.18	-1.11	<i>Tac2</i>	tachykinin 2	0007217 // tachykinin receptor signaling pathway // inferred from electronic annotation/
NM_026680	///NM				0.004			1.03	-1.08	-1.18	-1.02	<i>Golt1a///Kiss1</i>	golgi transport 1 homolog A (S. cerevisiae)///KISS-1 metastasis-suppressor	0006629 // lipid metabolic process // not recorded///0006810 // transport // inferred fr
NM_0013	0.0492	0.034						1.02	-1.11	-1.18	-1.12	<i>Gpr83</i>	G protein-coupled receptor 83	0007165 // signal transduction // inferred from electronic annotation///0007166 // cell s
NM_011680	///XM				0.01	0.022		1.06	1.01	-1.18	-1.10	<i>Usf2</i>	upstream transcription factor 2	0000432 // positive regulation of transcription from RNA polymerase II promoter by gluc
NM_001291065	///				0.022			1.05	1.02	-1.18	-1.08	<i>Foxa2</i>	forkhead box A2	0000432 // positive regulation of transcription from RNA polymerase II promoter by gluc
NM_008571	///XM				0.015			-1.04	-1.03	-1.18	-1.20	<i>Mcpt2</i>	mast cell protease 2	0006508 // proteolysis // inferred from electronic annotation///0016485 // protein proc
NM_011172	///XM				0.027			1.13	1.04	-1.18	-1.05	<i>Prodh</i>	proline dehydrogenase	0006560 // proline metabolic process // inferred from electronic annotation///0006562 /
NM_001168498	///				0.044			1.03	-1.09	-1.18	-1.09	<i>Ncmap</i>	noncompact myelin associated protein	0031643 // positive regulation of myelination // not recorded///0032290 // peripheral ne
NM_0011	0.0321							-1.27	1.01	-1.18	-1.33	<i>Clec4d</i>	C-type lectin domain family 4, member d	0002250 // adaptive immune response // inferred from mutant phenotype///0002292 //
NM_013750		0.039						-1.02	-1.11	-1.18	-1.13	<i>Phlda3</i>	pleckstrin homology-like domain, family A, member 3	0006915 // apoptotic process // inferred from electronic annotation///0042771 // intrin
NM_001001892	///				0.041			-1.07	1.05	-1.18	-1.08	<i>H2-K1///H2-D1</i>	histocompatibility 2, K1, K region///histocompatibility 2, D region locus 1///H-2 class I	0001916 // positive regulation of T cell mediated cytotoxicity // inferred from direct assa
NM_133831		0.046						1.10	1.14	-1.18	-1.20	<i>Gltscr2</i>	glioma tumor suppressor candidate region gene 2	
NM_0169	0.0032							-1.06	1.30	-1.18	-1.24	<i>Ptprcap</i>	protein tyrosine phosphatase, receptor type, C polypeptide-associated protein	0006468 // protein phosphorylation // inferred from direct assay///0006468 // protein p

RefSeq	Tri	p 24h	p 48h	p 72h	FD Air	FD 24h	FD 48h	FD 72h	Gene Symbol	Gene Title	Gene Ontology Biological Process
NM_153097		0.033			1.06	-1.10	-1.18	-1.08	<i>Trim60</i>	tripartite motif-containing 60	
NM_0540	0.0317				-1.02	-1.18	-1.18	-1.07	<i>Pnpla3</i>	patatin-like phospholipase domain containing 3	0006629 // lipid metabolic process // inferred from electronic annotation///0008152 // n
NM_001031622	///NM_00	0.047			1.00	-1.05	-1.18	-1.20	<i>Gm16367</i> ///Gm16427///Gm16513///Gm3	predicted gene 16367///predicted gene 16427///predicted gene, Gm16513///predicte	0008284 // positive regulation of cell proliferation // inferred from electronic annotation/
NM_0099	0.0187				-1.16	-1.04	-1.18	-1.19	<i>Cst7</i>	cystatin F (leukocystatin)	0010466 // negative regulation of peptidase activity // inferred from electronic annotatio
NM_0103	#####		0.02		-1.31	1.01	-1.18	-1.16	<i>H2-Q10</i>	histocompatibility 2, Q region locus 10	0002376 // immune system process // inferred from electronic annotation///0002474 //
NM_019540		0.027			1.01	-1.12	-1.18	-1.10	<i>Pfpl</i>	pore forming protein-like	
NM_153789		0.017			1.22	1.30	-1.18	1.07	<i>Mylip</i>	myosin regulatory light chain interacting protein	0006928 // movement of cell or subcellular component // not recorded///0007399 // nei
NM_009800	///XM	0.044			-1.02	-1.09	-1.18	-1.10	<i>Car11</i>	carbonic anhydrase 11	
NM_001077696	///	0.047			1.09	1.15	-1.18	1.13	<i>Hdac5</i>	histone deacetylase 5	0000122 // negative regulation of transcription from RNA polymerase II promoter // infer
NM_001190357	///	0.034			1.04	-1.02	-1.17	-1.12	<i>Carkd</i>	carbohydrate kinase domain containing	0008152 // metabolic process // inferred from electronic annotation
NM_0205	0.0418				1.14	-1.04	-1.17	1.05	<i>Slc25a20</i>	solute carrier family 25 (mitochondrial carnitine/acylcarnitine translocase), member 20	0006810 // transport // inferred from electronic annotation
NM_021287	///XM	0.049			1.04	-1.08	-1.17	-1.09	<i>Sptbn2</i>	spectrin beta, non-erythrocytic 2	0007416 // synapse assembly // inferred from mutant phenotype///0016079 // synaptic
NM_130903	///XM	0.047			-1.03	-1.05	-1.17	-1.16	<i>Cd209c</i>	CD209c antigen	
NM_001252565	///	0.009			1.02	-1.02	-1.17	-1.14	<i>Oprl1</i>	opioid receptor-like 1	0001934 // positive regulation of protein phosphorylation // not recorded///0007165 // :
NM_0118	0.0355	0.026			1.05	-1.01	-1.17	-1.08	<i>3-Sep</i>	septin 3	0007049 // cell cycle // inferred from electronic annotation///0051301 // cell division // i
NM_0254	0.0063				1.03	-1.65	-1.17	-1.05	<i>Rgcc</i>	regulator of cell cycle	0000082 // G1/S transition of mitotic cell cycle // not recorded///0001100 // negative reg
NM_018795	///XM	0.019	0.01		1.09	1.02	-1.17	-1.20	<i>Abcc6</i>	ATP-binding cassette, sub-family C (CFTR/MRP), member 6	0006810 // transport // inferred from electronic annotation///0008152 // metabolic pro
NM_0083	0.0035	0.001			1.10	-1.14	-1.17	-1.08	<i>Htr2b</i>	5-hydroxytryptamine (serotonin) receptor 2B	0001755 // neural crest cell migration // inferred from mutant phenotype///0001819 // t
NM_139299	///XM	0.0651	0.001		-1.02	-1.07	-1.17	-1.29	<i>Il31ra</i>	interleukin 31 receptor A	0002067 // glandular epithelial cell differentiation // inferred from mutant phenotype///
NM_0011	0.0369				-1.00	1.18	-1.17	1.07	<i>Pparg</i>	peroxisome proliferator activated receptor gamma	0000122 // negative regulation of transcription from RNA polymerase II promoter // infer
NM_010630	///XM	0.038			1.04	-1.01	-1.17	-1.00	<i>Kifc2</i>	kinesin family member C2	0007018 // microtubule-based movement // not recorded///0008152 // metabolic proce
NM_0074	0.0479		0.029		1.02	-1.12	-1.17	-1.17	<i>Aqp7</i>	aquaporin 7	0006810 // transport // inferred from electronic annotation///0006833 // water transpo
NM_027983			0.002		-1.03	-1.01	-1.17	-1.29	<i>Krt33a</i>	keratin 33A	
NM_0079	0.0212				1.05	-1.27	-1.17	1.12	<i>Ereg</i>	epiregulin	0000187 // activation of MAPK activity // not recorded///0001525 // angiogenesis // infe
NM_0013	0.0348				1.02	-1.15	-1.17	1.20	<i>Adamts14</i>	ADAMTS-like 4	0006508 // proteolysis // inferred from electronic annotation///0006915 // apoptotic pro
NM_008340	///XM	0.028			-1.00	-1.03	-1.17	-1.14	<i>Igfals</i>	insulin-like growth factor binding protein, acid labile subunit	0007155 // cell adhesion // inferred from electronic annotation
NM_007699	///XM	0.0649	0.046		-1.00	-1.04	-1.17	-1.19	<i>Chrm4</i>	cholinergic receptor, muscarinic 4	0007165 // signal transduction // inferred from electronic annotation///0007186 // G-pr
NM_001167691	///	0.04			1.03	-1.03	-1.17	-1.09	<i>Sirt4</i>	sirtuin 4	0000820 // regulation of glutamine family amino acid metabolic process // inferred fr
NM_001310639	///	0.011			1.09	1.28	-1.17	-1.10	<i>Stap1</i>	signal transducing adaptor family member 1	0007169 // transmembrane receptor protein tyrosine kinase signaling pathway // infere
NM_010670			0.043		1.02	1.02	-1.17	-1.05	<i>Krtap12-1</i>	keratin associated protein 12-1	
NM_011741	///XM	0.001			-1.01	-1.05	-1.17	-1.12	<i>Zan</i>	zonadhesin	0007155 // cell adhesion // inferred from electronic annotation///0007339 // binding of :
NM_0092	0.0358				1.10	-1.08	-1.17	-1.17	<i>Sts</i>	steroid sulfatase	0006629 // lipid metabolic process // inferred from electronic annotation///0007565 // f
NM_0082	0.0012				1.09	1.65	-1.17	-1.01	<i>Hhex</i>	hematopoietically expressed homeobox	0000122 // negative regulation of transcription from RNA polymerase II promoter // infer
NM_025987		0.035			1.05	1.01	-1.17	-1.09	<i>Ndufa6</i>	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 6 (B14)	0006810 // transport // inferred from electronic annotation///0006979 // response to ox
NM_1460	0.0166				1.05	-1.21	-1.17	-1.01	<i>Sec14l4</i>	SEC14-like lipid binding 4	0006810 // transport // inferred from electronic annotation
NM_0103	0.0415				1.06	-1.07	-1.17	1.18	<i>Grb7</i>	growth factor receptor bound protein 7	0007165 // signal transduction // traceable author statement///0009967 // positive regu
NM_016863	///XM	0.011			1.09	1.02	-1.17	-1.15	<i>Fkbp1b</i>	FK506 binding protein 1b	0000413 // protein peptidyl-prolyl isomerization // not recorded///0002027 // regulatio
NM_001039530	///	0.038			1.07	1.04	-1.17	1.13	<i>Parp14</i>	poly (ADP-ribose) polymerase family, member 14	0006351 // transcription, DNA-templated // inferred from electronic annotation///00063
NM_0098	0.0413	0.014			1.02	-1.12	-1.17	-1.16	<i>Entpd2</i>	ectonucleoside triphosphate diphosphohydrolase 2	0007186 // G-protein coupled receptor signaling pathway // inferred from direct assay///
NM_053122		0.02			1.08	-1.01	-1.17	-1.09	<i>Immp2l</i>	IMP2 inner mitochondrial membrane peptidase-like (S. cerevisiae)	0001541 // ovarian follicle development // inferred from mutant phenotype///0006465 /
NM_033037	///XR	0.033			1.11	-1.00	-1.17	-1.04	<i>Cdo1</i>	cysteine dioxygenase 1, cytosolic	0007595 // lactation // not recorded///0010243 // response to organonitrogen compou
NM_001002927	///	0.042			1.07	-1.06	-1.17	-1.06	<i>Penk</i>	preproenkephalin	0001662 // behavioral fear response // inferred from mutant phenotype///0001964 // st
NM_013491	///XM	0.05			1.06	-1.02	-1.17	-1.06	<i>Clcn1</i>	chloride channel, voltage-sensitive 1	0006810 // transport // inferred from electronic annotation///0006811 // ion transport /
		0.0035			-1.07	1.24	-1.17	-1.22	<i>Igkv3-12</i> ///Igkv3-7	immunoglobulin kappa variable 3-12///immunoglobulin kappa variable 3-7	0006898 // receptor-mediated endocytosis // ---///0006910 // phagocytosis, recognition
NM_0097	0.0197	0.004			1.10	-1.15	-1.17	1.05	<i>Chic1</i>	cysteine-rich hydrophobic domain 1	0006810 // transport // not recorded
NM_001252662	///	0.042			1.04	1.06	-1.17	-1.02	<i>Dmtn</i>	dematin actin binding protein	0006461 // protein complex assembly // inferred from direct assay///0006461 // protein
NM_145377	///XM	0.01			1.04	-1.06	-1.17	-1.03	<i>Trim41</i>	tripartite motif-containing 41	0016567 // protein ubiquitination // inferred from electronic annotation
NM_133191	///XM	0.037			1.03	-1.00	-1.17	1.12	<i>Eps8l2</i>	EPS8-like 2	0007266 // Rho protein signal transduction // not recorded///0016601 // Rac protein sig
NM_001310680	///	0.009			1.01	-1.02	-1.17	-1.01	<i>Scg2</i>	secretogranin II	0000165 // MAPK cascade // not recorded///0000165 // MAPK cascade // inferred from :
NM_001199123	///	0.017			-1.00	-1.11	-1.16	-1.13	<i>Spc25</i>	SPC25, NDC80 kinetochore complex component, homolog (S. cerevisiae)	0007049 // cell cycle // inferred from electronic annotation///0007052 // mitotic spindle
NM_0273	0.0471				1.02	-1.24	-1.16	-1.08	<i>lyd</i>	iodotyrosine deiodinase	0055114 // oxidation-reduction process // inferred from electronic annotation
NM_001122949	///	0.01			1.02	-1.03	-1.16	-1.09	<i>Mpl</i>	myeloproliferative leukemia virus oncogene	0010628 // positive regulation of gene expression // inferred from mutant phenotype///
NM_008824	///XM	0.034			1.04	-1.04	-1.16	-1.04	<i>Pfkfb1</i>	6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase 1	0006000 // fructose metabolic process // inferred from electronic annotation///0006003
NM_1768	0.026				-1.02	-1.22	-1.16	1.07	<i>Osbpl11</i>	oxysterol binding protein-like 11	0006810 // transport // inferred from electronic annotation///0006869 // lipid transport
NM_0012	0.0073				-1.14	-1.44	-1.16	-1.16	<i>Stf1</i>	suppression of tumorigenicity 7-like	0030198 // extracellular matrix organization // non-traceable author statement///003030
NM_1531	0.0392				-1.01	-1.30	-1.16	1.20	<i>Abca8a</i>	ATP-binding cassette, sub-family A (ABC1), member 8a	0006810 // transport // inferred from electronic annotation///0006869 // lipid transport
NM_0269	0.0417	0.007	0.023		1.07	-1.06	-1.16	-1.14	<i>Zg16</i>	zymogran granule protein 16	0006810 // transport // inferred from electronic annotation///0015031 // protein transp
NM_031172	///XM	0.037			1.03	1.02	-1.16	-1.12	<i>Trim17</i> ///Hist3h2a	tripartite motif-containing 17///histone cluster 3, H2a	0006914 // autophagy // not recorded///0016567 // protein ubiquitination // inferred fr
NM_0012	0.0111				-1.11	1.01	-1.16	-1.18	<i>Dmc1</i>	DMC1 dosage suppressor of mck1 homolog, meiosis-specific homologous recombination	0000730 // DNA recombinase assembly // not recorded///0001541 // ovarian follicle dev
NM_008154		0.028			1.04	-1.04	-1.16	-1.12	<i>Gpr3</i>	G-protein coupled receptor 3	0007165 // signal transduction // inferred from electronic annotation///0007186 // G-pr
NM_0011	0.0016	#####			1.06	-1.09	-1.16	-1.06	<i>Kif17</i>	kinesin family member 17	0006810 // transport // inferred from electronic annotation///0007017 // microtubule-b
NM_021409		0.004			1.13	1.06	-1.16	1.11	<i>Pard6b</i>	par-6 family cell polarity regulator beta	0006461 // protein complex assembly // not recorded///0007049 // cell cycle // inferred
NM_025347	///NM	0.008			1.14	1.16	-1.16	-1.07	<i>Ypel3</i>	yippee-like 3 (Drosophila)	0006915 // apoptotic process // inferred from electronic annotation///2000774 // positi
NM_0010	0.0369				1.06	-1.12	-1.16	-1.02	<i>Rusc2</i>	RUN and SH3 domain containing 2	

RefSeq	Tri	p 24h	p 48h	p 72h	FD Air	FD 24h	FD 48h	FD 72h	Gene Symbol	Gene Title	Gene Ontology Biological Process
NM_026419	///XM	0.042			-1.01	-1.08	-1.16	-1.17	<b>Cela3b</b>	chymotrypsin-like elastase family, member 3B	0006508 // proteolysis // not recorded///0008203 // cholesterol metabolic process // no
NM_001290561	///	0.004	0.005		1.02	-1.06	-1.16	-1.19	<b>Plp1</b>	proteolipid protein (myelin) 1	0006954 // inflammatory response // inferred from genetic interaction///0007229 // inte
NM_001290680	///	0.045	0.005		1.09	1.08	-1.16	-1.11	<b>Nsg2</b>	neuron specific gene family member 2	0007212 // dopamine receptor signaling pathway // inferred from electronic annotation//
XM_9773f	0.0345				-1.04	1.32	-1.16	-1.17	<b>Tcrb-J//LOC665506//Trbc1//Trbc2</b>	T cell receptor beta, joining region//T-cell receptor beta-2 chain C region-like//T cell receptor beta, constant region 1//T cell receptor beta, constant 2	
NM_026818		0.03	0.035		1.12	-1.05	-1.16	-1.14	<b>Clp2</b>	cartilage intermediate layer protein 2	
NM_0194	0.0164				1.03	-1.17	-1.16	1.03	<b>Hgfac</b>	hepatocyte growth factor activator	0006508 // proteolysis // inferred from electronic annotation
NM_1733f	0.0086				-1.11	1.05	-1.16	-1.17	<b>Xkr6</b>	X Kell blood group precursor related family member 6 homolog	
NM_0218	0.0077		0.025		-1.06	-1.44	-1.16	1.09	<b>Tmod1</b>	tropomodulin 1	0006936 // muscle contraction // inferred from mutant phenotype///0007015 // actin fil.
NM_001165934	///	0.039			-1.02	-1.13	-1.16	-1.12	<b>Rgs9</b>	regulator of G-protein signaling 9	0007186 // G-protein coupled receptor signaling pathway // traceable author statement//
NM_0080	0.0074				1.11	-1.53	-1.16	1.39	<b>Fmo3</b>	flavin containing monooxygenase 3	0017144 // drug metabolic process // not recorded///0055114 // oxidation-reduction prc
NM_0011	0.011				1.01	-1.22	-1.16	-1.08	<b>Smyd1</b>	SET and MYND domain containing 1	0006338 // chromatin remodeling // inferred from physical interaction///0006351 // trar
NM_0134	0.0496				-1.15	1.12	-1.16	-1.23	<b>Cd3d</b>	CD3 antigen, delta polypeptide	0006461 // protein complex assembly // non-traceable author statement///0007166 // c
NM_0100	0.0421				1.03	-1.30	-1.15	-1.08	<b>Cyp2b9</b>	cytochrome P450, family 2, subfamily b, polypeptide 9	0006805 // xenobiotic metabolic process // not recorded///0019373 // epoxygenase P45
NM_0292	0.0127				1.01	-1.14	-1.15	-1.13	<b>Spp2</b>	secreted phosphoprotein 2	0006461 // protein complex assembly // not recorded///0046849 // bone remodeling // i
NM_1454	0.0146	0.005	0.025		1.08	-1.06	-1.15	-1.07	<b>Csdc2</b>	cold shock domain containing C2, RNA binding	0006355 // regulation of transcription, DNA-templated // inferred from electronic annota
NM_0166	0.0148	0.021			1.18	-1.26	-1.15	1.07	<b>Reck</b>	reversion-inducing-cysteine-rich protein with kazal motifs	0001955 // blood vessel maturation // inferred from genetic interaction///0001955 // blk
XR_105122	///XR_107916		0.006		1.02	-1.02	-1.15	-1.22	<b>Gm9885</b>	predicted gene 9885	
NM_0214	0.0035				1.02	-1.09	-1.15	-1.11	<b>Mlxipl</b>	MLX interacting protein-like	0000122 // negative regulation of transcription from RNA polymerase II promoter // infer
NM_021879	///XM	0.011			1.08	-1.02	-1.15	-1.09	<b>Oca2</b>	oculocutaneous albinism II	0006810 // transport // inferred from electronic annotation///0007286 // spermatid dev
NM_0167	0.0155	0.01			1.07	-1.18	-1.15	-1.01	<b>Pgrmc1</b>	progesterone receptor membrane component 1	0007411 // axon guidance // inferred from electronic annotation
NM_0277f	0.0212				-1.00	-1.26	-1.15	1.10	<b>Nipbl</b>	Nipped-B homolog (Drosophila)	0000122 // negative regulation of transcription from RNA polymerase II promoter // not i
NM_001163486	///	0.034			1.00	-1.04	-1.15	-1.19	<b>Hsd17b13</b>	hydroxysteroid (17-beta) dehydrogenase 13	0008152 // metabolic process // inferred from electronic annotation///0046889 // posit
XR_871929	///XR_871929	0.013			1.07	-1.03	-1.15	1.04	<b>Igf1os</b>	insulin-like growth factor 1, opposite strand	
NM_016695f	///XM	0.015	0.022		1.07	1.02	-1.15	-1.13	<b>Mpp2</b>	membrane protein, palmitoylated 2 (MAGUK p55 subfamily member 2)	
NM_008212	0.045				1.06	1.04	-1.15	1.14	<b>Hadh</b>	hydroxyacyl-Coenzyme A dehydrogenase	0006629 // lipid metabolic process // inferred from electronic annotation///0006631 // f.
NM_001010941	///	0.047	0.027		1.01	-1.02	-1.15	-1.15	<b>Gpr12</b>	G-protein coupled receptor 12	0006874 // cellular calcium ion homeostasis // inferred from direct assay///0007165 // si
NR_02826	0.0457				1.02	-1.33	-1.15	-1.22	<b>Dleu2</b>	deleted in lymphocytic leukemia, 2	0010977 // negative regulation of neuron projection development // inferred from geneti
NM_027918f	///XM_006511	0.039			1.00	1.07	-1.15	-1.19	<b>1300017J02Rik</b>	RIKEN cDNA 1300017J02 gene	0043086 // negative regulation of catalytic activity // inferred from electronic annotation
NM_0076	0.0063				1.00	-1.30	-1.15	-1.14	<b>Serpina6</b>	serine (or cysteine) peptidase inhibitor, clade A, member 6	0006810 // transport // inferred from electronic annotation///0008211 // glucocorticoid
NM_011455f	///NM	0.043			1.05	-1.02	-1.15	-1.01	<b>Serpina9e//Serpina9f//Serpina9g</b>	predicted gene 11397//serine (or cysteine) peptidase inhibitor, clade B, member 9e//	0002244 // hematopoietic progenitor cell differentiation // inferred from mutant phenot
NM_182805	0.03				1.14	1.02	-1.15	1.02	<b>Gpt</b>	glutamic pyruvic transaminase, soluble	0009058 // biosynthetic process // inferred from electronic annotation///0042853 // L-al
NM_0100f	0.0297	0.016			1.07	-1.09	-1.15	-1.04	<b>Cyp2c38</b>	cytochrome P450, family 2, subfamily c, polypeptide 38	0006805 // xenobiotic metabolic process // not recorded///0019373 // epoxygenase P45
NM_001128605f	///	0.04			-1.04	-1.00	-1.15	-1.03	<b>Psen2</b>	presenilin 2	0000122 // negative regulation of transcription from RNA polymerase II promoter // infer
NM_001037098f	///NM_02f	0.003			-1.05	-1.20	-1.15	1.11	<b>Nacc2</b>	nucleus accumbens associated 2, BEN and BTB (POZ) domain containing	0008285 // negative regulation of cell proliferation // not recorded///0010608 // posttra
NM_027790f	///XM	0.014			1.05	-1.01	-1.15	-1.12	<b>Dhrs2</b>	dehydrogenase/reductase member 2	0008152 // metabolic process // inferred from electronic annotation///0009636 // respo
NM_0307	0.0419				-1.12	1.02	-1.15	-1.19	<b>Cxcr6</b>	chemokine (C-X-C motif) receptor 6	0006935 // chemotaxis // inferred from electronic annotation///0006954 // inflammator
NM_0112	0.0458	0.024			1.03	-1.09	-1.15	-1.12	<b>Pvt1</b>	plasmacytoma variant translocation 1	
NM_001110337f	///	0.011			1.06	-1.10	-1.15	1.01	<b>Gprc5c</b>	G protein-coupled receptor, family C, group 5, member C	0007165 // signal transduction // inferred from electronic annotation///0007186 // G-pr
NM_0012	0.014	0.012	0.035		1.01	-1.08	-1.15	-1.17	<b>Kcnma1</b>	potassium large conductance calcium-activated channel, subfamily M, alpha member	0001666 // response to hypoxia // inferred from direct assay///0001666 // response to h
NM_0012	0.0263	0.043			1.10	-1.08	-1.15	1.02	<b>Ttc28</b>	tetratricopeptide repeat domain 28	0007049 // cell cycle // inferred from electronic annotation///0007067 // mitotic nuclear
NM_013697		0.033			-1.32	-1.05	-1.15	-1.08	<b>Ttr</b>	transthyretin	0006810 // transport // inferred from electronic annotation///0042572 // retinol metab
NM_009766f	///XM	0.038			1.06	-1.01	-1.15	-1.08	<b>Brs3</b>	bombesin-like receptor 3	0007165 // signal transduction // inferred from electronic annotation///0007186 // G-pr
		0.018	0.019		-1.00	-1.04	-1.15	-1.28	<b>Gm8479</b>	thiopurine S-methyltransferase pseudogene	
NM_019510f	///XM	0.016			1.09	1.09	-1.15	1.01	<b>Trpc3</b>	transient receptor potential cation channel, subfamily C, member 3	0006810 // transport // inferred from electronic annotation///0006811 // ion transport /
NM_001083929f	///NM_00f	0.02			-1.08	-1.12	-1.15	1.15	<b>Gpx3</b>	glutathione peroxidase 3	0006749 // glutathione metabolic process // not recorded///0006979 // response to oxid
NM_001286396f	///	0.01			1.05	1.12	-1.15	-1.08	<b>Dao</b>	D-amino acid oxidase	0006551 // leucine metabolic process // inferred from mutant phenotype///0006562 // c
NM_1784	0.0157				-1.05	1.35	-1.15	-1.19	<b>Myo1g</b>	myosin IG	0002376 // adaptive immune response // inferred from electronic annotation///0002376
NM_1707	0.0381				-1.02	1.28	-1.14	1.01	<b>Cd300a</b>	CD300A antigen	0002376 // immune system process // inferred from electronic annotation///0002552 //
NM_0212	0.0283				1.02	-1.15	-1.14	-1.18	<b>Wnt1</b>	wingless-type MMTV integration site family, member 1	0000578 // embryonic axis specification // inferred from mutant phenotype///0001658 //
NM_080729f	///XM_006511f	0.036			-1.15	-1.01	-1.14	-1.02	<b>Il25</b>	interleukin 25	0002437 // inflammatory response to antigenic stimulus // not recorded///0006954 // in
NM_0271	0.0093	0.041			1.07	-1.12	-1.14	1.15	<b>Arhgef12</b>	Rho guanine nucleotide exchange factor (GEF) 12	0007186 // G-protein coupled receptor signaling pathway // not recorded///0035023 // r
NM_001142732f	///	0.005			1.11	-1.03	-1.14	-1.07	<b>Ttl3</b>	tubulin tyrosine ligase-like family, member 3	0006464 // cellular protein modification process // inferred from electronic annotation//
NM_0085	0.0393				1.15	1.88	-1.14	-1.46	<b>Ltb</b>	lymphotoxin B	0006955 // immune response // inferred from electronic annotation///0010467 // gene e
NM_028621	0.008				-1.00	-1.06	-1.14	-1.02	<b>Krtap21-1</b>	keratin associated protein 21-1	0001942 // hair follicle development // inferred from mutant phenotype///0007165 // si
NM_053227f	///XM	0.021	0.031		-1.01	-1.11	-1.14	-1.14	<b>Vmn1r44</b>	vomeronal 1 receptor 44	0007165 // signal transduction // inferred from electronic annotation///0007186 // G-pr
NM_0108	0.0276		0.044		-1.17	1.00	-1.14	-1.09	<b>Myoc</b>	myocilin	0001649 // osteoblast differentiation // inferred from direct assay///0001649 // osteobla
NM_0276	0.0176				1.06	-1.13	-1.14	-1.08	<b>Speer3</b>	spermatogenesis associated glutamate (E)-rich protein 3	
NM_020277f	///XM	0.037			1.03	-1.03	-1.14	-1.20	<b>Trpm5</b>	transient receptor potential cation channel, subfamily M, member 5	0006810 // transport // inferred from electronic annotation///0006811 // ion transport /
NM_053221	0.032	0.041			1.15	-1.03	-1.14	-1.10	<b>Vmn1r42</b>	vomeronal 1 receptor 42	0007165 // signal transduction // inferred from electronic annotation///0007186 // G-pr
NM_001111015f	///	0.008	0.007		1.07	-1.04	-1.14	-1.13	<b>Syn2</b>	synapsin II	0007269 // neurotransmitter secretion // inferred from genetic interaction///0007269 //
NM_0013f	0.0289				-1.17	1.05	-1.14	-1.16	<b>Ggt1</b>	gamma-glutamyltransferase 1	0002682 // regulation of immune system process // inferred from mutant phenotype//0
NM_023907	0.017				1.06	-1.07	-1.14	-1.10	<b>Foxi1</b>	forkhead box I1	0006351 // transcription, DNA-templated // inferred from electronic annotation///00063
NM_0096f	0.0345				-1.12	1.08	-1.14	-1.13	<b>Apob</b>	apolipoprotein B	0001701 // in utero embryonic development // inferred from mutant phenotype///0006f
NM_001007570	0.012				1.03	1.03	-1.14	-1.07	<b>Slc25a42</b>	solute carrier family 25, member 42	0006810 // transport // inferred from electronic annotation///0008152 // metabolic pro

RefSeq	Tri	p 24h	p 48h	p 72h	FD Air	FD 24h	FD 48h	FD 72h	Gene Symbol	Gene Title	Gene Ontology Biological Process
NM_027220		0.022			1.04	-1.05	-1.14	-1.12	<i>Prss32</i>	protease, serine 32	0006508 // proteolysis // inferred by curator
NM_008814		0.034			1.00	-1.08	-1.14	-1.15	<i>Pdx1</i>	pancreatic and duodenal homeobox 1	0000122 // negative regulation of transcription from RNA polymerase II promoter // infer
NM_175309		0.016			1.20	1.05	-1.14	1.18	<i>Upk3b</i>	uroplakin 3B	0010629 // negative regulation of gene expression // not recorded//0046325 // negativ
NM_001313956//		0.038			1.01	-1.05	-1.14	-1.04	<i>Krt14//Krt17</i>	keratin 14//keratin 17	0002009 // morphogenesis of an epithelium // inferred from genetic interaction//00071
NM_001037930//		0.013			1.01	-1.04	-1.14	-1.10	<i>Gm6787</i>	proteasome (prosome, macropain) subunit, beta type 7 pseudogene	
NM_0012		0.0222		0.005	1.13	-1.20	-1.14	1.03	<i>Polr3gl</i>	polymerase (RNA) III (DNA directed) polypeptide G like	0006359 // regulation of transcription from RNA polymerase III promoter // inferred from
NM_008936			0.03		1.04	-1.17	-1.14	-1.15	<i>Prop1</i>	paired like homeodomain factor 1	0000122 // negative regulation of transcription from RNA polymerase II promoter // infer
NM_0136		0.0183			-1.05	1.11	-1.14	-1.12	<i>Irf4</i>	interferon regulatory factor 4	0006351 // transcription, DNA-templated // inferred from electronic annotation//00063
NM_007771//XM_01124:			0.02		-1.45	-1.22	-1.14	1.00	<i>Cry1</i>	cryptochrome 1 (photolyase-like)	0000122 // negative regulation of transcription from RNA polymerase II promoter // infer
NM_0197		0.0163		0.009	1.10	-1.18	-1.14	-1.16	<i>Tmeff2</i>	transmembrane protein with EGF-like and two follistatin-like domains 2	
NM_0010	#####				-1.02	-1.24	-1.14	-1.10	<i>Limch1</i>	LIM and calponin homology domains 1	0031032 // actomyosin structure organization // inferred from electronic annotation
NM_0214		0.0107		0.044	1.10	-1.07	-1.14	1.01	<i>Mknk2</i>	MAP kinase-interacting serine/threonine kinase 2	0006417 // regulation of translation // inferred from electronic annotation//0006468 //
NM_009937//NM		0.027		0.022	1.07	-1.04	-1.14	-1.15	<i>Colq//Hacl1//LOC102639719</i>	collagen-like tail subunit (single strand of homotrimer) of asymmetric acetylcholinesterase	0001561 // fatty acid alpha-oxidation // not recorded//0006629 // lipid metabolic proce
NM_026335				0.005	1.04	-1.03	-1.14	-1.12	<i>Lce1h</i>	late cornified envelope 1H	0008544 // epidermis development // inferred from electronic annotation//0018149 //
NM_0540		0.0162			1.14	-1.16	-1.14	-1.04	<i>Psg28</i>	pregnancy-specific glycoprotein 28	0007565 // female pregnancy // inferred from electronic annotation
NM_015730//XM		0.014			1.00	1.00	-1.14	-1.14	<i>Chrna4</i>	cholinergic receptor, nicotinic, alpha polypeptide 4	0001508 // action potential // inferred from mutant phenotype//0001666 // response to
NM_176987//XM		0.029			1.07	1.05	-1.14	-1.07	<i>Simc1</i>	SUMO-interacting motifs containing 1	
NM_009510		0.017			1.06	-1.01	-1.14	1.03	<i>Ezr</i>	euzrin	0000122 // negative regulation of transcription from RNA polymerase II promoter // not r
NM_0107		0.0479			-1.07	1.01	-1.14	-1.10	<i>Mcpt4</i>	mast cell protease 4	0002002 // regulation of angiotensin levels in blood // inferred from genetic interaction//
NM_001291280//NM_02:			0.012		1.01	-1.01	-1.13	-1.15	<i>Nmb</i>	neuromedin B	0007204 // positive regulation of cytosolic calcium ion concentration // not recorded//0
NM_0213		0.0147		0.042	1.09	-1.13	-1.13	-1.02	<i>Pappa</i>	pregnancy-associated plasma protein A	0006508 // proteolysis // inferred from electronic annotation//0030154 // cell differenti
NM_0011		0.0267		0.018	1.05	-1.11	-1.13	1.12	<i>Fmo5</i>	flavin containing monooxygenase 5	0017144 // drug metabolic process // not recorded//0055114 // oxidation-reduction prc
NM_001081025//		0.031			1.09	-1.11	-1.13	-1.01	<i>Maats1</i>	MYCBP-associated, testis expressed 1	
NM_0010		0.0354			1.01	1.24	-1.13	1.14	<i>Hmga1//Hmga1-rs1</i>	high mobility group AT-hook 1//high mobility group AT-hook 1, related sequence 1	0006284 // base-excision repair // not recorded//0006351 // transcription, DNA-templa
NM_0011718//XM		0.007		0.028	1.11	1.04	-1.13	-1.13	<i>Wnt10b</i>	wingless-type MMTV integration site family, member 10B	0000086 // G2/M transition of mitotic cell cycle // inferred from genetic interaction//00
NM_0095		0.0048		0.016	1.07	-1.21	-1.13	1.06	<i>Abcg1</i>	ATP-binding cassette, sub-family G (WHITE), member 1	0006355 // regulation of transcription, DNA-templated // inferred from mutant phenoty
NM_0088		0.0468			-1.02	-1.20	-1.13	1.08	<i>Pkd2</i>	polycystic kidney disease 2	0001658 // branching involved in ureteric bud morphogenesis // inferred from electronic
NM_1530		0.0118		0.029	1.05	-1.11	-1.13	-1.05	<i>Slc18a1</i>	solute carrier family 18 (vesicular monoamine), member 1	0006810 // transport // inferred from electronic annotation//0006836 // neurotransmit
NM_001289468//		0.01			1.04	1.02	-1.13	-1.05	<i>Tcl1</i>	T cell lymphoma breakpoint 1	0010629 // negative regulation of gene expression // inferred from mutant phenotype//
NM_0089		0.0124			1.04	-1.16	-1.13	-1.15	<i>Prop1</i>	paired like homeodomain factor 1	0000122 // negative regulation of transcription from RNA polymerase II promoter // infer
NM_0094		0.0302		0.022	1.11	-1.09	-1.13	-1.14	<i>Trh</i>	thyrotropin releasing hormone	0001666 // response to hypoxia // inferred from electronic annotation//0001692 // hist
NM_008764		0.019			1.05	1.03	-1.13	-1.05	<i>Tnfrsf11b</i>	tumor necrosis factor receptor superfamily, member 11b (osteoprotegerin)	0006915 // apoptotic process // inferred from electronic annotation//0006954 // inflam
NM_008262			0.022		-1.03	1.10	-1.13	-1.24	<i>Onecut1</i>	one cut domain, family member 1	0001889 // liver development // inferred from genetic interaction//0001952 // regulati
NM_0011		0.001		0.028	1.05	-1.09	-1.13	-1.05	<i>Ralbp1</i>	ralA binding protein 1	0006810 // transport // not recorded//0006897 // endocytosis // not recorded//00070
NM_001048139//		0.005		0.033	1.18	1.06	-1.13	-1.05	<i>Bdnf</i>	brain derived neurotrophic factor	0001657 // ureteric bud development // inferred from direct assay//0001662 // behavi
NM_009710//XM		0.045			-1.01	-1.00	-1.13	-1.11	<i>Art1</i>	ADP-ribosyltransferase 1	0006471 // protein ADP-ribosylation // inferred from direct assay
NM_0135		0.0117			1.03	1.31	-1.13	-1.16	<i>Itgb7</i>	integrin beta 7	0003366 // cell-matrix adhesion involved in ameoboidal cell migration // not recorded//0
NM_0010		0.0147			-1.20	1.04	-1.13	-1.13	<i>Dnah1</i>	dynein, axonemal, heavy chain 1	0003341 // cilium movement // inferred from electronic annotation//0003354 // epithe
NM_013803//XM		0.043			1.06	-1.08	-1.13	-1.06	<i>Casr</i>	calcium-sensing receptor	0001503 // ossification // not recorded//0006816 // calcium ion transport // not record
NM_030259		0.047			-1.01	-1.02	-1.13	-1.09	<i>Rilpl2</i>	Rab interacting lysosomal protein-like 2	0003382 // epithelial cell morphogenesis // inferred from mutant phenotype//0006810
NM_0011		0.0026		0.032	1.04	-1.04	-1.13	1.01	<i>Hopx</i>	HOP homeobox	0000122 // negative regulation of transcription from RNA polymerase II promoter // infer
NM_026447//NM		0.024			1.04	1.09	-1.13	-1.08	<i>Ppm1m</i>	protein phosphatase 1M	0006470 // protein dephosphorylation // inferred from direct assay
NM_001110780//		0.029			1.01	-1.11	-1.13	-1.09	<i>Syn1</i>	synapsin I	0007269 // neurotransmitter secretion // inferred from genetic interaction//0007269 //
NM_0118		0.026			1.02	-1.15	-1.13	-1.04	<i>Aadat</i>	aminoadipate aminotransferase	0006103 // 2-oxoglutarate metabolic process // not recorded//0006536 // glutamate m
NM_0010		0.0467			1.09	-1.00	-1.13	1.13	<i>Atxn7f3</i>	ataxin 7-like 3	0006351 // transcription, DNA-templated // inferred from electronic annotation//00063
NM_028176//XM_00653:			0.023		-1.21	-1.04	-1.13	1.03	<i>Cda</i>	cytidine deaminase	0009972 // cytidine deamination // not recorded//0030308 // negative regulation of cel
NM_0107		0.0188			-1.02	1.27	-1.13	-1.09	<i>Lst1</i>	leukocyte specific transcript 1	0000902 // cell morphogenesis // inferred from electronic annotation//0002376 // imm
NM_0013		0.0398			1.01	-1.20	-1.13	-1.14	<i>Slc16a4</i>	solute carrier family 16 (monocarboxylic acid transporters), member 4	0006810 // transport // inferred from electronic annotation//0015718 // monocarboxyl
NM_0136		0.0447			1.14	-1.35	-1.13	-1.02	<i>Mt1</i>	metallothionein 1	0000032 // cell wall mannoprotein biosynthetic process // ---//0006486 // protein glyco
NM_130860//XM		0.037			1.09	1.10	-1.13	-1.08	<i>Cdk9</i>	cyclin-dependent kinase 9 (CDC2-related kinase)	0006281 // DNA repair // inferred from electronic annotation//0006282 // regulation of
NM_001291149//		0.044		0.034	1.07	-1.06	-1.13	-1.14	<i>Ptprt</i>	protein tyrosine phosphatase, receptor type, T	0006470 // protein dephosphorylation // inferred from direct assay//0006470 // protei
NM_1454		0.0191			-1.09	1.06	-1.13	-1.14	<i>Cd300ld</i>	CD300 molecule-like family member d	0002376 // immune system process // inferred from electronic annotation//0032675 //
NM_010645			0.003		1.05	-1.13	-1.13	-1.21	<i>Klk1b1</i>	kallikrein 1-related peptidase b1	0002255 // tissue kallikrein-kinin cascade // inferred from mutant phenotype//0002936
NM_0010		0.0278			-1.04	1.07	-1.13	-1.06	<i>Fmn1</i>	formin-like 1	0006929 // substrate-dependent cell migration // inferred from mutant phenotype//000
NM_008530//XM		0.028			1.01	-1.20	-1.13	1.03	<i>Ly6f</i>	lymphocyte antigen 6 complex, locus F	0006461 // protein complex assembly // not recorded//0006811 // ion transport // not r
NM_0012		0.0225			-1.07	1.03	-1.13	-1.19	<i>Add2</i>	adducin 2 (beta)	0030433 // ER-associated ubiquitin-dependent protein catabolic process // not recorded
NM_0224		0.011			-1.08	1.02	-1.13	-1.03	<i>Tmub1</i>	transmembrane and ubiquitin-like domain containing 1	0006805 // xenobiotic metabolic process // not recorded//0019373 // epoxygenase P45
NM_0287		0.0427			1.03	-1.14	-1.13	1.09	<i>Cyp2s1</i>	cytochrome P450, family 2, subfamily 5, polypeptide 1	0006805 // proteolysis // inferred from electronic annotation
NM_013906			#####		-1.11	-1.15	-1.13	1.12	<i>Adams28</i>	a disintegrin-like and metallopeptidase (reprolysin type) with thrombospondin type 1 r	0007288 // sperm axoneme assembly // inferred from mutant phenotype//0021591 // v
NM_0157		0.0352			1.03	-1.23	-1.13	-1.05	<i>Spag6</i>	sperm associated antigen 6	0007165 // signal transduction // inferred from electronic annotation//0007186 // G-pr
NM_013533//XM_00650:		0.023			1.01	1.04	-1.13	-1.17	<i>Gpr162</i>	G protein-coupled receptor 162	0000387 // spliceosomal snRNP assembly // not recorded//0000398 // mRNA splicing, v
NM_0168		0.0401			-1.12	1.04	-1.13	-1.15	<i>Sart1</i>	squamous cell carcinoma antigen recognized by T cells 1	0001967 // suckling behavior // inferred from mutant phenotype//0003360 // brainsten
NM_001136056//NM_00		0.027			1.03	-1.06	-1.13	-1.16	<i>Cntfr</i>	ciliary neurotrophic factor receptor	
NM_133359			0.043		1.01	-1.04	-1.13	-1.20	<i>Krtap19-9b</i>	keratin associated protein 19-9B	



RefSeq	Tri	p 24h	p 48h	p 72h	FD Air	FD 24h	FD 48h	FD 72h	Gene Symbol	Gene Title	Gene Ontology Biological Process
NM_0118		0.0365			-1.06	1.10	-1.13	-1.13	<i>Hcst</i>	hematopoietic cell signal transducer	0006468 // protein phosphorylation // not recorded//0014068 // positive regulation of
NM_007818			0.039		-1.44	-1.14	-1.13	-1.16	<i>Cyp3a11</i>	cytochrome P450, family 3, subfamily a, polypeptide 11	0055114 // oxidation-reduction process // inferred from electronic annotation
NM_0242		0.0382			-1.24	-1.33	-1.12	-1.34	<i>Mxra8</i>	matrix-remodelling associated 8	0060857 // establishment of glial blood-brain barrier // inferred from expression pattern
NM_001037859	///		0.04		1.01	1.03	-1.12	-1.02	<i>Csf1r</i>	colony stimulating factor 1 receptor	0001934 // positive regulation of protein phosphorylation // not recorded//0002376 // i
NM_001081445	///		0.029		1.01	-1.03	-1.12	-1.07	<i>Ncam1</i>	neural cell adhesion molecule 1	0001928 // regulation of exocyst assembly // inferred from mutant phenotype//000715:
NM_0012		0.0382			-1.11	-1.32	-1.12	-1.03	<i>Trim3</i>	tripartite motif-containing 3	0006810 // transport // inferred from electronic annotation//0015031 // protein transp
NM_0010		0.0196	0.036		1.12	-1.07	-1.12	-1.02	<i>Zfr2</i>	zinc finger RNA binding protein 2	0006955 // immune response // inferred from electronic annotation//0008152 // metab
NM_009043		0.012	0.019		1.07	-1.10	-1.12	-1.12	<i>Reg2</i>	regenerating islet-derived 2	0001967 // suckling behavior // inferred from mutant phenotype//0042552 // myelinati
NM_153119	///XM		0.003		1.04	1.12	-1.12	1.08	<i>Plekho2</i>	pleckstrin homology domain containing, family O member 2	
NM_028149	///NM		0.032		1.03	1.03	-1.12	1.04	<i>Fbxl20</i>	F-box and leucine-rich repeat protein 20	0001662 // behavioral fear response // inferred from mutant phenotype//0016567 // pr
NM_1725		0.0116	0.011	0.011	1.08	-1.06	-1.12	-1.14	<i>Klhl11</i>	kelch-like 11	
NM_0080		0.0455	0.003		1.11	-1.00	-1.12	-1.06	<i>Gas1</i>	growth arrest specific 1	0002053 // positive regulation of mesenchymal cell proliferation // inferred from mutant
NM_011274	///XM		0.032		1.01	1.00	-1.12	1.01	<i>Uri1</i>	URI1, prefoldin-like chaperone	0000122 // negative regulation of transcription from RNA polymerase II promoter // not i
NM_001252501	///NM_00		0.046		-1.01	1.01	-1.12	-1.17	<i>Sorcs1</i>	sortilin-related VPS10 domain containing receptor 1	
NM_0075		0.0281			-1.12	1.17	-1.12	-1.13	<i>Cxcr5</i>	chemokine (C-X-C motif) receptor 5	0006935 // chemotaxis // inferred from electronic annotation//0006955 // immune res
NM_0166		0.018			1.00	1.14	-1.12	1.01	<i>Il27ra</i>	interleukin 27 receptor, alpha	0002827 // positive regulation of T-helper 1 type immune response // inferred from muta
NM_012034	///XM_00652		0.035		-1.05	-1.16	-1.12	-1.29	<i>Tpsg1</i>	tryptase gamma 1	0006508 // proteolysis // inferred from electronic annotation
NM_001316370	///NM_00		0.038		-1.66	-1.71	-1.12	1.05	<i>P4ha1</i>	procollagen-proline, 2-oxoglutarate 4-dioxygenase (proline 4-hydroxylase), alpha 1 pol	0018401 // peptidyl-proline hydroxylation to 4-hydroxy-L-proline // inferred from direct
NM_008878			0.048		-1.02	-1.01	-1.12	-1.19	<i>Serpinf2</i>	serine (or cysteine) peptidase inhibitor, clade F, member 2	0002034 // regulation of blood vessel size by renin-angiotensin // inferred from mutant p
NM_080448	///NM		0.047		1.03	-1.10	-1.12	1.01	<i>Srgap3</i>	SLIT-ROBO Rho GTPase activating protein 3	0007165 // signal transduction // inferred from electronic annotation//0030336 // nega
NM_1447		0.0171	0.043		1.14	-1.09	-1.12	-1.13	<i>Wt1</i>	Wilms tumor 1 homolog	0000122 // negative regulation of transcription from RNA polymerase II promoter // not i
NM_001146215	///		0.015		1.09	1.03	-1.12	-1.10	<i>Msh5</i>	mutS homolog 5 (E. coli)	0000710 // meiotic mismatch repair // --//0006298 // mismatch repair // inferred from
NM_001244198	///		0.009		1.12	1.05	-1.12	-1.09	<i>Pax6</i>	paired box 6	0000122 // negative regulation of transcription from RNA polymerase II promoter // infer
NM_0202		0.0168			1.04	-1.14	-1.12	-1.10	<i>Cldn9</i>	claudin 9	0016338 // calcium-independent cell-cell adhesion via plasma membrane cell-adhesion n
NM_1537		0.027	0.004	0.003	1.06	-1.06	-1.12	-1.23	<i>Rel12</i>	REL1-like 2	0010811 // positive regulation of cell-substrate adhesion // inferred from direct assay
NM_1340		0.0011	0.043		1.12	-1.11	-1.12	-1.06	<i>Tbc1d10a</i>	TBC1 domain family, member 10a	0042147 // retrograde transport, endosome to Golgi // not recorded//0043547 // posit
NM_1332		0.0087	0.034		1.11	-1.24	-1.12	1.06	<i>Zfp704</i>	zinc finger protein 704	
NM_001290792	///		0.036		1.01	1.06	-1.12	1.07	<i>Wdr45</i>	WD repeat domain 45	0000045 // autophagosome assembly // not recorded//0000422 // mitophagy // not rec
NM_001276676	///NM_00		0.007		1.09	1.07	-1.12	-1.26	<i>Syt6</i>	synaptotagmin VI	0006906 // vesicle fusion // --//0007340 // acrosome reaction // inferred from direct as
NM_0136		0.0232	0.018		1.00	-1.15	-1.12	-1.00	<i>Mt3</i>	metallothionein 3	0000060 // protein import into nucleus, translocation // inferred from sequence or struct
NM_001081363	///XM_00		0.017		-1.11	1.00	-1.12	1.12	<i>Cenpf</i>	centromere protein F	0000278 // mitotic cell cycle // not recorded//0002724 // regulation of T cell cytokine pr
NM_030678			0.023		-1.11	-1.01	-1.12	1.01	<i>Gys1</i>	glycogen synthase 1, muscle	0005977 // glycogen metabolic process // not recorded//0005978 // glycogen biosynthe
NM_0011		0.0353			1.02	-1.24	-1.12	-1.09	<i>Pclo</i>	piccolo (presynaptic cytomatrix protein)	0007010 // cytoskeleton organization // inferred from direct assay//0007416 // synapse
NM_001139520	///		0.021		1.09	1.07	-1.12	1.04	<i>Samhd1</i>	SAM domain and HD domain, 1	0002376 // immune system process // inferred from electronic annotation//0006203 //
NM_0011		0.0196			-1.00	-1.18	-1.12	1.02	<i>Mak</i>	male germ cell-associated kinase	0006351 // transcription, DNA-templated // inferred from electronic annotation//00063
NM_011850			0.016		1.03	1.05	-1.12	-1.10	<i>Nr0b2</i>	nuclear receptor subfamily 0, group B, member 2	0000122 // negative regulation of transcription from RNA polymerase II promoter // not i
NM_0010		0.0262	0.017		1.02	-1.28	-1.12	1.10	<i>Chka</i>	choline kinase alpha	0006580 // ethanolamine metabolic process // not recorded//0006629 // lipid metaboli
NM_013772	///XM		0.045	0.027	1.02	-1.05	-1.12	-1.16	<i>LOC100041483//Tcl1b3</i>	protein TCL1B3//T cell leukemia/lymphoma 1B, 3	
NM_008175			0.006		1.06	1.03	-1.12	1.06	<i>Grrn</i>	granulin	0001835 // blastocyst hatching // inferred from direct assay//0007566 // embryo implar
NM_0011		0.0139			-1.09	1.05	-1.12	-1.16	<i>Tcf7l2</i>	transcription factor 7 like 2, T cell specific, HMG box	0000122 // negative regulation of transcription from RNA polymerase II promoter // infer
NM_0202		0.0258			-1.18	-1.03	-1.12	-1.15	<i>Magea4</i>	melanoma antigen, family A, 4	
NM_0010		0.0348			1.02	-1.08	-1.12	-1.12	<i>Oxtr</i>	oxytocin receptor	0001967 // suckling behavior // not recorded//0001975 // response to amphetamine //
NM_1772		0.0207			-1.03	1.10	-1.12	-1.13	<i>Trac//Tnpo3//Traj15//Trav6-7-dv9//Tr</i>	T cell receptor alpha constant//transportin 3//T cell receptor alpha joining 15//T ce	0050852 // T cell receptor signaling pathway // --//0006606 // protein import into nucl
NM_0281		0.0047			1.04	-1.15	-1.12	-1.01	<i>Nkd2</i>	naked cuticle 2 homolog (Drosophila)	0006810 // transport // inferred from electronic annotation//0006887 // exocytosis // ir
NM_011663		0.013			1.06	-1.19	-1.12	1.02	<i>Zrsr1</i>	zinc finger (CCCH type), RNA binding motif and serine/arginine rich 1	
NM_029096	///NM		0.027	0.01	1.04	1.04	-1.12	-1.10	<i>Rita1</i>	RBPJ interacting and tubulin associated 1	0007219 // Notch signaling pathway // inferred from electronic annotation//0007399 //
NM_009718		0.018			1.07	-1.05	-1.12	-1.10	<i>Neurog2</i>	neurogenin 2	0001764 // neuron migration // inferred from mutant phenotype//0006351 // transcrip/
NM_0012		0.0412			1.05	-1.12	-1.12	1.09	<i>Scnn1b</i>	sodium channel, nonvoltage-gated 1 beta	0001666 // response to hypoxia // inferred from electronic annotation//0002028 // regu
NM_0081		0.0045	#####		1.04	-1.17	-1.12	-1.24	<i>Gpr33</i>	G protein-coupled receptor 33	0007165 // signal transduction // inferred from electronic annotation//0007186 // G-pr
NM_001315503	///		0.032		1.05	-1.08	-1.12	-1.11	<i>Adcyap1</i>	adenylate cyclase activating polypeptide 1	0001541 // ovarian follicle development // not recorded//0001662 // behavioral fear re
NM_001136064	///		0.05		1.05	1.04	-1.12	1.05	<i>Bscl2</i>	Berardinelli-Seip congenital lipodystrophy 2 homolog (seipin)	0006629 // lipid metabolic process // inferred from electronic annotation//0016042 // li
NM_016982	///NM		0.026		1.04	-1.04	-1.12	-1.07	<i>Vpreb1//Vpreb2</i>	pre-B lymphocyte gene 1//pre-B lymphocyte gene 2	0000902 // cell morphogenesis // inferred from genetic interaction//0002377 // immun
NM_0087		0.0471			1.05	-1.20	-1.12	-1.15	<i>Ints6</i>	integrator complex subunit 6	0016180 // snRNA processing // not recorded
NM_0082		0.0125			1.08	-1.37	-1.12	1.18	<i>Hpgd</i>	hydroxyprostaglandin dehydrogenase 15 (NAD)	0006629 // lipid metabolic process // inferred from electronic annotation//0006631 // f.
NM_144524	///XM		0.033		1.07	1.04	-1.12	-1.02	<i>Angel1</i>	angel homolog 1 (Drosophila)	
NM_0089		0.006			-1.03	-1.19	-1.12	1.00	<i>Npepps</i>	aminopeptidase puromycin sensitive	0006508 // proteolysis // inferred from electronic annotation//0043171 // peptide catal
NM_026261		0.012	0.016		1.11	-1.03	-1.12	-1.09	<i>Ubl4b</i>	ubiquitin-like 4B	1903955 // positive regulation of protein targeting to mitochondrion // not recorded
NM_0012		0.0252			1.01	-1.13	-1.12	-1.18	<i>Cdh23</i>	cadherin 23 (otocadherin)	0006816 // calcium ion transport // not recorded//0007155 // cell adhesion // traceable
NM_001198835	///NM_00		0.035		1.02	-1.03	-1.12	-1.15	<i>Coch</i>	coagulation factor C homolog (Limulus polyphemus)	0007605 // sensory perception of sound // inferred from mutant phenotype//0008360 //
NM_0100		0.0236			1.03	-1.18	-1.12	1.06	<i>Dspp</i>	dentin sialophosphoprotein	0031214 // biomineral tissue development // inferred from electronic annotation//0071
NM_0093		0.0413	0.02	0.028	1.09	-1.09	-1.12	-1.19	<i>Tecta</i>	tectorin alpha	0007160 // cell-matrix adhesion // inferred from electronic annotation//0007605 // sen:
NM_0302		0.0478			-1.01	1.09	-1.11	-1.10	<i>Aacs</i>	acetoacetyl-CoA synthetase	0001889 // liver development // not recorded//0006629 // lipid metabolic process // inf
NM_008108	///XM_00650		0.022		-1.03	1.02	-1.11	-1.19	<i>Gdf3</i>	growth differentiation factor 3	0001501 // skeletal system development // not recorded//0001654 // eye development
NM_0012		0.03	0.037	0.006	1.15	1.00	-1.11	-1.16	<i>Nxf2</i>	nuclear RNA export factor 2	0006405 // RNA export from nucleus // inferred from direct assay//0006405 // RNA exp

RefSeq	Tri	p 24h	p 48h	p 72h	FD Air	FD 24h	FD 48h	FD 72h	Gene Symbol	Gene Title	Gene Ontology Biological Process
NM_178020			0.044	-1.07	1.00	-1.11	-1.26		<i>Hyal3</i>	hyaluronoglucosaminidase 3	0005975 // carbohydrate metabolic process // inferred from electronic annotation//0000001702 // gastrulation with mouth forming second // non-traceable author statement//
NM_023160//XM		0.043		1.01	-1.05	-1.11	-1.13		<i>Cml1</i>	camello-like 1	0016567 // protein ubiquitination // inferred from electronic annotation//0035556 // in
NM_133346			0.045	-1.01	-1.09	-1.11	-1.11		<i>Asb6</i>	ankyrin repeat and SOCS box-containing 6	0001694 // histamine biosynthetic process // not recorded//0006955 // immune respon
NM_0169	0.0486			1.02	-1.09	-1.11	-1.14		<i>Prg3</i>	proteoglycan 3	0006508 // proteolysis // inferred from electronic annotation//0008283 // cell proliferat
NM_0012	0.0134			1.11	-1.02	-1.11	-1.02		<i>Rhbdf1</i>	rhomboid family 1 (Drosophila)	0001819 // positive regulation of cytokine production // inferred from direct assay//000
NM_019450			0.05	1.03	-1.04	-1.11	-1.13		<i>Il1f6</i>	interleukin 1 family, member 6	0006468 // protein phosphorylation // not recorded//0007346 // regulation of mitotic c
NM_0088	0.0062			-1.11	1.29	-1.11	1.01		<i>Pim1</i>	proviral integration site 1	0000122 // negative regulation of transcription from RNA polymerase II promoter // infer
NM_031184//XM	0.036	0.024		1.08	1.08	-1.11	-1.05		<i>Glis2</i>	GLIS family zinc finger 2	0001570 // vasculogenesis // inferred from mutant phenotype//0001701 // in utero em
NM_001033402//	0.022	0.008		1.12	1.00	-1.11	-1.12		<i>Zmiz1</i>	zinc finger, MIZ-type containing 1	0006810 // transport // inferred from electronic annotation//0006811 // ion transport
NM_030687//XM	0.029	0.04		1.08	1.00	-1.11	-1.04		<i>Slco1a4</i>	solute carrier organic anion transporter family, member 1a4	0001503 // ossification // not recorded//0001954 // positive regulation of cell-matrix ad
NM_001113529//	0.011			1.10	1.06	-1.11	1.05		<i>Csf1</i>	colony stimulating factor 1 (macrophage)	0000122 // negative regulation of transcription from RNA polymerase II promoter // infer
NM_0119	0.0397			-1.15	-1.04	-1.11	-1.14		<i>Vax2</i>	ventral anterior homeobox 2	0006915 // apoptotic process // inferred from electronic annotation//0007165 // signal
NM_025886//XM	0.039			1.14	1.06	-1.11	1.00		<i>Rassf7</i>	Ras association (RalGDS/AF-6) domain family (N-terminal) member 7	0001666 // response to hypoxia // inferred from electronic annotation//0002028 // regu
NM_009301			0.019	-1.07	1.01	-1.11	-1.05		<i>Svs5</i>	seminal vesicle secretory protein 5	0007244 // negative regulation of thymocyte apoptotic process // inferred from mutant p
NM_008712//XM_006530	0.022			-1.02	-1.03	-1.11	-1.20		<i>Nos1</i>	nitric oxide synthase 1, neuronal	0006810 // transport // inferred from electronic annotation//0006886 // intracellular pr
NM_011195	0.032			1.08	-1.11	-1.11	-1.07		<i>Ptcr</i>	pre T cell antigen receptor alpha	0007155 // cell adhesion // inferred from electronic annotation//0007156 // homophilic
NM_001136259//	0.023			1.04	1.04	-1.11	1.06		<i>Tom1</i>	target of myb1 homolog (chicken)	0006810 // transport // inferred from electronic annotation//0006811 // ion transport
NM_153112		0.049		-1.10	-1.09	-1.11	-1.23		<i>Cadm4</i>	cell adhesion molecule 4	0001502 // ossification // not recorded//0001954 // positive regulation of cell-matrix ad
NM_031396//XM	0.004	0.022		1.11	-1.01	-1.11	-1.13		<i>Cnnm1</i>	cyclin M1	0005975 // carbohydrate metabolic process // inferred from electronic annotation//000
NM_001302397//	0.048			1.15	1.00	-1.11	1.05		<i>Phf1</i>	PHD finger protein 1	0008152 // metabolic process // inferred from electronic annotation
NM_013630//XM	0.011			1.11	-1.12	-1.11	1.15		<i>Pkd1</i>	polycystic kidney disease 1 homolog	0006351 // transcription, DNA-templated // inferred from electronic annotation//00063
NM_021715//XR_0029			0.029	1.08	1.00	-1.11	-1.13		<i>Chst7</i>	carbohydrate (N-acetylglucosamino) sulfotransferase 7	0009060 // aerobic respiration // not recorded//0033617 // mitochondrial respiratory cl
XR_389155//XR_393665//	0.048		0.029	1.01	1.00	-1.11	-1.18		<i>Myo15b</i>	myosin XVb	0001826 // inner cell mass cell differentiation // inferred from mutant phenotype//0006
NM_008022			0.029	-1.05	-1.07	-1.11	-1.40		<i>Foxd4</i>	forkhead box D4	0000122 // negative regulation of transcription from RNA polymerase II promoter // infer
NM_0253	0.0375			-1.09	1.12	-1.11	-1.06		<i>Chchd5</i>	coiled-coil-helix-coiled-coil-helix domain containing 5	0001701 // in utero embryonic development // inferred from mutant phenotype//0006:
NM_001285807//NM_00	0.04			-1.06	-1.10	-1.11	1.03		<i>Dtna</i>	dystrobrevin alpha	0000122 // negative regulation of transcription from RNA polymerase II promoter // infer
NM_0012	0.049			1.08	-1.09	-1.11	-1.09		<i>Tet1</i>	tet methylcytosine dioxygenase 1	0001666 // response to hypoxia // inferred from electronic annotation//0002028 // regu
NM_008835//NR_028271	0.021			-1.02	-1.12	-1.11	-1.18		<i>Phxr4</i>	per-hexamer repeat gene 4	0007244 // negative regulation of thymocyte apoptotic process // inferred from mutant p
NM_001316360//	0.025			1.07	1.34	-1.11	1.10		<i>Bmp4</i>	bone morphogenetic protein 4	0006810 // transport // inferred from electronic annotation//0006811 // ion transport
NM_0079	0.0266			1.09	-1.20	-1.11	-1.18		<i>Endog</i>	endonuclease G	0001502 // ossification // not recorded//0001954 // positive regulation of cell-matrix ad
NM_024432//XM	0.034			1.12	1.02	-1.11	-1.08		<i>Ubxn6</i>	UBX domain protein 6	0006351 // transcription, DNA-templated // inferred from electronic annotation//00063
NM_001008542//	0.006			1.10	1.04	-1.11	1.07		<i>Mxi1</i>	MAX interactor 1, dimerization protein	0001502 // ossification // not recorded//0001954 // positive regulation of cell-matrix ad
NM_001142335//	0.038	0.03		1.13	1.32	-1.11	-1.15		<i>Lmo2</i>	LIM domain only 2	0000122 // negative regulation of transcription from RNA polymerase II promoter // infer
NM_144518//XM	0.043			1.14	-1.00	-1.11	-1.07		<i>2900011008Rik</i>	RIKEN cDNA 2900011008 gene	00035162 // embryonic hemopoiesis // inferred from genetic interaction//0042789 // mF
NM_001042528//NM_00	0.014			-1.01	-1.06	-1.11	-1.15		<i>Cacna1b</i>	calcium channel, voltage-dependent, N type, alpha 1B subunit	0007026 // negative regulation of microtubule depolymerization // inferred from mutant
NM_0011 #####	0.027			1.15	-1.09	-1.11	-1.00		<i>Abl1</i>	c-abl oncogene 1, non-receptor tyrosine kinase	0001956 // positive regulation of neurotransmitter secretion // not recorded//0006810
NM_0313	0.0019			1.04	-1.13	-1.11	-1.02		<i>Tex13</i>	testis expressed gene 13	0001922 // B-1 B cell homeostasis // inferred from mutant phenotype//0001934 // posi
NM_001301805//NM_00	0.017			1.06	1.03	-1.11	-1.22		<i>Hes2</i>	hairy and enhancer of split 2 (Drosophila)	0006351 // transcription, DNA-templated // inferred from electronic annotation//00063
NM_011040//XM_00649	0.036			-1.17	-1.09	-1.11	-1.07		<i>Pax8</i>	paired box 8	0001655 // urogenital system development // inferred from genetic interaction//00016:
NM_001081306//NM_00	0.029			-1.16	-1.08	-1.11	-1.05		<i>Ptprz1</i>	protein tyrosine phosphatase, receptor type Z, polypeptide 1	0002244 // hematopoietic progenitor cell differentiation // inferred from mutant phenot
NM_007817	0.027			-1.01	-1.14	-1.11	1.18		<i>Cyp2f2</i>	cytochrome P450, family 2, subfamily f, polypeptide 2	0006805 // xenobiotic metabolic process // not recorded//0009636 // response to toxic
NM_153558//XM_00649	0.005			-1.12	-1.09	-1.11	1.03		<i>Obp2a</i>	odorant binding protein 2A	0006810 // transport // inferred from electronic annotation
NM_015779	0.045			1.00	1.01	-1.11	-1.18		<i>Elane</i>	elastase, neutrophil expressed	0000122 // negative regulation of transcription from RNA polymerase II promoter // not i
NM_0012	0.0151			1.02	-1.15	-1.11	1.00		<i>Anks1</i>	ankyrin repeat and SAM domain containing 1	0006929 // substrate-dependent cell migration // inferred from direct assay//0016322
NM_1452	0.0479	0.02		1.25	-1.06	-1.11	1.22		<i>App12</i>	adaptor protein, phosphotyrosine interaction, PH domain and leucine zipper containin	0007049 // cell cycle // inferred from electronic annotation//0008283 // cell proliferatio
NM_0278	0.0113			1.02	-1.09	-1.11	-1.06		<i>Fam110c</i>	family with sequence similarity 110, member C	0030335 // positive regulation of cell migration // not recorded//0051897 // positive reg
NM_0292	0.0201			1.05	1.23	-1.11	1.03		<i>Rnf19b</i>	ring finger protein 19B	0000209 // protein polyubiquitination // not recorded//0002250 // adaptive immune re
NM_009482			0.02	1.04	-1.03	-1.11	-1.16		<i>Utf1</i>	undifferentiated embryonic cell transcription factor 1	0006351 // transcription, DNA-templated // inferred from electronic annotation//00063
NM_0079	0.0015	0.017	0.005	1.07	-1.11	-1.11	-1.18		<i>Etv2</i>	ets variant 2	0001701 // in utero embryonic development // inferred from mutant phenotype//0001:
NM_138955//XM_01124	0.04			1.03	1.00	-1.11	-1.10		<i>Abcg4</i>	ATP-binding cassette, sub-family G (WHITE), member 4	0006355 // regulation of transcription, DNA-templated // inferred from mutant phenoty
NM_0011	0.0207			1.03	-1.10	-1.11	-1.10		<i>Rab17</i>	RAB17, member RAS oncogene family	0002415 // immunoglobulin transcytosis in epithelial cells mediated by polymeric immun
NM_001290574//	0.031			1.09	1.02	-1.11	-1.08		<i>Ppp1r3f</i>	protein phosphatase 1, regulatory (inhibitor) subunit 3F	0005979 // regulation of glycogen biosynthetic process // not recorded//2000465 // reg
NM_0115	0.0035			1.04	-1.10	-1.11	-1.12		<i>Sry</i>	sex determining region of Chr Y	0000122 // negative regulation of transcription from RNA polymerase II promoter // infer
NM_0104	0.0229			1.05	-1.15	-1.11	-1.11		<i>Hoxc6</i>	homeobox C6	0006351 // transcription, DNA-templated // inferred from electronic annotation//00063
NM_001311152//	0.026			1.06	1.09	-1.11	-1.00		<i>Rnf123</i>	ring finger protein 123	0016567 // protein ubiquitination // inferred from electronic annotation
NM_029658			0.016	-1.02	-1.09	-1.11	-1.18		<i>Fam101b</i>	family with sequence similarity 101, member B	0001837 // epithelial to mesenchymal transition // inferred from genetic interaction//0C
NM_008003			0.017	1.03	1.01	-1.11	-1.14		<i>Fgf15</i>	fibroblast growth factor 15	0001755 // neural crest cell migration // inferred from mutant phenotype//0001934 // i
NR_001463//NR_0002	0.013	0.003		1.03	-1.04	-1.11	-1.10		<i>Xist</i>	inactive X specific transcripts	0009048 // dosage compensation by inactivation of X chromosome // inferred from direc
NM_009253//XM_00651	0.019			-1.14	-1.09	-1.11	1.00		<i>Serpina3m</i>	serine (or cysteine) peptidase inhibitor, clade A, member 3M	0010466 // negative regulation of peptidase activity // inferred from electronic annotatio
NM_0194	0.0227			1.05	-1.20	-1.11	1.15		<i>Epb414b</i>	erythrocyte membrane protein band 4.1 like 4b	0010628 // positive regulation of gene expression // not recorded//0031032 // actomyo
NM_007848			0.016	-1.01	1.02	-1.10	-1.17		<i>Defa-rs7</i>	defensin, alpha, related sequence 7	0006952 // defense response // inferred from electronic annotation//0042742 // defens
NM_175244//XR_0036			0.036	1.08	-1.01	-1.10	1.01		<i>Hectd3</i>	HECT domain containing 3	0016567 // protein ubiquitination // inferred from electronic annotation//0016567 // pr
NM_133235//XR_373242	0.02			1.06	-1.03	-1.10	-1.20		<i>Khdrbs2</i>	KH domain containing, RNA binding, signal transduction associated 2	0006351 // transcription, DNA-templated // inferred from electronic annotation//00063
NM_0076	0.0097	0.016		1.08	-1.03	-1.10	1.26		<i>Cbr2</i>	carbonyl reductase 2	0006116 // NADH oxidation // traceable author statement//0008152 // metabolic proce

RefSeq	Tri	p 24h	p 48h	p 72h	FD Air	FD 24h	FD 48h	FD 72h	Gene Symbol	Gene Title	Gene Ontology Biological Process
NM_0217		0.0358	0.039		-1.26	-1.07	-1.10	-1.14	<b>Trappc4</b>	trafficking protein particle complex 4	0006810 // transport // inferred from electronic annotation//0006888 // ER to Golgi ves
NM_001308327	///	0.008			1.06	1.13	-1.10	-1.15	<b>Enpp1</b>	ectonucleotide pyrophosphatase/phosphodiesterase 1	0006091 // generation of precursor metabolites and energy // not recorded//0006796 /
NM_146064	///XM	0.045			1.05	1.05	-1.10	1.02	<b>Soat2</b>	sterol O-acyltransferase 2	0006629 // lipid metabolic process // inferred from electronic annotation//0008202 // s
NM_0296		0.0475			-1.14	1.03	-1.10	-1.09	<b>Stambpl1</b>	STAM binding protein like 1	0006508 // proteolysis // inferred from electronic annotation
NM_198108		0.05	0.031		1.05	1.03	-1.10	-1.11	<b>Morn4</b>	MORN repeat containing 4	
NM_025716		0.048			1.05	1.06	-1.10	1.10	<b>Spryd4</b>	SPRY domain containing 4	
NM_008759		0.025	0.035		1.03	-1.10	-1.10	-1.16	<b>Sebox</b>	SEBOX homeobox	0006351 // transcription, DNA-templated // inferred from electronic annotation//00063
NM_001177594	///	0.028			1.09	-1.01	-1.10	1.04	<b>Slc8b1</b>	solute carrier family 8 (sodium/lithium/calcium exchanger), member B1	0006810 // transport // inferred from electronic annotation//0006811 // ion transport /
NM_0198		0.0063			1.06	1.40	-1.10	1.36	<b>Dusp14</b>	dual specificity phosphatase 14	0000188 // inactivation of MAPK activity // inferred from electronic annotation//00064;
NM_133643	///XM	0.00651	0.007		-1.00	-1.01	-1.10	-1.22	<b>Edaradd</b>	EDAR (ectodysplasin-A receptor)-associated death domain	0001942 // hair follicle development // inferred from genetic interaction//0007165 // si
NM_0010		0.0171			1.05	-1.49	-1.10	1.33	<b>Rtkn2</b>	rhotekin 2	0008284 // positive regulation of cell proliferation // inferred from direct assay//003009
NM_010149	///XM	0.003	0.025		1.10	1.05	-1.10	-1.12	<b>Epor</b>	erythropoietin receptor	0003007 // heart morphogenesis // traceable author statement//0007165 // signal tran
NM_001145876	///	0.006			1.05	-1.01	-1.10	1.06	<b>Slc25a44</b>	solute carrier family 25, member 44	0006810 // transport // inferred from electronic annotation//0055085 // transmembrar
NM_054095	///XM	0.045		0.002	1.06	-1.02	-1.10	-1.13	<b>Necab2</b>	N-terminal EF-hand calcium binding protein 2	0042984 // regulation of amyloid precursor protein biosynthetic process // not recorded
NM_138955	///XM	0.013			1.03	-1.05	-1.10	-1.10	<b>Abcg4</b>	ATP-binding cassette, sub-family G (WHITE), member 4	0006355 // regulation of transcription, DNA-templated // inferred from mutant phenoty
NM_0012		0.0383	0.007	0.012	1.05	-1.11	-1.10	-1.12	<b>Pde10a</b>	phosphodiesterase 10A	0006198 // cAMP catabolic process // not recorded//0007165 // signal transduction // i
NM_001285487	///	0.025			1.06	1.04	-1.10	1.01	<b>Mknk1</b>	MAP kinase-interacting serine/threonine kinase 1	0006417 // regulation of translation // inferred from electronic annotation//0006446 // i
NM_0010		0.0045			1.07	-1.17	-1.10	1.17	<b>5330417C22Rik</b>	RIKEN cDNA 5330417C22 gene	0006914 // autophagy // inferred from electronic annotation//0009267 // cellular respo
NM_0011		0.0081		0.043	1.09	-1.14	-1.10	-1.03	<b>Rapgef3</b>	Rap guanine nucleotide exchange factor (GEF) 3	0001525 // angiogenesis // inferred from electronic annotation//0001932 // regulation
NM_080555			0.015		1.03	-1.01	-1.10	-1.06	<b>Ppp3</b>	phospholipid phosphatase 3	0001568 // blood vessel development // inferred from mutant phenotype//0001702 // g
NM_0297		0.002			-1.16	1.13	-1.10	1.01	<b>Rps9</b>	ribosomal protein S9	0006412 // translation // not recorded//0008284 // positive regulation of cell proliferat
NM_133902	///XM	0.01124	0.01		-1.05	1.08	-1.10	-1.29	<b>Sds1</b>	serine dehydratase-like	0006565 // L-serine catabolic process // not recorded//0006567 // threonine catabolic c
NM_0011		0.0011	0.019		1.03	-1.10	-1.10	-1.10	<b>Cd160</b>	CD160 antigen	0007165 // signal transduction // ---//0007165 // signal transduction // inferred from el
NM_008167	///XM	0.00650	0.007		1.00	-1.04	-1.10	-1.17	<b>Grid2</b>	glutamate receptor, ionotropic, delta 2	0006810 // transport // inferred from electronic annotation//0006811 // ion transport /
NM_0114		0.0207			1.01	-1.17	-1.10	1.08	<b>Sox13</b>	SRY (sex determining region Y)-box 13	0006351 // transcription, DNA-templated // inferred from electronic annotation//00063
NM_0256		0.0055			1.02	-1.22	-1.10	-1.13	<b>Mis18a</b>	MIS18 kinetochore protein homolog A (S. pombe)	0007049 // cell cycle // inferred from electronic annotation//0007059 // chromosome s
NM_0011		0.0106			1.05	-1.18	-1.10	-1.08	<b>Cbfa2t3</b>	core-binding factor, runt domain, alpha subunit 2, translocated to, 3 (human)	0000122 // negative regulation of transcription from RNA polymerase II promoter // infer
NM_009430			0.014		-1.01	1.04	-1.10	-1.18	<b>Prss2</b>	protease, serine 2	0006508 // proteolysis // not recorded//0007584 // response to nutrient // inferred fro
NM_0095		0.041			1.27	-1.44	-1.10	-1.13	<b>Plagl1</b>	pleiomorphic adenoma gene-like 1	0006351 // transcription, DNA-templated // inferred from electronic annotation//00063
		0.0283			-1.05	-1.19	-1.10	-1.23	<b>BC038268</b>	cDNA sequence BC038268	0001503 // ossification // inferred from electronic annotation//0001822 // kidney devel
NM_0254		0.0274			-1.01	-1.28	-1.10	-1.17	<b>Arl4d</b>	ADP-ribosylation factor-like 4D	0007264 // small GTPase mediated signal transduction // inferred from electronic annota
NM_0096		0.0444	0.013	0.017	-1.99	-1.23	-1.10	-1.08	<b>Alb</b>	albumin	0001895 // retina homeostasis // inferred from electronic annotation//0006810 // trans
NM_1453		0.024	0.041		1.07	-1.09	-1.10	-1.05	<b>Mrgprf</b>	MAS-related GPR, member F	0007165 // signal transduction // inferred from electronic annotation//0007186 // G-pr
NM_133980	///XM	0.038	0.011		1.06	-1.06	-1.10	-1.16	<b>Slc22a13</b>	solute carrier family 22 (organic cation transporter), member 13	0015747 // urate transport // not recorded//0055085 // transmembrane transport // nc
NM_0290	#####				-1.03	-1.39	-1.10	-1.11	<b>Spsb1</b>	splA/ryanodine receptor domain and SOCS box containing 1	0016567 // protein ubiquitination // inferred from electronic annotation//0035556 // i
NM_021316	///XM	0.00653	0.024		1.05	-1.01	-1.10	-1.14	<b>Cend1</b>	cell cycle exit and neuronal differentiation 1	0007628 // adult walking behavior // inferred from mutant phenotype//0021549 // cere
NM_144790	///XM	0.00652	0.043		1.04	-1.09	-1.10	-1.20	<b>Ankrd33</b>	ankyrin repeat domain 33	0000122 // negative regulation of transcription from RNA polymerase II promoter // infer
XM_006504541	///XM	0.006	0.043		1.02	-1.03	-1.10	-1.21	<b>Muc3</b>	mucin 3, intestinal	0001975 // cellular homeostasis // traceable author statement
NM_144820	///XM	0.00651	0.036		1.02	-1.08	-1.10	-1.14	<b>Ccdc28a</b>	coiled-coil domain containing 28A	
NM_0012		0.002			1.03	-1.04	-1.10	1.22	<b>Ager</b>	advanced glycosylation end product-specific receptor	0001666 // response to hypoxia // inferred from mutant phenotype//0001933 // negati
NM_028625			0.038		1.02	-1.11	-1.10	-1.17	<b>Lce1a2</b>	late cornified envelope 1A2	0008544 // epidermis development // inferred from electronic annotation//0018149 // i
NM_013822	///XM	0.01123	0.029		-1.05	-1.01	-1.10	1.03	<b>Jag1</b>	jagged 1	0001974 // blood vessel remodeling // inferred from mutant phenotype//0002011 // mc
NM_058214	///XM	0.00652	0.028		1.03	1.03	-1.10	-1.14	<b>Recq4</b>	RecQ protein-like 4	0000733 // DNA strand renaturation // not recorded//0001501 // skeletal system devel
NM_1455		0.027			1.13	-1.04	-1.10	-1.06	<b>Ccm1</b>	cerebral cavernous malformation 2-like	0003209 // cardiac atrium morphogenesis // inferred from genetic interaction//0003222
NM_021452	///XM	0.007			1.19	1.05	-1.10	1.09	<b>Kcnmb4</b>	potassium large conductance calcium-activated channel, subfamily M, beta member 4	0001508 // action potential // not recorded//0005513 // detection of calcium ion // not
NM_011434		0.018			-1.01	-1.11	-1.10	-1.13	<b>Sod1</b>	superoxide dismutase 1, soluble	0000187 // activation of MAPK activity // inferred from direct assay//0000302 // respon
NM_026273	///XM	0.024			1.10	-1.06	-1.10	-1.07	<b>4930453N24Rik</b>	RIKEN cDNA 4930453N24 gene	0006915 // apoptotic process // inferred from electronic annotation
NM_0010		0.0355			1.06	-1.19	-1.10	-1.03	<b>Rgs11</b>	regulator of G-protein signaling 11	0007186 // G-protein coupled receptor signaling pathway // traceable author statement/
NM_0012		0.0239			-1.04	1.12	-1.10	-1.17	<b>Socs1</b>	suppressor of cytokine signaling 1	0001932 // regulation of protein phosphorylation // inferred from direct assay//000646
NM_0010		0.0264			1.27	-1.21	-1.10	1.62	<b>Gpr155</b>	G protein-coupled receptor 155	0035556 // intracellular signal transduction // inferred from electronic annotation//0005
NM_0087		0.0437			1.02	-1.08	-1.10	-1.09	<b>Pcp4</b>	Purkinje cell protein 4	0006469 // negative regulation of protein kinase activity // not recorded//0010976 // pc
NM_1789		0.0033			-1.08	1.50	-1.10	-1.05	<b>Pld4</b>	phospholipase D family, member 4	0002244 // hematopoietic progenitor cell differentiation // inferred from mutant phenot
NM_011437	///XM	0.00652	0.002		1.03	1.00	-1.09	-1.09	<b>Sox10</b>	SRY (sex determining region Y)-box 10	0001701 // in utero embryonic development // inferred from genetic interaction//0001:
NM_028216		0.001			1.06	1.06	-1.09	-1.17	<b>Psca</b>	prostate stem cell antigen	
NM_026716		0.033			-1.00	1.01	-1.09	-1.11	<b>Syca</b>	syncollin	0006887 // exocytosis // inferred from electronic annotation
NM_012013	///XM	0.00650	0.026		-1.07	1.01	-1.09	-1.33	<b>Figla</b>	folliculogenesis specific basic helix-loop-helix	0006351 // transcription, DNA-templated // inferred from electronic annotation//00063
NM_0287		0.0144			-1.02	-1.15	-1.09	-1.17	<b>Slc7a13</b>	solute carrier family 7, (cationic amino acid transporter, y+ system) member 13	0003333 // amino acid transmembrane transport // not recorded//0006810 // transpor
NM_0296		0.0064	0.003		1.10	-1.00	-1.09	1.06	<b>Abhd14b</b>	abhydrolase domain containing 14b	0008152 // metabolic process // not recorded//0045944 // positive regulation of transcr
NM_027454	///NM	0.17321	0.024		1.07	-1.07	-1.09	-1.18	<b>Chrb3</b>	cholinergic receptor, nicotinic, beta polypeptide 3	0006810 // transport // inferred from electronic annotation//0006811 // ion transport /
NM_019741	///XM	0.037	0.003		1.07	1.01	-1.09	-1.16	<b>Slc2a5</b>	solute carrier family 2 (facilitated glucose transporter), member 5	0006810 // transport // inferred from electronic annotation//0008643 // carbohydrate t
NM_008818		0.033			-1.05	-1.02	-1.09	-1.23	<b>Rhox5</b>	reproductive homeobox 5	0000122 // negative regulation of transcription from RNA polymerase II promoter // infer
NM_001081373	///	0.027	0.001		1.05	1.04	-1.09	-1.23	<b>Cep164</b>	centrosomal protein 164	0006281 // DNA repair // inferred from electronic annotation//0006974 // cellular resp
NM_1455		0.0293	0.032	0.036	1.04	-1.08	-1.09	-1.09	<b>Myopop</b>	Myb-related transcription factor, partner of profilin	0000122 // negative regulation of transcription from RNA polymerase II promoter // infer
NM_0011		0.041			1.09	-1.22	-1.09	1.13	<b>Trim32</b>	tripartite motif-containing 32	0000209 // protein polyubiquitination // not recorded//0001894 // tissue homeostasis /

RefSeq	Tri.p	24h	p	48h	p	72h	FD Air	FD 24h	FD 48h	FD 72h	Gene Symbol	Gene Title	Gene Ontology Biological Process	
NM_008410			0.031				1.01	-1.03	-1.09	-1.03	<i>Itm2b</i>	integral membrane protein 2B	0042985 // negative regulation of amyloid precursor protein biosynthetic process // not r	
NM_0134	0.031						1.02	-1.25	-1.09	1.15	<i>Aldh1a1</i>	aldehyde dehydrogenase family 1, subfamily A1	0001822 // kidney development // inferred from electronic annotation//0001889 // live	
NM_0093	0.0117						1.17	-1.01	-1.09	1.13	<i>Inmt</i>	indolethylamine N-methyltransferase	0009308 // amine metabolic process // not recorded//0009636 // response to toxic sub:	
NM_0012	0.0371	0.027					1.10	-1.09	-1.09	-1.07	<i>Slc4a10</i>	solute carrier family 4, sodium bicarbonate cotransporter-like, member 10	0006486 // protein glycosylation // not recorded//0006810 // transport // inferred from	
NM_026602//XM_006501			0.01				-1.21	-1.08	-1.09	1.13	<i>Bcas2</i>	breast carcinoma amplified sequence 2	0000398 // mRNA splicing, via spliceosome // not recorded//0006397 // mRNA processi	
NM_017373//XM_0024			0.024				-1.53	-1.31	-1.09	-1.34	<i>Nfil3</i>	nuclear factor, interleukin 3, regulated	0000122 // negative regulation of transcription from RNA polymerase II promoter // not i	
NM_1336	0.0187						1.07	-1.18	-1.09	-1.06	<i>Ppp1r32</i>	protein phosphatase 1, regulatory subunit 32		
NM_0010	0.0204						-1.01	-1.20	-1.09	-1.03	<i>Sorbs1</i>	sorbin and SH3 domain containing 1	0006810 // transport // inferred from electronic annotation//0007015 // actin filament	
NM_0298	0.0201						-1.04	-1.19	-1.09	1.13	<i>Gppb11i</i>	GC-rich promoter binding protein 1-like 1	0006351 // transcription, DNA-templated // inferred from electronic annotation//00063	
NM_0011	0.0433						1.02	1.34	-1.09	-1.03	<i>Arhgap4</i>	Rho GTPase activating protein 4	0007165 // signal transduction // inferred from electronic annotation//0010764 // nega	
NM_0011	0.001						1.06	-1.11	-1.09	-1.06	<i>Syt3</i>	synaptotagmin III	0006906 // vesicle fusion // ---//0016079 // synaptic vesicle exocytosis // not recorded//	
NM_025402		0.042					1.01	1.06	-1.09	-1.04	<i>Ogfod3</i>	2-oxoglutarate and iron-dependent oxygenase domain containing 3	0055114 // oxidation-reduction process // inferred from electronic annotation	
							0.018	-1.02	-1.01	-1.09	<i>D4Ert4117e</i>	DNA segment, Chr 4, ERATO Doi 117, expressed		
NM_145156//XM_0014			0.014				1.05	1.12	-1.09	-1.11	<i>Slc25a28</i>	solute carrier family 25, member 28	0006810 // transport // inferred from electronic annotation//0006811 // ion transport /	
NM_0103	#####	0.003	0.027				1.08	-1.16	-1.09	-1.06	<i>H2-Ea-ps</i>	histocompatibility 2, class II antigen E alpha, pseudogene	0002376 // immune system process // inferred from electronic annotation//0002504 //	
NM_001048190//			0.029				1.10	-1.01	-1.09	-1.02	<i>Agbl5</i>	ATP/GTP binding protein-like 5	0006508 // proteolysis // inferred from electronic annotation//0035608 // protein degl	
NM_0213	#####						1.04	-1.34	-1.09	-1.14	<i>Klf13</i>	Kruppel-like factor 13	0006351 // transcription, DNA-templated // inferred from electronic annotation//00063	
NM_013809		0.044					1.10	-1.05	-1.09	-1.17	<i>Cyp2g1</i>	cytochrome P450, family 2, subfamily g, polypeptide 1	0006805 // xenobiotic metabolic process // not recorded//0019373 // epoxygenase P45	
NM_133185//XM_01124			0.009				1.03	1.13	-1.09	-1.11	<i>Rogdi</i>	rogdi homolog (Drosophila)	0007420 // brain development // not recorded//0008284 // positive regulation of cell p	
NM_0107	0.0044						1.03	1.80	-1.09	-1.03	<i>Ly6d</i>	lymphocyte antigen 6 complex, locus D	0030098 // lymphocyte differentiation // inferred from expression pattern//0035634 //	
NM_0012	0.0315	0.024	0.009				1.11	-1.00	-1.09	-1.13	<i>Pla2g10</i>	phospholipase A2, group X	0006629 // lipid metabolic process // inferred from electronic annotation//0006644 // p	
NM_0215	0.0033						-1.01	1.17	-1.09	1.12	<i>Chst12</i>	carbohydrate sulfotransferase 12	0005975 // carbohydrate metabolic process // inferred from electronic annotation//001	
NM_0010	0.0268						1.01	-1.12	-1.09	-1.03	<i>Mrpl44</i>	mitochondrial ribosomal protein L44	0006396 // RNA processing // inferred from electronic annotation//0070125 // mitocho	
NM_0013	0.0322						-1.11	-1.37	-1.09	-1.01	<i>Figf</i>	c-fos induced growth factor	0001525 // angiogenesis // inferred from electronic annotation//0001666 // response t	
NM_033320//XM_006511			0.024				-1.06	-1.07	-1.09	1.13	<i>Glce</i>	glucuronyl C5-epimerase	0006024 // glycosaminoglycan biosynthetic process // inferred from electronic annotat	
NM_001146707//			0.001	0.037			1.05	-1.06	-1.09	-1.03	<i>Gm4204//Nap11</i>	nucleosome assembly protein 1-like 1 pseudogene//nucleosome assembly protein 1-	0006334 // nucleosome assembly // inferred from electronic annotation//0014010 // Sc	
NM_175133//XM_0021			0.021				1.05	-1.02	-1.09	-1.05	<i>Gucd1</i>	guanylyl cyclase domain containing 1		
NM_0011	0.0264	0.033					1.12	-1.06	-1.09	1.21	<i>Dhrs3</i>	dehydrogenase/reductase (SDR family) member 3	0001523 // retinoid metabolic process // inferred from mutant phenotype//0003151 //	
NM_029360		0.016					1.08	1.08	-1.09	-1.03	<i>Tm4sf5</i>	transmembrane 4 superfamily member 5		
NM_0294	0.0042						-1.07	-1.37	-1.09	-1.09	<i>Them4</i>	thioesterase superfamily member 4	0006629 // lipid metabolic process // inferred from electronic annotation//0006631 // f.	
NM_0261	0.0326						1.07	-1.13	-1.09	-1.11	<i>Ppp1r2-ps9</i>	protein phosphatase 1, regulatory (inhibitor) subunit 2, pseudogene 9		
NM_0080	0.0073						1.01	-1.29	-1.09	-1.08	<i>Gata2</i>	GATA binding protein 2	0000122 // negative regulation of transcription from RNA polymerase II promoter // infer	
NM_0187	0.005						-1.04	-1.42	-1.09	1.08	<i>Cpq</i>	carboxypeptidase Q	0006508 // proteolysis // not recorded//0006590 // thyroid hormone generation // not	
NM_001025599//			0.011	0.041			1.07	-1.01	-1.09	-1.03	<i>Trim26</i>	tripartite motif-containing 26	0045087 // innate immune response // not recorded//0046597 // negative regulation of	
NM_010791		0.008					-1.01	-1.02	-1.09	-1.17	<i>Meox1</i>	mesenchyme homeobox 1	0001757 // somite specification // inferred from genetic interaction//0006351 // transcr	
NM_011246		0.014					1.03	-1.01	-1.09	-1.13	<i>Rasgrp1</i>	RAS guanyl releasing protein 1	0001816 // cytokine production // inferred from mutant phenotype//0001934 // positiv	
NM_025974//NR_110499			0.028				-1.07	-1.02	-1.09	-1.12	<i>Rpl14//Rpl14-ps1</i>	ribosomal protein L14//ribosomal protein L14, pseudogene 1	0006364 // rRNA processing // not recorded//0006412 // translation // inferred from el	
NM_0010	0.0076						0.038	1.11	-1.06	-1.09	1.01	<i>Mink1</i>	missshapen-like kinase 1 (zebrafish)	0000165 // MAPK cascade // not recorded//0001952 // regulation of cell-matrix adhesi
NM_0012	0.0372						1.06	-1.06	-1.09	-1.21	<i>Dtx2</i>	deltex 2 homolog (Drosophila)	0007219 // Notch signaling pathway // inferred from direct assay//0007219 // Notch sig	
NM_0113	0.0122						1.06	1.41	-1.09	-1.30	<i>Spi1</i>	spleen focus forming virus (SFFV) proviral integration oncogene	0000122 // negative regulation of transcription from RNA polymerase II promoter // infer	
NM_0012	0.001						1.04	1.52	-1.08	1.04	<i>Lrmp</i>	lymphoid-restricted membrane protein	0002376 // immune system process // inferred from electronic annotation//0007338 //	
NM_177242		0.043					1.04	-1.08	-1.08	1.00	<i>Pptc7</i>	PTC7 protein phosphatase homolog (S. cerevisiae)	0006470 // protein dephosphorylation // inferred from electronic annotation//0008152	
NM_0106	0.0204						1.00	1.25	-1.08	1.02	<i>Lcp2</i>	lymphocyte cytosolic protein 2	0006955 // immune response // not recorded//0007169 // transmembrane receptor pr	
NM_0117	0.0275						-1.11	-1.00	-1.08	-1.16	<i>Xcr1</i>	chemokine (C motif) receptor 1	0006935 // chemotaxis // inferred from direct assay//0007165 // signal transduction // i	
NM_008763		0.045					-1.08	-1.20	-1.08	-1.01	<i>Olfr16</i>	olfactory receptor 16	0007165 // signal transduction // inferred from electronic annotation//0007186 // G-pr	
NM_0010	0.0154						1.08	-1.13	-1.08	-1.05	<i>Lgr6</i>	leucine-rich repeat-containing G protein-coupled receptor 6	0007165 // signal transduction // inferred from electronic annotation//0007186 // G-pr	
NM_031379		0.038					1.03	-1.04	-1.08	-1.15	<i>Tktl1</i>	transketolase-like 1	0008152 // metabolic process // inferred from electronic annotation	
NM_016875//XM_0033			0.033				1.11	1.02	-1.08	-1.12	<i>Ybx2</i>	Y box protein 2	0006355 // regulation of transcription, DNA-templated // inferred from electronic annot	
NM_008911//XM_0037			0.037				1.08	1.04	-1.08	-1.00	<i>Ppox</i>	protoporphyrinogen oxidase	0006779 // porphyrin-containing compound biosynthetic process // not recorded//0006	
NM_009314		0.033					1.03	-1.03	-1.08	-1.11	<i>Tacr2</i>	tachykinin receptor 2	0007165 // signal transduction // inferred from electronic annotation//0007166 // cell s	
NM_0084	0.0474						-1.08	1.02	-1.08	-1.12	<i>Krt4</i>	keratin 4	0007010 // cytoskeleton organization // not recorded//0009790 // embryo developmen	
NM_0217	0.0358						1.06	1.23	-1.08	1.15	<i>Myg1</i>	melanocyte proliferating gene 1	0035641 // locomotory exploration behavior // inferred from mutant phenotype	
NM_001177773//NM_0017			0.017				-1.14	-1.20	-1.08	-1.05	<i>Fbxw7</i>	F-box and WD-40 domain protein 7	0001570 // vasculogenesis // inferred from mutant phenotype//0001944 // vasculature	
NM_0274	0.0232						1.03	-1.19	-1.08	1.12	<i>Zcchc8</i>	zinc finger, CCHC domain containing 8	0006397 // mRNA processing // inferred from electronic annotation//0008380 // RNA s	
NM_1489	0.0441						-1.06	1.02	-1.08	-1.21	<i>Usp9y</i>	ubiquitin specific peptidase 9, Y chromosome	0006508 // proteolysis // inferred from electronic annotation//0006511 // ubiquitin-dep	
NM_0011	0.0171						-1.00	1.10	-1.08	-1.12	<i>Ppfia4</i>	protein tyrosine phosphatase, receptor type, f polypeptide (PTPRF), interacting protein	(liprin), alpha 4	
NM_001113408//			0.028				1.34	1.32	-1.08	1.13	<i>Ldb1</i>	LIM domain binding 1	0000972 // transcription-dependent tethering of RNA polymerase II gene DNA at nuclear	
NM_030890//XM_006524			0.003				1.03	-1.06	-1.08	-1.14	<i>Prrt1</i>	proline-rich transmembrane protein 1	0009607 // response to biotic stimulus // inferred from electronic annotation	
NM_0269	0.0273						1.05	-1.03	-1.08	1.00	<i>Snx15</i>	sorting nexin 15	0006810 // transport // inferred from electronic annotation//0007165 // signal transduc	
NM_001316710//NM_01			0.039				1.01	-1.01	-1.08	-1.16	<i>Gprin1</i>	G protein-regulated inducer of neurite outgrowth 1	0031175 // neuron projection development // inferred from direct assay	
NM_001276298//NM_00			0.007				1.10	1.01	-1.08	-1.15	<i>Avpr2</i>	arginine vasopressin receptor 2	0001992 // regulation of systemic arterial blood pressure by vasopressin // not recorded//	
NM_0285	0.0428						-1.09	1.02	-1.08	-1.26	<i>1700080E11Rik</i>	RIKEN cDNA 1700080E11 gene	0008152 // metabolic process // inferred from electronic annotation	
NM_001272024//NM_01	#####						1.03	1.01	-1.08	-1.17	<i>Sema6c</i>	sema domain, transmembrane domain (TM), and cytoplasmic domain, (semaphorin) 6	0001755 // neural crest cell migration // not recorded//0007275 // multicellular organis	
NM_0110	0.0235						-1.09	1.07	-1.08	-1.13	<i>Otp</i>	orthopedia homolog (Drosophila)	0002052 // positive regulation of neuroblast proliferation // inferred from mutant pheno	

RefSeq	Tri	p 24h	p 48h	p 72h	FD Air	FD 24h	FD 48h	FD 72h	Gene Symbol	Gene Title	Gene Ontology Biological Process
NM_0012		0.0115			1.08	-1.26	-1.08	1.07	<i>Bcl2l1</i>	BCL2-like 1	0000910 // cytokinesis // not recorded//0001541 // ovarian follicle development // infer
NM_0087		0.0499			1.05	-1.41	-1.08	1.01	<i>Ogn</i>	osteoglycin	0018146 // keratan sulfate biosynthetic process // not recorded//0035385 // Roundab
NM_0195		0.0176		0.022	1.10	-1.08	-1.08	-1.16	<i>Plac1</i>	placental specific protein 1	0001890 // placenta development // inferred from expression pattern//0001890 // plac
NM_0011		0.0024			1.21	-1.06	-1.08	1.10	<i>Ngef</i>	neuronal guanine nucleotide exchange factor	0007275 // multicellular organismal development // inferred from electronic annotation/
NM_0013		0.0485	0.041		1.02	-1.08	-1.08	-1.06	<i>Rab7b</i>	RAB7B, member RAS oncogene family	0006810 // transport // inferred from electronic annotation//0006886 // intracellular pr
NM_145746	///XM_00653		0.017		1.10	-1.02	-1.08	-1.10	<i>Odf4</i>	outer dense fiber of sperm tails 4	0007275 // multicellular organismal development // inferred from electronic annotation/
NM_001293630	///	0.014			1.13	1.08	-1.08	-1.01	<i>Slc37a4</i>	solute carrier family 37 (glucose-6-phosphate transporter), member 4	0001780 // neutrophil homeostasis // inferred from mutant phenotype//0001816 // cyt
NM_0012		0.0032			1.11	1.58	-1.08	1.02	<i>Cd37</i>	CD37 antigen	0002639 // positive regulation of immunoglobulin production // inferred from mutant ph
NM_0010	#####				-1.02	-1.40	-1.08	1.12	<i>Fam178a</i>	family with sequence similarity 178, member A	0006281 // DNA repair // inferred from electronic annotation//0006974 // cellular resp
NM_001267625	///NM_00		0.018		1.05	-1.02	-1.08	-1.17	<i>Dpf3</i>	D4, zinc and double PHD fingers, family 3	0002230 // positive regulation of defense response to virus by host // not recorded//000
NM_0202		0.0171			1.06	-1.14	-1.08	-1.18	<i>Klk1b27</i>	kallikrein 1-related peptidase b27	0002526 // acute inflammatory response // ---//0003073 // regulation of systemic arteri
NM_023910	///NM		0.005		1.14	1.15	-1.08	-1.24	<i>Tsc22d4</i>	TSC22 domain family, member 4	0006351 // transcription, DNA-templated // inferred from electronic annotation//00063
NM_0105		0.0483			-1.03	1.29	-1.08	1.28	<i>Ifit3</i>	interferon-induced protein with tetratricopeptide repeats 3	0002376 // immune system process // inferred from electronic annotation//0008285 //
NM_1462		0.0251			1.04	-1.26	-1.08	1.04	<i>Wdr78</i>	WD repeat domain 78	0002244 // hematopoietic progenitor cell differentiation // inferred from mutant phenoty
NM_0012		0.0271			-1.08	1.04	-1.08	-1.26	<i>Wnk2</i>	WNK lysine deficient protein kinase 2	0006468 // protein phosphorylation // inferred from direct assay//0006468 // protein p
NM_026780		0.045			1.04	-1.03	-1.08	1.17	<i>Syf2</i>	SYF2 homolog, RNA splicing factor (S. cerevisiae)	0000398 // mRNA splicing, via spliceosome // not recorded//0001701 // in utero embry
NM_0231		0.0062			1.03	-1.10	-1.08	-1.12	<i>Ctrl</i>	chymotrypsin-like	0006508 // proteolysis // inferred from direct assay//0006508 // proteolysis // not recor
		0.021			1.19	1.04	-1.08	1.02	<i>D12Ert123e</i>	DNA segment, Chr 12, ERATO Doi 123, expressed	
NM_013730	///XM_00649		0.026		1.06	1.09	-1.08	-1.14	<i>Slamf1</i>	signaling lymphocytic activation molecule family member 1	0001778 // natural killer cell differentiation // inferred from mutant phenotype//00017
NM_028953	///XM_00652		0.048		1.03	-1.02	-1.08	-1.17	<i>Tmc1</i>	transmembrane channel-like gene family 1	0006810 // transport // inferred from electronic annotation//0006811 // ion transport /
NM_013651	///XM		0.047		1.13	1.07	-1.08	-1.12	<i>Sf3a2</i>	splicing factor 3a, subunit 2	0002245 // spliceosome complex assembly // not recorded//0000375 // RNA splicing, v
NM_0119		0.0361	0.009		1.12	-1.05	-1.08	-1.14	<i>Sema4g</i>	sema domain, immunoglobulin domain (Ig), transmembrane domain (TM) and short cy	0001755 // neural crest cell migration // not recorded//0007275 // multicellular organis
NM_019975	///XM		0.035		1.04	-1.02	-1.08	-1.06	<i>Hact1</i> ///Colg	2-hydroxyacyl-CoA lyase 1//collagen-like tail subunit (single strand of homotrimer) of	0001561 // fatty acid alpha-oxidation // not recorded//0006629 // lipid metabolic proce
NM_0120		0.0378			1.10	-1.14	-1.08	-1.11	<i>Ppnr</i>	per-pentamer repeat gene	
NM_0010		0.0255			-1.01	1.35	-1.08	-1.10	<i>Hvcn1</i>	hydrogen voltage-gated channel 1	0006810 // transport // inferred from electronic annotation//0006811 // ion transport /
NM_1531		0.009			1.03	-1.10	-1.08	1.10	<i>Svil</i>	supervillin	0007010 // cytoskeleton organization // inferred from electronic annotation//0007519 /
NM_007745			0.038		1.03	1.05	-1.08	-1.15	<i>Cort</i>	cortistatin	0007193 // adenylate cyclase-inhibiting G-protein coupled receptor signaling pathway //
NM_008429	///XM_00649		0.049		1.07	-1.02	-1.08	-1.22	<i>Kcnj9</i>	potassium inwardly-rectifying channel, subfamily J, member 9	0006810 // transport // inferred from electronic annotation//0006811 // ion transport /
NM_029938		0.028			1.09	1.01	-1.08	-1.10	<i>H2afv</i>	H2A histone family, member V	0006325 // chromatin organization // not recorded//0006342 // chromatin silencing // i
NM_001037940	///	0.018			1.05	-1.06	-1.08	1.05	<i>Dnajb6</i>	Dnaj (Hsp40) homolog, subfamily B, member 6	0006457 // protein folding // not recorded//0030036 // actin cytoskeleton organization
NM_001289507	///NM_00		0.029		-1.02	-1.04	-1.08	-1.24	<i>Tjr2</i>	transferin receptor 2	0006879 // cellular iron ion homeostasis // traceable author statement//0006898 // rec
NM_0266		0.0033	0.039		1.04	-1.15	-1.08	1.02	<i>Rbm28</i>	RNA binding motif protein 28	0006397 // mRNA processing // inferred from electronic annotation//0008380 // RNA sp
NM_011134	///XM		0.022		1.12	-1.05	-1.08	1.29	<i>Pon1</i>	paraoxonase 1	0006470 // protein dephosphorylation // ---//0006470 // protein dephosphorylation // i
NM_025595		0.047	0.042		1.04	-1.00	-1.08	-1.08	<i>Mrp151</i>	mitochondrial ribosomal protein L51	0006412 // translation // inferred from direct assay//0032543 // mitochondrial translati
NM_144919	///XM		0.014		1.11	1.07	-1.08	-1.02	<i>Hdac11</i>	histone deacetylase 11	0006351 // transcription, DNA-templated // inferred from electronic annotation//00063
NM_015809		0.041			1.06	1.00	-1.08	-1.10	<i>Krtap5-4</i>	keratin associated protein 5-4	
NM_010030			0.005		1.02	-1.02	-1.08	-1.21	<i>Defb2</i>	defensin beta 2	0006952 // defense response // inferred from electronic annotation//0042742 // defens
NM_001164607	///	0.034			1.04	1.07	-1.08	-1.10	<i>Maf1</i>	MAF1 homolog (S. cerevisiae)	0006351 // transcription, DNA-templated // inferred from electronic annotation//00063
NM_0093		0.0466			-1.05	-1.48	-1.08	1.04	<i>Thbd</i>	thrombomodulin	0007165 // signal transduction // inferred from electronic annotation//0007565 // fema
NM_145479	///XM		0.02		1.03	-1.05	-1.08	-1.07	<i>Klhl22</i>	kelch-like 22	0000070 // mitotic sister chromatid segregation // not recorded//0006513 // protein m
NM_001278581	///NM_00		0.038		1.06	1.07	-1.08	-1.13	<i>Pomc</i>	pro-opiomelanocortin-alpha	0006091 // generation of precursor metabolites and energy // not recorded//0007165 /
NM_019663	///XM		0.023		1.11	-1.01	-1.08	1.16	<i>Pias1</i>	protein inhibitor of activated STAT 1	0000082 // G1/S transition of mitotic cell cycle // not recorded//0000122 // negative re
NM_148953			0.019		1.03	-1.01	-1.07	-1.14	<i>Asb16</i>	ankyrin repeat and SOCS box-containing 16	0016567 // protein ubiquitination // inferred from electronic annotation//0035556 // in
NM_0011		0.0428			1.09	-1.07	-1.07	-1.10	<i>Dctn1</i>	dynactin 1	0006810 // transport // inferred from electronic annotation//0008152 // metabolic pro
NM_019701	///XM_00653		0.04		-1.01	1.03	-1.07	-1.20	<i>Clnkb</i>	chloride channel, voltage-sensitive Kb	0006810 // transport // inferred from electronic annotation//0006811 // ion transport /
NM_145564	///XM		0.008	0.046	1.12	1.03	-1.07	-1.03	<i>Fbxo21</i>	F-box protein 21	
NM_001013360	///	0.014			1.02	-1.01	-1.07	-1.10	<i>Npcd</i> ///Nptxr	neuronal pentraxin chromo domain//neuronal pentraxin receptor	0000122 // negative regulation of transcription from RNA polymerase II promoter // infer
NM_009620			0.038		1.05	1.00	-1.07	-1.06	<i>Adam4</i>	a disintegrin and metallopeptidase domain 4	0006508 // proteolysis // inferred from electronic annotation//0007229 // integrin-med
NM_001040136	///NM_00		0.049		-1.01	-1.02	-1.07	-1.16	<i>Pdzd9</i>	PDZ domain containing 9	
XM_9935		0.0102			1.07	1.20	-1.07	-1.16	<i>LOC672450</i> ///Ilgk-V21	V(kappa) gene product//immunoglobulin kappa chain variable 21 (V21)//immunogl	0006898 // receptor-mediated endocytosis // not recorded//0006910 // phagocytosis, r
NM_009438	///NM_01352		0.047		-1.01	1.04	-1.07	-1.05	<i>Rpl13a</i> ///Ftl3	ribosomal protein L13A//FMS-like tyrosine kinase 3 ligand//60S ribosomal protein L1	0006412 // translation // inferred from electronic annotation//0006417 // regulation of
NM_025414	///XM_00653		0.013		-1.09	-1.04	-1.07	1.05	<i>Myo19</i>	myosin XIX	0008152 // metabolic process // inferred from electronic annotation//0034642 // mitoc
NM_001159520	///NM_00		0.002		-1.00	-1.03	-1.07	-1.18	<i>Pax3</i>	paired box 3	0000122 // negative regulation of transcription from RNA polymerase II promoter // infer
NM_0264		0.0431			-1.16	-1.07	-1.07	-1.14	<i>Mtjp1</i>	mitochondrial fission process 1	0000266 // mitochondrial fission // not recorded//0006915 // apoptotic process // infer
NM_134000	///XM		0.005	0.004	1.10	1.11	-1.07	-1.08	<i>Traf3ip2</i>	TRAF3 interacting protein 2	0001783 // B cell apoptotic process // inferred from mutant phenotype//0002230 // po
NM_0265		0.0233			1.16	-1.06	-1.07	-1.09	<i>Bambi</i>	BMP and activin membrane-bound inhibitor	0007179 // transforming growth factor beta receptor signaling pathway // not recorded,
NM_0120		0.0346			-1.04	1.08	-1.07	-1.14	<i>Pla2g2e</i>	phospholipase A2, group IIE	0006629 // lipid metabolic process // inferred from electronic annotation//0006644 // p
NM_001166642	///	0.042			1.10	-1.01	-1.07	-1.01	<i>Bcas3</i>	breast carcinoma amplified sequence 3	0001525 // angiogenesis // inferred from electronic annotation//0006351 // transcrip
NM_0011		0.034			1.02	-1.05	-1.07	-1.04	<i>Prph</i>	peripherin	0045104 // intermediate filament cytoskeleton organization // inferred from direct assay,
NM_1308		0.0147	0.002		1.05	-1.03	-1.07	-1.06	<i>Nxph3</i>	neurexophilin 3	
NM_0012		0.0273			1.03	-1.14	-1.07	-1.02	<i>Pbx1</i>	pre B cell leukemia homeobox 1	0001655 // urogenital system development // inferred from mutant phenotype//00016
NM_1341		0.0311		0.048	-1.05	1.15	-1.07	1.07	<i>Pla1a</i>	phospholipase A1 member A	0006629 // lipid metabolic process // inferred from electronic annotation//0016042 // li
NM_001289729	///NM_13		0.028		-1.01	-1.14	-1.07	-1.16	<i>Xpnpep2</i>	X-prolyl aminopeptidase (aminopeptidase P) 2, membrane-bound	0006508 // proteolysis // inferred from electronic annotation//0008152 // metabolic pr
NM_0010		0.0472			1.05	-1.05	-1.07	-1.24	<i>Cdc102a</i>	coiled-coil domain containing 102A	0008152 // metabolic process // inferred from electronic annotation

RefSeq	Tri	p 24h	p 48h	p 72h	FD Air	FD 24h	FD 48h	FD 72h	Gene Symbol	Gene Title	Gene Ontology Biological Process
NM_023697	///XM	0.025			1.03	-1.06	-1.07	-1.09	<b>Rdh14</b>	retinol dehydrogenase 14 (all-trans and 9-cis)	0001649 // osteoblast differentiation // not recorded///0008152 // metabolic process //
NM_0113	0.0314				1.06	-1.15	-1.07	1.26	<b>Scnn1a</b>	sodium channel, nonvoltage-gated 1 alpha	0006810 // transport // inferred from electronic annotation///0006811 // ion transport //
NM_145940		0.044			1.02	-1.03	-1.07	1.02	<b>Wipi1</b>	WD repeat domain, phosphoinositide interacting 1	0000045 // autophagosome assembly // not recorded///0000422 // mitophagy // not rec
NM_029624	///NR_045520	0.031			-1.03	1.03	-1.07	1.13	<b>Lmf1</b>	lipase maturation factor 1	0006888 // ER to Golgi vesicle-mediated transport // inferred from mutant phenotype///
NM_0011	0.0117				-1.01	1.09	-1.07	-1.12	<b>Dbn1</b>	drebrin 1	0007015 // actin filament organization // inferred from direct assay///0007275 // multic
NM_0011	0.0487				-1.03	-1.32	-1.07	1.06	<b>Lpin1</b>	lipin 1	0000122 // negative regulation of transcription from RNA polymerase II promoter // infer
NM_138655		0.043			1.02	-1.01	-1.07	-1.12	<b>Tmc2</b>	transmembrane channel-like gene family 2	0006810 // transport // inferred from electronic annotation///0006811 // ion transport //
NM_144523		0.02			-1.01	-1.03	-1.07	-1.22	<b>Zfp622</b>	zinc finger protein 622	0008631 // intrinsic apoptotic signaling pathway in response to oxidative stress // not rec
NM_148938			0.031		1.08	-1.04	-1.07	1.04	<b>Slc1a3</b>	solute carrier family 1 (glial high affinity glutamate transporter), member 3	0002230 // positive regulation of defense response to virus by host // not recorded///000
NM_1455	0.0162	0.009			1.03	-1.21	-1.07	1.03	<b>Tmem159</b>	transmembrane protein 159	
NM_0111	0.0488				-1.03	1.27	-1.07	-1.04	<b>Pstpip1</b>	proline-serine-threonine phosphatase-interacting protein 1	0000910 // cytokinesis // inferred by curator///0002376 // immune system process // inf
NM_008803		0.009			1.11	-1.06	-1.07	1.11	<b>Pde8a</b>	phosphodiesterase 8A	0006198 // cAMP catabolic process // inferred from electronic annotation///0006355 // i
NM_0088	0.0328				1.11	-1.06	-1.07	1.11	<b>Pde8a</b>	phosphodiesterase 8A	0006198 // cAMP catabolic process // inferred from electronic annotation///0006355 // i
NM_0294	0.0159				-1.05	1.09	-1.07	-1.03	<b>Epsti1</b>	epithelial stromal interaction 1 (breast)	
NM_1528	0.025	0.003			1.11	-1.04	-1.07	1.05	<b>Ccdc137</b>	coiled-coil domain containing 137	
NM_0168	0.0478				-1.12	1.03	-1.07	-1.14	<b>Avpr1a</b>	arginine vasopressin receptor 1A	0001992 // regulation of systemic arterial blood pressure by vasopressin // inferred from
NM_011973	///XM_006515	0.018			1.03	1.03	-1.07	-1.12	<b>Mok</b>	MOK protein kinase	0006468 // protein phosphorylation // inferred from electronic annotation///0016310 //
NM_024230	///XM_006500	0.04			1.06	-1.08	-1.07	-1.23	<b>Smtnl1</b>	smoothelin-like 1	0014823 // response to activity // inferred from mutant phenotype///0018105 // peptid
NM_0013	0.0339				-1.03	-1.18	-1.07	1.15	<b>Nek7</b>	NIMA (never in mitosis gene a)-related expressed kinase 7	0006468 // protein phosphorylation // not recorded///0016310 // phosphorylation // inf
NM_0299	0.0435				-1.08	-1.02	-1.07	-1.10	<b>Sla2</b>	Src-like-adapter 2	0000122 // negative regulation of transcription from RNA polymerase II promoter // not r
NM_0198	0.0114				-1.03	1.20	-1.07	1.03	<b>Gsk3b</b>	glycogen synthase kinase 3 beta	0000320 // re-entry into mitotic cell cycle // inferred from direct assay///0001837 // epit
NM_001130419	///	0.022	0.003		1.15	-1.03	-1.07	-1.24	<b>Hpca</b>	hippocalcin	0007420 // brain development // inferred from electronic annotation///0010518 // posit
NM_007811			0.014		-1.04	1.01	-1.07	-1.24	<b>Cyp26a1</b>	cytochrome P450, family 26, subfamily a, polypeptide 1	0007417 // central nervous system development // inferred from genetic interaction///0
NM_008899		0.047			1.04	-1.03	-1.07	-1.07	<b>Pou3f2</b>	POU domain, class 3, transcription factor 2	0006351 // transcription, DNA-templated // inferred from electronic annotation///00063
NM_030714	///XM	0.045			1.15	1.02	-1.07	1.22	<b>Dtx3</b>	deltex 3 homolog (Drosophila)	0007219 // Notch signaling pathway // inferred from direct assay///0007219 // Notch sig
NM_0220	#####				-1.01	1.14	-1.07	1.05	<b>Dusp10</b>	dual specificity phosphatase 10	0000188 // inactivation of MAPK activity // not recorded///0002819 // regulation of ada
NM_0264	0.0339				-1.05	1.07	-1.07	-1.01	<b>Coq9</b>	coenzyme Q9 homolog (yeast)	0006120 // mitochondrial electron transport, NADH to ubiquinone // inferred from muta
NM_1789	0.0449				-1.04	-1.36	-1.07	1.05	<b>Mal2</b>	mal, T cell differentiation protein 2	
NM_1813	0.0082		0.021		1.09	-1.10	-1.07	-1.15	<b>Cwh43</b>	cell wall biogenesis 43 C-terminal homolog (S. cerevisiae)	0006506 // GPI anchor biosynthetic process // inferred from electronic annotation
NM_1980	#####				1.04	-1.08	-1.07	-1.15	<b>Tnrc6c</b>	trinucleotide repeat containing 6C	0001706 // endoderm formation // inferred from mutant phenotype///0006417 // regula
NM_001313928	///NM_00	0.009			-1.02	1.01	-1.07	-1.15	<b>Crrh1</b>	corticotropin releasing hormone receptor 1	0001666 // response to hypoxia // not recorded///0007165 // signal transduction // infer
NM_0260	0.0489				1.01	-1.12	-1.07	-1.02	<b>Gemin6</b>	gem (nuclear organelle) associated protein 6	0000245 // spliceosomal complex assembly // inferred from electronic annotation///000
NM_144867	///XM_006525	0.038			-1.03	-1.03	-1.07	-1.14	<b>Simo1</b>	slowmo homolog 1 (Drosophila)	0015914 // phospholipid transport // not recorded///1903955 // positive regulation of pi
NM_033146	///XM	0.007	0.024		1.16	1.11	-1.07	-1.21	<b>Emc9</b>	ER membrane protein complex subunit 9	
NM_0085	0.0453				-1.01	1.06	-1.07	-1.19	<b>Mageb1</b> /// <b>Mage2</b> /// <b>Mageb3</b>	melanoma antigen, family B, 1///melanoma antigen, family B, 2///melanoma antigen, family B, 3	0006750 // glutathione biosynthetic process // inferred from electronic annotation///001
NM_001039509	///NM_01	0.007			1.06	-1.11	-1.07	-1.12	<b>Pnk4</b>	paroxysmal nonkinesinogenic dyskinesia	0001889 // liver development // inferred from electronic annotation///0006139 // nuclei
NM_0011	0.0471		0.023		1.03	-1.07	-1.07	-1.13	<b>Ak4</b>	adenylate kinase 4	0006464 // cellular protein modification process // inferred from electronic annotation///
NM_0116	0.0261				-1.04	-1.11	-1.07	-1.06	<b>Uba1y</b>	ubiquitin-activating enzyme, Chr Y	0006006 // glucose metabolic process // inferred from electronic annotation///0006915
NM_0226	0.0035	0.008			1.06	-1.09	-1.07	-1.08	<b>Nisch</b>	nischarin	0098734 // macromolecule depalmitoylation // not recorded
NM_001302393	///	0.039			1.04	-1.02	-1.07	1.02	<b>Ppt2</b>	palmitoyl-protein thioesterase 2	0007017 // microtubule-based process // inferred from physical interaction///0008104 //
NM_0013	0.0275				1.02	-1.11	-1.07	1.05	<b>Kifap3</b>	kinesin-associated protein 3	0007155 // cell adhesion // inferred from electronic annotation///0032225 // regulati
NM_1304	0.0145				1.05	-1.14	-1.07	-1.06	<b>Cntnap4</b>	contactin associated protein-like 4	0001782 // B cell homeostasis // inferred from mutant phenotype///0002250 // adaptiv
NM_0010	0.0119				-1.06	1.10	-1.07	-1.10	<b>Pik3cd</b>	phosphatidylinositol 3-kinase catalytic delta polypeptide	0007275 // multicellular organismal development // inferred from electronic annotation/
NM_007792		0.02			-1.02	-1.12	-1.06	1.10	<b>Csrp2</b>	cysteine and glycine-rich protein 2	0001774 // microglial cell activation // not recorded///0002052 // positive regulation of r
NM_0099	0.032				-1.03	1.15	-1.06	-1.04	<b>Cx3cr1</b>	chemokine (C-X3-C motif) receptor 1	1902042 // negative regulation of extrinsic apoptotic signaling pathway via death domain
NM_0013	0.0033				1.02	-1.15	-1.06	1.01	<b>Tnfrsf23</b>	tumor necrosis factor receptor superfamily, member 23	0006120 // mitochondrial electron transport, NADH to ubiquinone // inferred from electr
NM_0242	0.035				1.02	-1.07	-1.06	1.05	<b>LOC102641347</b> /// <b>Ndufc2</b>	NADH dehydrogenase [ubiquinone] 1 subunit C2///NADH dehydrogenase (ubiquinone	0007031 // peroxisome organization // not recorded///0007165 // signal transduction //
NM_0110	0.0314				-1.00	-1.31	-1.06	1.02	<b>Pex11a</b>	peroxisomal biogenesis factor 11 alpha	1901386 // negative regulation of voltage-gated calcium channel activity // not recorded
NM_0011	0.0477				1.17	-1.00	-1.06	-1.02	<b>Charp</b>	calcium channel, voltage-dependent, beta subunit associated regulatory protein	0001207 // histone displacement // inferred from mutant phenotype///0006338 // chr
NM_0010	0.0339				-1.05	1.12	-1.06	-1.10	<b>Brdt</b>	bromodomain, testis-specific	0006629 // lipid metabolic process // inferred from electronic annotation///0006694 // s
NM_0532	0.01	0.008			1.13	-1.02	-1.06	1.12	<b>Hsd17b11</b>	hydroxysteroid (17-beta) dehydrogenase 11	
NM_023816	///XM_006514	0.045			1.09	-1.04	-1.06	-1.11	<b>Ankrd36</b>	ankyrin repeat domain 36	0006810 // transport // inferred from electronic annotation///0007165 // signal transdu
NM_0010	0.0251	0.04			1.07	-1.14	-1.06	1.02	<b>Agap1</b>	ArfGAP with GTPase domain, ankyrin repeat and PH domain 1	0006952 // defense response // inferred from electronic annotation
NM_0011	0.021	0.045			1.35	-1.10	-1.06	-1.13	<b>Ankrd33b</b>	ankyrin repeat domain 33B	0002244 // hematopoietic progenitor cell differentiation // inferred from genetic interact
NM_007845		0.034			-1.05	1.02	-1.06	-1.10	<b>Defa-rs10</b>	defensin, alpha, related sequence 10	0006468 // protein phosphorylation // not recorded///0019835 // cytolysis // inferred fr
NM_001146021	///NM_02	0.016			1.02	1.03	-1.06	-1.22	<b>Lrrc18</b>	leucine rich repeat containing 18	0007017 // microtubule-based process // inferred from electronic annotation///0008152
NM_0012	0.0427				-1.08	1.05	-1.06	-1.14	<b>Kcnab2</b>	potassium voltage-gated channel, shaker-related subfamily, beta member 2	0002244 // hematopoietic progenitor cell differentiation // inferred from genetic interact
NM_175217	///XM_006504	0.032			1.03	-1.09	-1.06	-1.18	<b>Mmd2</b>	monocyte to macrophage differentiation-associated 2	0006468 // protein phosphorylation // not recorded///0019835 // cytolysis // inferred fr
NM_0013	0.0433				-1.17	1.05	-1.06	-1.05	<b>Tuba4a</b>	tubulin, alpha 4A	0007017 // microtubule-based process // inferred from electronic annotation///0008152
NM_028658		0.03	0.031		1.02	-1.06	-1.06	-1.06	<b>Ppp1r21</b>	protein phosphatase 1, regulatory subunit 21	0000165 // MAPK cascade // inferred from electronic annotation///0000186 // activator
NM_1456	0.0285				-1.04	-1.11	-1.06	-1.15	<b>BC021891</b>	cDNA sequence BC021891	
NM_144872	///XM	0.019			1.19	1.39	-1.06	1.26	<b>Eml3</b>	echinoderm microtubule associated protein like 3	0006749 // glutathione metabolic process // not recorded///0008152 // metabolic proce
NM_0103	0.0226				1.00	-1.08	-1.06	1.22	<b>Gstm1</b>	glutathione S-transferase, mu 1	0000060 // protein import into nucleus, translocation // inferred from direct assay///000
NM_0109	0.0336	0.043			1.08	-1.15	-1.06	-1.17	<b>Nfkbia</b>	nuclear factor of kappa light polypeptide gene enhancer in B cells inhibitor, alpha	

RefSeq	Tri	p 24h	p 48h	p 72h	FD Air	FD 24h	FD 48h	FD 72h	Gene Symbol	Gene Title	Gene Ontology Biological Process
NM_013811	///XM	0.017			1.14	1.05	-1.06	-1.04	<i>Dnah8</i>	dynein, axonemal, heavy chain 8	0007018 // microtubule-based movement // inferred from electronic annotation//0008:
NM_0010	0.0207				1.09	-1.14	-1.06	-1.08	<i>Car1</i>	carbonic anhydrase 1	0006730 // one-carbon metabolic process // inferred from electronic annotation
NM_0198	0.0223				1.01	-1.13	-1.06	-1.18	<i>Copz2</i>	coatomer protein complex, subunit zeta 2	0006810 // transport // inferred from electronic annotation//0015031 // protein transp
NM_0089	0.0155				1.03	-1.25	-1.06	1.33	<i>Ptrf</i>	polymerase I and transcript release factor	0006351 // transcription, DNA-templated // inferred from electronic annotation//00063
NM_1340	0.0023				1.09	-1.14	-1.06	-1.04	<i>Chmp7</i>	charged multivesicular body protein 7	0000920 // cell separation after cytokinesis // not recorded//0006810 // transport // inf
NM_0158	0.0157				1.04	-1.15	-1.06	-1.11	<i>Capn15</i>	calpain 15	0006508 // proteolysis // not recorded
NM_0013	0.0351				1.07	-1.15	-1.06	-1.04	<i>Zfp423</i>	zinc finger protein 423	0006351 // transcription, DNA-templated // inferred from electronic annotation//00063
NM_001033499	///	0.015			1.06	1.09	-1.06	1.07	<i>Sh2d1b1///Sh2d1b2</i>	SH2 domain containing 1B1//SH2 domain containing 1B2	0002366 // leukocyte activation involved in immune response // inferred from direct ass
NM_009855	///XM	0.0652	0.015		-1.05	-1.05	-1.06	-1.22	<i>Cd80</i>	CD80 antigen	0031295 // T cell costimulation // inferred from direct assay//0042102 // positive regula
NM_0013	0.0459				1.09	-1.05	-1.06	-1.03	<i>Slc27a3</i>	solute carrier family 27 (fatty acid transporter), member 3	0001676 // long-chain fatty acid metabolic process // traceable author statement//0006
NM_0220	0.0354				-1.08	1.05	-1.06	-1.09	<i>Ube4b</i>	ubiquitination factor E4B	0000209 // protein polyubiquitination // inferred from direct assay//0000209 // protein
NM_0282	0.0261	0.027			1.08	-1.06	-1.06	1.07	<i>Sgol1</i>	shugoshin-like 1 (S. pombe)	0007049 // cell cycle // inferred from electronic annotation//0007059 // chromosome s
NM_0011	0.0479				1.03	-1.08	-1.06	-1.12	<i>Smax</i>	spermine oxidase	0006598 // polyamine catabolic process // not recorded//0046208 // spermine cataboli
NM_013774	///XM	0.0651	0.036		1.05	1.01	-1.06	-1.05	<i>Tcl1b4</i>	T cell leukemia/lymphoma 1B, 4	
NM_030262	///XR	380457	0.046		-1.13	-1.12	-1.06	1.07	<i>Pofut2</i>	protein O-fucosyltransferase 2	0001707 // mesoderm formation // inferred from mutant phenotype//0005975 // carb
NM_008474	///XM	0.0652	0.036		-1.06	-1.06	-1.06	-1.32	<i>Krt84</i>	keratin 84	0045616 // regulation of keratinocyte differentiation // inferred from direct assay
NM_011723	///XM	#####			1.18	1.03	-1.06	1.31	<i>Xdh///Cwc22</i>	xanthine dehydrogenase//CWC22 spliceosome-associated protein homolog (S. cerevi	0001933 // negative regulation of protein phosphorylation // not recorded//0001937 //
NM_145926		0.05			1.16	1.13	-1.06	-1.16	<i>Mgat4b</i>	mannoside acetylglucosaminyltransferase 4, isoenzyme B	0005975 // carbohydrate metabolic process // inferred from electronic annotation//000
NM_1818	0.0451				-1.01	-1.12	-1.06	1.01	<i>Hcfc1r1</i>	host cell factor C1 regulator 1 (XPO1-dependent)	
NM_001038700	///	0.032			1.08	1.05	-1.06	1.01	<i>Fnbp1</i>	formin binding protein 1	0006897 // endocytosis // inferred from electronic annotation//0007399 // nervous syst
NM_0076	0.0133				1.06	1.29	-1.06	-1.15	<i>Cdkn2b</i>	cyclin-dependent kinase inhibitor 2B (p15, inhibits CDK4)	0000079 // regulation of cyclin-dependent protein serine/threonine kinase activity // not
NM_001204129	///NM_00	0.01			1.03	-1.04	-1.06	-1.09	<i>C1qtnf1</i>	C1q and tumor necrosis factor related protein 1	0007204 // positive regulation of cytosolic calcium ion concentration // not recorded//0
NM_0087	0.0395	0.007			1.04	-1.08	-1.06	-1.18	<i>Dusp8</i>	dual specificity phosphatase 8	0000188 // inactivation of MAPK activity // inferred from electronic annotation//00064
NM_133351	///XM	0.017			1.14	1.15	-1.06	1.19	<i>Prss8</i>	protease, serine 8 (prostasin)	0001942 // hair follicle development // inferred from mutant phenotype//0006508 // pr
NM_023377		0.008			-1.02	-1.10	-1.06	1.12	<i>Stard5</i>	STAR-related lipid transfer (START) domain containing 5	0006810 // transport // inferred from electronic annotation//0006869 // lipid transport,
NM_022411	///XM	0.0653	0.036		1.03	1.02	-1.06	-1.15	<i>Slc13a2</i>	solute carrier family 13 (sodium-dependent dicarboxylate transporter), member 2	0006810 // transport // inferred from electronic annotation//0006811 // ion transport /
NM_1727	0.0305	0.007			1.22	1.10	-1.06	1.05	<i>Lang8</i>	leukocyte receptor cluster (LRC) member 8	
NM_1393	0.0409	0.048			1.11	-1.02	-1.06	-1.02	<i>Mllt6</i>	myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Drosophila); translocated to, 6	0007165 // signal transduction // inferred from electronic annotation
NM_0166	0.0303	0.013			1.11	-1.03	-1.06	-1.04	<i>Hpcal1</i>	hippocalcin-like 1	0001881 // receptor recycling // inferred from mutant phenotype//0007173 // epiderm:
NM_0075	0.0125	0.022			1.06	-1.05	-1.06	-1.03	<i>Cam1</i>	calcium modulating ligand	0006629 // lipid metabolic process // inferred from electronic annotation//0006694 // s
NM_0013	0.0126				1.11	-1.08	-1.06	-1.16	<i>Fdx1</i>	ferredoxin 1	0007165 // signal transduction // inferred from electronic annotation//0007166 // cell s
NM_0086	0.0066				1.04	-1.09	-1.06	-1.01	<i>Mtnr1a</i>	melatonin receptor 1A	0006629 // lipid metabolic process // inferred from electronic annotation//0006631 // f.
NM_153807	///XR	0.034			1.09	1.04	-1.06	1.12	<i>Acsf2</i>	acyl-CoA synthetase family member 2	0006955 // immune response // inferred from electronic annotation//0008152 // metab
NM_001159934	///NM_14	0.024			1.12	-1.04	-1.06	-1.12	<i>Oas1h</i>	2'-5' oligoadenylate synthetase 1H	0006468 // protein phosphorylation // not recorded//0006979 // response to oxidativ
NM_133985	///NR	0.45693	0.045		-1.08	-1.15	-1.06	1.12	<i>Oxsr1</i>	oxidative-stress responsive 1	0006629 // lipid metabolic process // inferred from electronic annotation
NM_0188	0.008	0.011			1.25	-1.04	-1.06	1.01	<i>Pnlprp1</i>	pancreatic lipase related protein 1	0006412 // translation // not recorded//0032543 // mitochondrial translation // not rec
NM_025606		0.013			1.12	1.15	-1.06	1.05	<i>Mrp116</i>	mitochondrial ribosomal protein L16	0006351 // transcription, DNA-templated // inferred from electronic annotation//00063
NM_133968	///XM	0.017			1.13	1.07	-1.06	-1.02	<i>Snopc2</i>	small nuclear RNA activating complex, polypeptide 2	0006351 // transcription, DNA-templated // inferred from electronic annotation//00063
NM_0011	0.0081	0.019			1.06	-1.24	-1.06	1.16	<i>Lpin2</i>	lipin 2	0007165 // signal transduction // inferred from electronic annotation//0007166 // cell s
NM_1391	0.0056				-1.03	1.21	-1.06	1.05	<i>Adgre4</i>	adhesion G protein-coupled receptor E4	0006898 // receptor-mediated endocytosis // not recorded//0007275 // multicellular or
NM_033603		0.04			1.07	1.02	-1.06	-1.13	<i>Amn</i>	amniotless	0008152 // metabolic process // inferred from electronic annotation
NM_0255	0.0168				-1.07	1.08	-1.06	-1.13	<i>Nudt8</i>	nudix (nucleoside diphosphate linked moiety X)-type motif 8	000165 // MAPK cascade // not recorded//0000302 // response to reactive oxygen spe
NM_0011	0.0066				-1.01	1.29	-1.06	1.09	<i>Ptk2b</i>	PTK2 protein tyrosine kinase 2 beta	0006351 // transcription, DNA-templated // inferred from electronic annotation//00063
NM_001101502	///	0.042			1.12	1.15	-1.06	-1.03	<i>Zfp703</i>	zinc finger protein 703	0001889 // liver development // inferred from mutant phenotype//0001947 // heart loc
NM_007685		0.036			-1.01	1.09	-1.06	-1.15	<i>Cfc1</i>	cripto, FRL-1, cryptic family 1	0000122 // negative regulation of transcription from RNA polymerase II promoter // infer
NM_001098203	///	0.049	0.006		1.20	1.09	-1.06	-1.08	<i>Hic1</i>	hypermethylated in cancer 1	0000122 // negative regulation of transcription from RNA polymerase II promoter // infer
NM_0010	0.042				1.20	1.09	-1.06	-1.08	<i>Hic1</i>	hypermethylated in cancer 1	0008544 // epidermis development // traceable author statement//0018149 // peptide
NM_009374	///XM	0.0649	0.034		1.06	-1.01	-1.06	-1.13	<i>Tgm3</i>	transglutaminase 3, E polypeptide	0000435 // positive regulation of transcription from RNA polymerase II promoter by gala
NM_0108	#####	0.003			1.07	-1.09	-1.06	-1.04	<i>Ncoa1</i>	nuclear receptor coactivator 1	0006351 // transcription, DNA-templated // inferred from electronic annotation//00063
NM_0010	0.0062				1.03	-1.10	-1.06	-1.10	<i>Zfp518b</i>	zinc finger protein 518B	
NM_001161741	///NM_01	0.01			-1.11	1.04	-1.06	1.06	<i>Reg3d</i>	regenerating islet-derived 3 delta	0006810 // transport // inferred from electronic annotation//0006844 // acyl carnitine t
NM_1813	0.0053				1.02	-1.15	-1.06	-1.15	<i>Slc25a29</i>	solute carrier family 25 (mitochondrial carrier, palmitoylcarnitine transporter), membe	0000132 // establishment of mitotic spindle orientation // not recorded//0007049 // cel
NM_027411	///XM	0.028			-1.25	-1.09	-1.06	-1.03	<i>Spdl1</i>	spindle apparatus coiled-coil protein 1	0000398 // mRNA splicing, via spliceosome // not recorded//0009725 // response to ho
NM_001082961	///	0.02			1.02	1.04	-1.06	-1.03	<i>Snrpn///Snrp///Gm35595</i>	small nuclear ribonucleoprotein N//SNRPN upstream reading frame//predicted gene	0003091 // renal water homeostasis // inferred from mutant phenotype//0006171 // cA
NM_007405	///XM	0.017			1.06	-1.02	-1.06	1.13	<i>Adcy6</i>	adenylate cyclase 6	0003149 // membranous septum morphogenesis // inferred from genetic interaction//0
NM_0205	0.0234				1.08	1.32	-1.06	-1.05	<i>Fzd2</i>	frizzled homolog 2 (Drosophila)	0007155 // cell adhesion // inferred from electronic annotation//0007159 // leukocyte c
NM_1537	0.0168				1.14	1.40	-1.06	1.03	<i>Fermt3</i>	fermitin family homolog 3 (Drosophila)	
NM_0213	0.0231				-1.12	1.05	-1.06	-1.06	<i>Vstm2b</i>	V-set and transmembrane domain containing 2B	0001503 // ossification // inferred from direct assay//0001889 // liver development // ir
NM_008973	///XM	0.0650	0.027		1.02	1.05	-1.06	-1.27	<i>Ptn</i>	pleiotrophin	0006508 // proteolysis // inferred from electronic annotation//0007039 // protein catab
NM_001024698	///	0.026			-1.16	-1.08	-1.05	-1.23	<i>Cpa2</i>	carboxypeptidase A2, pancreatic	0000122 // negative regulation of transcription from RNA polymerase II promoter // not i
NM_009045	///XM	0.0653	0.018		1.12	1.13	-1.05	1.06	<i>Rela</i>	v-rel reticuloendotheliosis viral oncogene homolog A (avian)	0006351 // transcription, DNA-templated // inferred from electronic annotation//00063
NM_023773	///XM	0.043	0.021		1.01	-1.02	-1.05	-1.11	<i>Mphosph8</i>	M-phase phosphoprotein 8	0007165 // signal transduction // inferred from electronic annotation//0035556 // intra
NM_0011	0.0146				1.02	-1.24	-1.05	1.04	<i>Chn2</i>	chimerin 2	0006629 // lipid metabolic process // inferred from electronic annotation//0006631 // f.
NM_1456	0.0483	0.042			-1.02	-1.10	-1.05	-1.20	<i>Alox12e</i>	arachidonate lipoxygenase, epidermal	

RefSeq	Tri	p 24h	p 48h	p 72h	FD Air	FD 24h	FD 48h	FD 72h	Gene Symbol	Gene Title	Gene Ontology Biological Process
NM_0264	0.0471				-1.00	-1.19	-1.05	1.34	<i>Tppp3</i>	tubulin polymerization-promoting protein family member 3	0001578 // microtubule bundle formation // not recorded//0046785 // microtubule pol
NM_053249			0.004		1.09	-1.07	-1.05	-1.24	<i>Krt82</i>	keratin 82	
NM_0233	0.0394				-1.15	1.15	-1.05	-1.22	<i>Samsn1</i>	SAM domain, SH3 domain and nuclear localization signals, 1	0002820 // negative regulation of adaptive immune response // inferred from mutant ph
NM_020279//XM_00651	0.027				1.03	1.01	-1.05	-1.10	<i>Ccl28</i>	chemokine (C-C motif) ligand 28	0001954 // positive regulation of cell-matrix adhesion // not recorded//0006935 // cher
NM_001190466//	0.038				1.11	1.11	-1.05	1.04	<i>Dact1</i>	dapper homolog 1, antagonist of beta-catenin (xenopus)	0000122 // negative regulation of transcription from RNA polymerase II promoter // not
NM_1818	0.0391				-1.11	1.02	-1.05	-1.13	<i>Tpte</i>	transmembrane phosphatase with tensin homology	0006470 // protein dephosphorylation // inferred from electronic annotation//0016311
NM_029798		0.032			1.07	1.01	-1.05	-1.17	<i>Flywch2</i>	FLYWCH family member 2	
NM_130886//XM_00653	0.01				-1.03	-1.02	-1.05	-1.13	<i>Card14</i>	caspace recruitment domain family, member 14	0001934 // positive regulation of protein phosphorylation // not recorded//0006915 //
NM_024479//XM_0031	0.031				1.07	1.05	-1.05	-1.05	<i>Wbscr27</i>	Williams Beuren syndrome chromosome region 27 (human)	0008152 // metabolic process // inferred from electronic annotation//0032259 // meth
NM_0013	0.0095				1.05	-1.14	-1.05	-1.09	<i>Vsx2</i>	visual system homeobox 2	0006351 // transcription, DNA-templated // inferred from electronic annotation//00063
NM_027203		0.042	0.01		-1.17	1.00	-1.05	-1.03	<i>Leng1</i>	leukocyte receptor cluster (LRC) member 1	
NM_001003918//	0.016				1.03	-1.04	-1.05	1.01	<i>Usp7</i>	ubiquitin specific peptidase 7	0006281 // DNA repair // inferred from electronic annotation//0006283 // transcription
NM_023312//XM_00650	0.018				1.05	-1.05	-1.05	-1.28	<i>Ndufa13//Yjefn3</i>	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 13//Yjef N-terminal domain	0006915 // apoptotic process // inferred from electronic annotation//0030308 // negati
NM_001316699//NM_02	0.015				1.04	-1.01	-1.05	-1.19	<i>Mier2</i>	mesoderm induction early response 1, family member 2	0006351 // transcription, DNA-templated // inferred from electronic annotation//00063
NM_001163770//	0.048				1.06	1.08	-1.05	1.03	<i>Dxo</i>	decapping exoribonuclease	0006402 // mRNA catabolic process // inferred from mutant phenotype//0008152 // me
NM_0081	0.0071				-1.06	-1.57	-1.05	1.22	<i>Glul</i>	glutamate-ammonia ligase (glutamine synthetase)	0006536 // glutamate metabolic process // not recorded//0006542 // glutamine biosyn
NM_0082	0.007				1.06	1.51	-1.05	-1.26	<i>Map4k1</i>	mitogen-activated protein kinase kinase kinase kinase 1	0000165 // MAPK cascade // not recorded//0000185 // activation of MAPKKK activity //
NM_146240//XM_00651	0.005				-1.15	-1.07	-1.05	1.08	<i>Rassf9</i>	Ras association (RalGDS/AF-6) domain family (N-terminal) member 9	0007165 // signal transduction // inferred from electronic annotation//0046907 // intra
NM_011592		0.046			1.04	1.00	-1.05	1.11	<i>Timm44</i>	translocase of inner mitochondrial membrane 44	0006810 // transport // inferred from electronic annotation//0006886 // intracellular pr
NM_0010	0.0271		0.043		1.10	-1.03	-1.05	1.39	<i>Fgfr1</i>	fibroblast growth factor receptor 1	0000122 // negative regulation of transcription from RNA polymerase II promoter // infer
NM_0011	0.039				-1.10	1.07	-1.05	-1.14	<i>Trp63</i>	transformation related protein 63	0000122 // negative regulation of transcription from RNA polymerase II promoter // infer
NM_007813//XM_00653	0.003				1.07	-1.01	-1.05	-1.13	<i>Cyp2b13</i>	cytochrome P450, family 2, subfamily b, polypeptide 13	0006805 // xenobiotic metabolic process // not recorded//0019373 // epoxygenase P45
NM_0011	0.0182				-1.07	-1.39	-1.05	-1.32	<i>Banp</i>	BTG3 associated nuclear protein	0006351 // transcription, DNA-templated // inferred from electronic annotation//00063
NM_028055//XM_00653	0.042				-1.02	1.07	-1.05	-1.30	<i>Btbd17</i>	BTB (POZ) domain containing 17	
NM_010758//XM_00653	0.026				1.08	1.08	-1.05	-1.07	<i>Mag</i>	myelin-associated glycoprotein	0007155 // cell adhesion // inferred from electronic annotation//0007399 // nervous sy
NM_0013	0.0203				-1.01	1.17	-1.05	-1.02	<i>Grhpr</i>	glyoxylate reductase/hydroxypyruvate reductase	0007588 // excretion // not recorded//0008152 // metabolic process // inferred from el
NM_1535	0.0012				1.20	-1.12	-1.05	1.20	<i>Tns2</i>	tensin 2	0001822 // kidney development // inferred from mutant phenotype//0006470 // protei
NM_0137	0.0112				-1.13	1.19	-1.05	-1.01	<i>LOC102642963//Rps26</i>	40S ribosomal protein S26-like//ribosomal protein S26	0006412 // translation // inferred from electronic annotation//0033119 // negative regu
NM_0010	0.0396				1.03	-1.22	-1.05	1.11	<i>Pdgfra</i>	platelet derived growth factor receptor, alpha polypeptide	0001553 // luteinization // inferred from genetic interaction//0001553 // luteinization /
NM_0092	0.0226				-1.02	-1.21	-1.05	-1.03	<i>Snta1</i>	syntrophin, acidic 1	0002027 // regulation of heart rate // not recorded//0003117 // regulation of vasocon
NM_018780		0.036			-1.00	1.02	-1.05	-1.18	<i>Sfrp5</i>	secreted frizzled-related sequence protein 5	0007275 // multicellular organismal development // inferred from electronic annotati
NM_053178//XM_0007	0.007				-1.13	-1.12	-1.05	-1.12	<i>Acsbg1</i>	acyl-CoA synthetase bubblegum family member 1	0000038 // very long-chain fatty acid metabolic process // not recorded//0000038 // ve
NM_1338	0.0072				1.02	-1.17	-1.05	1.10	<i>Bsd1</i>	BSD domain containing 1	
NM_0012	0.0076				1.04	-1.18	-1.05	1.01	<i>Rora</i>	RAR-related orphan receptor alpha	0001525 // angiogenesis // not recorded//0006351 // transcription, DNA-templated // i
NM_0013	0.0436				1.07	-1.15	-1.05	1.10	<i>Trpc1</i>	transient receptor potential cation channel, subfamily C, member 1	0006810 // transport // inferred from electronic annotation//0006811 // ion transport /
NM_0013	0.0124				-1.03	1.13	-1.05	-1.09	<i>Car7</i>	carbonic anhydrase 7	0002230 // positive regulation of defense response to virus by host // not recorded//00
NM_001290789//NM_02	0.032				1.07	-1.03	-1.05	-1.17	<i>Shroom1</i>	shroom family member 1	0000902 // cell morphogenesis // inferred from direct assay//0051017 // actin filament
NM_008997//XM_0022	0.022				1.14	1.08	-1.05	1.08	<i>Rab11b</i>	RAB11B, member RAS oncogene family	0001881 // receptor recycling // inferred from mutant phenotype//0006810 // transpor
NR_02832	0.0374				1.05	-1.10	-1.05	-1.01	<i>Appbp2os</i>	amyloid beta precursor protein (cytoplasmic tail) binding protein 2, opposite strand	
NM_001085348//NM_00	0.014				1.04	-1.07	-1.05	-1.20	<i>Rhox2a//Rhox2b//Rhox2e</i>	reproductive homeobox 2A//reproductive homeobox 2B//reproductive homeobox 2	0000122 // negative regulation of transcription from RNA polymerase II promoter // infer
NM_172665//XM_0037	0.037				1.15	1.08	-1.05	-1.01	<i>Pdk1</i>	pyruvate dehydrogenase kinase, isoenzyme 1	0005975 // carbohydrate metabolic process // inferred from electronic annotation//000
NM_024264//XM_0039	0.039				1.09	1.01	-1.05	-1.07	<i>Cyp27a1</i>	cytochrome P450, family 27, subfamily a, polypeptide 1	0008203 // cholesterol metabolic process // not recorded//0036378 // calcitriol biosyn
NM_016852//XM_0049	0.049				-1.01	1.02	-1.05	1.18	<i>Wbp2</i>	WW domain binding protein 2	0045184 // establishment of protein localization // not recorded//0045815 // positive re
NM_0090	0.0066	0.005	0.001		-1.00	-1.01	-1.05	1.01	<i>Rps29</i>	ribosomal protein S29	0006412 // translation // not recorded
NM_024190//NM_02592	0.033				-1.11	-1.01	-1.05	1.15	<i>2610002M06Rik//Chmp1b</i>	RIKEN cDNA 2610002M06 gene//charged multivesicular body protein 1B	0000920 // cell separation after cytokinesis // not recorded//0006810 // transport // inf
NM_0011	0.0487				-1.05	1.07	-1.05	-1.11	<i>6-Sep</i>	septin 6	0007049 // cell cycle // inferred from electronic annotation//0051301 // cell division // i
NM_001310766//NM_02	0.004				1.01	-1.06	-1.05	-1.13	<i>B3gat1</i>	beta-1,3-glucuronyltransferase 1 (glucuronosyltransferase P)	0005975 // carbohydrate metabolic process // not recorded//0006486 // protein glycos
NM_2072	0.0274				1.06	1.19	-1.05	-1.26	<i>Mrps26</i>	mitochondrial ribosomal protein S26	
NM_0257	0.0136				-1.05	1.09	-1.05	-1.08	<i>Adat2</i>	adenosine deaminase, tRNA-specific 2	0002100 // tRNA wobble adenosine to inosine editing // inferred from electronic annotat
NM_0010	0.0332				-1.05	1.17	-1.05	-1.08	<i>Lif</i>	leukemia inhibitory factor	0001974 // blood vessel remodeling // inferred from genetic interaction//0006955 // im
NM_0012	0.0244				1.05	-1.17	-1.05	1.07	<i>Birc2</i>	baculoviral IAP repeat-containing 2	0000209 // protein polyubiquitination // not recorded//0001666 // response to hypoxia
NM_0013	0.0016				1.01	2.38	-1.05	-1.06	<i>Coro1a</i>	coronin, actin binding protein 1A	0001845 // phagolysosome assembly // not recorded//0006816 // calcium ion transport
NM_0013	0.0166				-1.00	1.54	-1.05	-1.16	<i>Prkcb</i>	protein kinase C, beta	0001666 // response to hypoxia // inferred from direct assay//0002250 // adaptive imm
NM_172676//XM_0023	0.023				1.10	-1.00	-1.05	1.04	<i>Samd10</i>	sterile alpha motif domain containing 10	
NM_0010	0.007				1.04	-1.25	-1.05	1.07	<i>Dock9</i>	dedicator of cytokinesis 9	0007264 // small GTPase mediated signal transduction // inferred from electronic annota
NM_001039653//NM_01	0.019				1.03	-1.05	-1.05	-1.20	<i>Lhx3</i>	LIM homeobox protein 3	0001890 // placenta development // inferred from genetic interaction//0006351 // tran
NM_0106	0.0028				-1.04	-1.70	-1.05	-1.01	<i>Klf9</i>	Kruppel-like factor 9	0006351 // transcription, DNA-templated // inferred from electronic annotation//00063
NM_145394		0.025			-1.10	-1.03	-1.05	1.11	<i>Slc44a3</i>	solute carrier family 44, member 3	
NM_0012	0.0167				-1.01	1.40	-1.05	-1.10	<i>Fyb</i>	FYN binding protein	0006955 // immune response // inferred from electronic annotation//0045576 // mast c
NM_011616		0.033			-1.00	-1.08	-1.05	-1.18	<i>Cd40lg</i>	CD40 ligand	0002839 // positive regulation of immune response to tumor cell // not recorded//0006
NM_0010	0.0018	0.011			1.07	-1.12	-1.05	-1.05	<i>Cmc4//Mtcp1</i>	C-x(9)-C motif containing 4//mature T cell proliferation 1	
NM_175667		0.022			1.07	-1.04	-1.05	-1.18	<i>Ankfn1</i>	ankyrin repeat and EF-hand domain containing 1	
NM_013851//XM_0038	0.038				1.16	1.05	-1.05	-1.08	<i>Abca8b</i>	ATP-binding cassette, sub-family A (ABC1), member 8b	0006810 // transport // not recorded//0006869 // lipid transport // not recorded//000
NM_0118	0.0198				-1.03	-1.17	-1.05	-1.04	<i>Mmp17</i>	matrix metalloproteinase 17	0006508 // proteolysis // inferred from electronic annotation



RefSeq	Tri.p	24h	p	48h	p	72h	FD Air	FD 24h	FD 48h	FD 72h	Gene Symbol	Gene Title	Gene Ontology Biological Process
NM_0094	0.0188						1.03	-1.12	-1.05	1.14	<i>Tst</i>	thiosulfate sulfurtransferase, mitochondrial	0008152 // metabolic process // inferred from electronic annotation//0030855 // epith
NM_0010	0.0478						-1.11	1.04	-1.05	1.05	<i>11-Sep</i>	septin 11	0007049 // cell cycle // inferred from electronic annotation//0051291 // protein hetero
NM_0086	0.0104						1.10	-1.08	-1.05	1.16	<i>Mmp15</i>	matrix metalloproteinase 15	0006508 // proteolysis // inferred from electronic annotation//0032355 // response to e
NM_007435		0.034					1.10	1.17	-1.04	1.12	<i>Abcd1</i>	ATP-binding cassette, sub-family D (ALD), member 1	0006635 // fatty acid beta-oxidation // inferred from mutant phenotype//0006635 // fa
NM_0104	0.0257						-1.06	-1.13	-1.04	-1.04	<i>Hexa</i>	hexosaminidase A	0001501 // skeletal system development // inferred from genetic interaction//0005975 ,
NM_1445	0.032						-1.12	1.04	-1.04	-1.07	<i>Fcgr4</i>	Fc receptor, IgG, low affinity IV	0001866 // NK T cell proliferation // not recorded//0051930 // regulation of sensory per
NM_0012	0.0301						-1.05	1.07	-1.04	-1.07	<i>Nppb</i>	natriuretic peptide type B	0001666 // response to hypoxia // inferred from electronic annotation//0003085 // neg
NM_020289			0.032				1.05	1.00	-1.04	-1.22	<i>Olfir544</i>	olfactory receptor 544	0007165 // signal transduction // not recorded//0007186 // G-protein coupled receptor
NM_001285845	///	0.018					1.11	1.10	-1.04	1.12	<i>Paqr7</i>	progesterin and adipoQ receptor family member VII	0006810 // multicellular organismal development // inferred from electronic annotation/
NM_011121		0.032					1.10	1.03	-1.04	1.04	<i>Plk1</i>	polo-like kinase 1	0000070 // mitotic sister chromatid segregation // not recorded//0000086 // G2/M tran
NM_0010	0.0031						-1.00	1.13	-1.04	1.11	<i>Thoc6</i>	THO complex 6 homolog (Drosophila)	0006397 // mRNA processing // inferred from electronic annotation//0006406 // mRNA
NM_001162485	///	0.032					1.05	1.08	-1.04	1.00	<i>Aradc1</i>	arrestin domain containing 1	
NM_0012	0.046		0.022				1.09	1.00	-1.04	-1.06	<i>Ranbp3</i>	RAN binding protein 3	0006810 // transport // inferred from electronic annotation//0015031 // protein transp
NM_001146153	///NM_01	0.038					1.01	1.03	-1.04	-1.21	<i>Homer3</i>	homer homolog 3 (Drosophila)	0006810 // G-protein coupled glutamate receptor signaling pathway // traceable author :
NM_027122		0.038					1.03	-1.02	-1.04	-1.19	<i>Mfsd3</i>	major facilitator superfamily domain containing 3	0006810 // transport // not recorded//0015992 // proton transport // ---//0055085 // :
NM_0101	0.0044		0.012				1.10	-1.04	-1.04	-1.07	<i>Ext2</i>	exostosins (multiple) 2	0001503 // ossification // not recorded//0001707 // mesoderm formation // inferred fr
NM_0101	0.0044						-1.09	1.15	-1.04	-1.13	<i>Fcgr1</i>	Fc receptor, IgG, high affinity I	0001788 // antibody-dependent cellular cytotoxicity // inferred from mutant phenotype/
NM_0010	0.0105						-1.01	-1.13	-1.04	1.14	<i>Zfp57</i>	zinc finger protein 57	0000122 // negative regulation of transcription from RNA polymerase II promoter // infer
NM_144913		0.021					1.10	1.08	-1.04	1.00	<i>Mepece</i>	methylphosphate capping enzyme	0000122 // negative regulation of transcription from RNA polymerase II promoter // infer
NM_0011	0.0393						1.05	-1.09	-1.04	-1.03	<i>Tmem184a</i>	transmembrane protein 184a	0006810 // transport // ---//0018992 // germ-line sex determination // inferred from m
NM_145490	///XM	0.044					1.14	1.00	-1.04	1.02	<i>Zfp959</i>	zinc finger protein 959	0006355 // regulation of transcription, DNA-templated // not recorded
NM_001003815	///	0.017					1.11	1.02	-1.04	-1.02	<i>Epb411</i>	erythrocyte membrane protein band 4.1 like 1	0001558 // regulation of cell growth // inferred from electronic annotation//0007010 //
NM_172439	///XM_006514	0.024					1.04	-1.02	-1.04	-1.04	<i>Inpp5j</i>	inositol polyphosphate 5-phosphatase J	0006470 // protein dephosphorylation // inferred from direct assay//0006470 // protei
NM_0095	0.027	0.034					1.06	-1.04	-1.04	1.03	<i>Vpreb3</i>	pre-B lymphocyte gene 3	0002377 // immunoglobulin production // ---//0006955 // immune response // ---//00:
NM_028071	#####						1.04	1.12	-1.04	1.04	<i>Cot1</i>	coactosin-like 1 (Dictyostelium)	0019370 // leukotriene biosynthetic process // inferred from electronic annotation//00:
NM_012042	///XM_006506	0.022					-1.23	1.03	-1.04	1.16	<i>Cul1</i>	cullin 1	0006511 // ubiquitin-dependent protein catabolic process // inferred by curator//00065
NM_1752	0.0034						1.11	-1.21	-1.04	1.00	<i>Arid2</i>	AT rich interactive domain 2 (ARID, RFX-like)	0006337 // nucleosome disassembly // not recorded//0006355 // regulation of transcrip
NM_0296	0.0235						1.04	1.17	-1.04	1.10	<i>Plet1</i>	placenta expressed transcript 1	0001953 // negative regulation of cell-matrix adhesion // inferred from mutant phenoty
NM_0012	0.0169						-1.05	1.38	-1.04	1.06	<i>Irx3</i>	Iroquois related homeobox 3	0001656 // metanephros development // inferred from expression pattern//0001822 //
NM_011910		0.025					1.09	-1.10	-1.04	-1.20	<i>Uts2</i>	urotensin 2	0001666 // response to hypoxia // inferred from electronic annotation//0003105 // neg
NM_001171024	///NM_01	0.036					1.04	1.05	-1.04	-1.21	<i>Gm21948</i> /// <i>Il4i1</i>	predicted gene, 21948//interleukin 4 induced 1	0006351 // transcription, DNA-templated // ---//0006351 // transcription, DNA-templat
NM_013581	///XM_006536	0.005					1.03	1.05	-1.04	-1.06	<i>Cog1</i> /// <i>LOC102641618</i>	component of oligomeric golgi complex 1//conserved oligomeric Golgi complex subur	0000301 // retrograde transport, vesicle recycling within Golgi // not recorded//0006811
NM_018730	///XM_006524	0.027					1.04	1.16	-1.04	-1.26	<i>Rpl36</i> /// <i>Rpl36-ps2</i> /// <i>Gm4604</i>	ribosomal protein L36//ribosomal protein L36, pseudogene 2//predicted gene 4604	0002181 // cytoplasmic translation // ---//0006412 // translation // inferred from elect
NM_1530	0.043						-1.09	1.03	-1.04	-1.14	<i>Tmem5</i>	transmembrane protein 5	0006486 // protein glycosylation // inferred from electronic annotation//0035269 // prc
NM_001287514	///	0.001					1.08	1.02	-1.04	1.05	<i>Cebpa</i>	CCAAT/enhancer binding protein (C/EBP), alpha	0000050 // urea cycle // inferred from direct assay//0000122 // negative regulation of t
NM_0011	0.0063						1.18	1.05	-1.04	-1.02	<i>Zfp574</i>	zinc finger protein 574	0006351 // transcription, DNA-templated // inferred from electronic annotation//00063
NM_0213	0.0147	0.047					-1.17	1.02	-1.04	-1.04	<i>Cd200r1</i>	CD200 receptor 1	
NM_015803	///XM_006515	0.017					1.05	-1.07	-1.04	-1.27	<i>Atp8a2</i>	ATPase, aminophospholipid transporter-like, class I, type 8A, member 2	0003011 // involuntary skeletal muscle contraction // inferred from mutant phenotype//,
NM_001031667	///	0.016					1.06	1.04	-1.04	-1.03	<i>Gsk3a</i>	glycogen synthase kinase 3 alpha	0003073 // regulation of systemic arterial blood pressure // inferred from mutant phenot
NM_144829	///XM_006534	0.019					-1.04	1.03	-1.04	1.12	<i>Aarsd1</i>	alanyl-tRNA synthetase domain containing 1	0006412 // translation // inferred from electronic annotation//0006419 // alanyl-tRNA e
NM_0294	0.0298	0.03	0.01				1.09	-1.06	-1.04	-1.18	<i>Klf17</i>	Kruppel-like factor 17	0000122 // negative regulation of transcription from RNA polymerase II promoter // infer
NM_028636	///XM_006511	0.014					1.10	1.00	-1.04	-1.01	<i>Man2c1</i>	mannosidase, alpha, class 2C, member 1	0005975 // carbohydrate metabolic process // inferred from electronic annotation//000
NM_0232	0.0477						1.17	1.06	-1.04	1.07	<i>Fastk</i>	Fas-activated serine/threonine kinase	0006468 // protein phosphorylation // not recorded//0006915 // apoptotic process // ir
NM_153053		0.045	0.04				1.04	1.06	-1.04	-1.14	<i>Sf3b4</i>	splicing factor 3b, subunit 4	0006397 // mRNA processing // inferred from electronic annotation//0008380 // RNA sp
NM_0085	0.0418		0.048				1.14	1.49	-1.04	-1.20	<i>Blink</i>	B cell linker	0006955 // immune response // not recorded//0007169 // transmembrane receptor pr
NM_0011	0.0164						1.03	1.30	-1.04	-1.08	<i>Fcrla</i>	Fc receptor-like A	0030154 // cell differentiation // inferred from electronic annotation
NM_0011	0.0141						-1.01	1.72	-1.04	-1.05	<i>Sell</i>	selectin, lymphocyte	0007155 // cell adhesion // inferred from electronic annotation//0033198 // response to
NM_173382		0.034					-1.01	1.02	-1.04	-1.22	<i>Proser1</i>	proline and serine rich 1	
NM_0010	0.0167						1.07	-1.17	-1.04	-1.07	<i>Unc13b</i>	unc-13 homolog B (C. elegans)	0006887 // exocytosis // inferred from electronic annotation//0007165 // signal transdu
NM_001290508	///	0.027					1.07	1.09	-1.04	-1.03	<i>Dolpp1</i>	dolichyl pyrophosphate phosphatase 1	0006486 // protein glycosylation // inferred from electronic annotation//0006487 // prc
NM_153570		0.007					1.08	1.07	-1.04	-1.08	<i>Noc4l</i>	nucleolar complex associated 4 homolog (S. cerevisiae)	0042254 // ribosome biogenesis // inferred from electronic annotation
NM_026849	///XM_006506	0.042					1.09	-1.05	-1.04	-1.13	<i>Mtmt14</i>	myotubularin related protein 14	0006470 // protein dephosphorylation // ---//0006470 // protein dephosphorylation // i
NM_001045520	///XM_006	0.037					-1.11	-1.02	-1.04	1.13	<i>Clint1</i>	clathrin interactor 1	0006897 // endocytosis // inferred from electronic annotation//0016192 // vesicle-medi
NM_001310587	///	0.006	0.033				1.10	1.04	-1.04	-1.05	<i>Mef2d</i>	myocyte enhancer factor 2D	0001649 // osteoblast differentiation // inferred from genetic interaction//0001958 // e
NM_0011	0.0412						-1.09	-1.03	-1.04	-1.05	<i>Gtse1</i>	G two S phase expressed protein 1	
NM_001243049	///	0.042					1.16	1.21	-1.04	1.19	<i>Atp6v0a1</i>	ATPase, H+ transporting, lysosomal V0 subunit A1	0006810 // transport // inferred from electronic annotation//0006811 // ion transport /
NM_001307989	///NM_01	0.042					1.01	1.03	-1.04	-1.19	<i>Nr4a3</i>	nuclear receptor subfamily 4, group A, member 3	0000122 // negative regulation of transcription from RNA polymerase II promoter // infer
NM_0118	0.0203						-1.05	1.11	-1.04	1.01	<i>Med24</i>	mediator complex subunit 24	0006351 // transcription, DNA-templated // inferred from electronic annotation//00063
NM_0013	0.0053		0.01				1.05	-1.12	-1.04	-1.12	<i>Arx</i>	aristaeless related homeobox	0000122 // negative regulation of transcription from RNA polymerase II promoter // infer
NM_0085	#####						1.06	-1.50	-1.04	1.04	<i>Mertk</i>	c-mer proto-oncogene tyrosine kinase	0001779 // natural killer cell differentiation // inferred from genetic interaction//00064
NM_033523	///XM	0.023					1.05	-1.01	-1.04	1.08	<i>Spred2</i>	sprouty-related, EVH1 domain containing 2	0000188 // inactivation of MAPK activity // inferred from mutant phenotype//0007275 ,
NM_001081277	///XM_006	0.028					1.12	1.09	-1.04	-1.05	<i>Ak5</i>	adenylate kinase 5	0006139 // nucleobase-containing compound metabolic process // inferred from electri
NM_0806	0.023						1.00	-1.28	-1.04	-1.01	<i>Caskin2</i>	CASK-interacting protein 2	
NM_001205396	///NM_05	0.016					1.06	1.07	-1.04	-1.20	<i>Gprc5d</i>	G protein-coupled receptor, family C, group 5, member D	0007165 // signal transduction // inferred from electronic annotation//0007186 // G-prc

RefSeq	Tri p	24h	p	48h	p	72h	FD Air	FD 24h	FD 48h	FD 72h	Gene Symbol	Gene Title	Gene Ontology Biological Process
NM_1832	0.0232						-1.01	-1.12	-1.04	-1.05	<i>Rnmt1</i>	RNA methyltransferase like 1	0001510 // RNA methylation // not recorded//0006364 // rRNA processing // inferred fr
NM_0013	0.0052						1.08	1.53	-1.04	-1.16	<i>Ccr7</i>	chemokine (C-C motif) receptor 7	0001768 // establishment of T cell polarity // traceable author statement//0002408 // r
NM_0011	0.0189						1.01	1.15	-1.04	-1.02	<i>Ccm2</i>	cerebral cavernous malformation 2	0001568 // blood vessel development // inferred from mutant phenotype//0001570 // \
NM_011790	//XM	0.019					1.07	1.14	-1.04	1.01	<i>Arih2</i>	ariadne homolog 2 (Drosophila)	0000209 // protein polyubiquitination // not recorded//0006511 // ubiquitin-dependen
NM_0094	0.0447						1.02	-1.18	-1.04	-1.28	<i>Tpst2</i>	protein-tyrosine sulfotransferase 2	0006478 // peptidyl-tyrosine sulfation // inferred from mutant phenotype//0007342 // l
NM_145374	//XM	0.007					1.05	1.07	-1.04	1.05	<i>Mios</i>	missing oocyte, meiosis regulator, homolog (Drosophila)	0032008 // positive regulation of TOR signaling // not recorded//0034198 // cellular res
NM_001037801	//NM_001	#####					1.09	1.03	-1.04	-1.12	<i>Cd6</i>	CD6 antigen	0001771 // immunological synapse formation // inferred from sequence or structural sim
NM_001289442	//NM_001	0.021					1.01	1.07	-1.04	-1.13	<i>Grap2</i>	GRB2-related adaptor protein 2	
NM_0011	0.006						-1.30	1.14	-1.04	-1.04	<i>Apoc1</i>	apolipoprotein C-I	0006641 // triglyceride metabolic process // inferred from mutant phenotype//0006810
NM_2076	0.0124						-1.00	-1.44	-1.04	1.02	<i>Fndc3a</i>	fibronectin type III domain containing 3A	0007286 // spermatid development // inferred from mutant phenotype//0009566 // fer
NM_018730	//XM	0.0652	0.037				1.06	1.16	-1.04	-1.23	<i>Rpl36</i>	ribosomal protein L36//ribosomal protein L36, pseudogene 2//predicted gene 4604	0002181 // cytoplasmic translation // ---//0006412 // translation // inferred from electr
NM_0011	0.0098						1.06	-1.05	-1.04	1.10	<i>Kat7</i>	K(lysine) acetyltransferase 7	0006260 // DNA replication // not recorded//0006351 // transcription, DNA-templated ,
NM_175275	//NM_17738	0.044					1.13	-1.03	-1.04	-1.15	<i>Cntln</i>	centlein, centrosomal protein	0010457 // centriole-centriole cohesion // not recorded//0033365 // protein localizatio
NM_0012	0.0107						1.09	-1.06	-1.03	1.01	<i>Osbpl6</i>	oxysterol binding protein-like 6	0006810 // transport // inferred from electronic annotation//0006869 // lipid transport
NM_0011	0.037						1.12	1.35	-1.03	1.10	<i>Fcrl1</i>	Fc receptor-like 1	
NM_0012	0.0489						-1.03	1.19	-1.03	-1.19	<i>Cmtm7</i>	CKLF-like MARVEL transmembrane domain containing 7	0002337 // B-1a B cell differentiation // inferred from mutant phenotype//0006935 // c
NM_0110	0.0491						-1.07	1.10	-1.03	-1.15	<i>Pitx1</i>	paired-like homeodomain transcription factor 1	0001501 // skeletal system development // inferred from mutant phenotype//0006351 ,
NM_1789	0.0354						-1.10	-1.01	-1.03	-1.09	<i>Hic2</i>	hypermethylated in cancer 2	0006351 // transcription, DNA-templated // inferred from electronic annotation//00063
NM_0289	0.0397	0.03					1.02	-1.05	-1.03	-1.08	<i>Gorasp1</i>	golgi reassembly stacking protein 1	0006487 // protein N-linked glycosylation // inferred from mutant phenotype//0006810
NM_0254	0.0406						1.08	-1.08	-1.03	-1.03	<i>1700018B24Rik</i>	enhancer of rudimentary homolog pseudogene	0006221 // pyrimidine nucleotide biosynthetic process // inferred from electronic annota
NM_0010	0.0364						-1.20	-1.60	-1.03	-1.09	<i>Gprasp1</i>	G protein-coupled receptor associated sorting protein 1	0008333 // endosome to lysosome transport // not recorded//1990172 // G-protein cot
NM_0076	0.0065						1.08	2.18	-1.03	-1.15	<i>Ms4a1</i>	membrane-spanning 4-domains, subfamily A, member 1	0042113 // B cell activation // inferred from electronic annotation
NM_0012	0.002						-1.00	-1.26	-1.03	1.14	<i>Cav1</i>	caveolin 1, caveolae protein	0001122 // negative regulation of transcription from RNA polymerase II promoter // infer
NM_0080	0.0457						1.10	-1.01	-1.03	1.03	<i>Fzd8</i>	frizzled homolog 8 (Drosophila)	0001122 // negative regulation of transcription from RNA polymerase II promoter // infer
NM_0010	0.0342						1.16	-1.12	-1.03	1.09	<i>Zscan26</i>	zinc finger and SCAN domain containing 26	0006351 // transcription, DNA-templated // inferred from electronic annotation//00063
NM_0011	0.0457	0.011					-1.15	-1.02	-1.03	1.00	<i>Zfp937</i>	zinc finger protein 937	
NM_0198	0.0396						-1.07	1.05	-1.03	-1.13	<i>Abcb9</i>	ATP-binding cassette, sub-family B (MDR/TAP), member 9	0006810 // transport // inferred from electronic annotation//0008152 // metabolic pro
NM_0281	0.033						-1.06	1.09	-1.03	-1.03	<i>Cep89</i>	centrosomal protein 89	0030030 // cell projection organization // inferred from electronic annotation//0035058
NM_0011	0.0477						-1.33	-1.83	-1.03	-1.41	<i>Cdkn1a</i>	cyclin-dependent kinase inhibitor 1A (P21)	0000079 // regulation of cyclin-dependent protein serine/threonine kinase activity // infe
NM_0012	0.0167						-1.05	-1.41	-1.03	-1.20	<i>Jdp2</i>	Jun dimerization protein 2	0001122 // negative regulation of transcription from RNA polymerase II promoter // infer
NM_1810	0.0142						1.08	-1.09	-1.03	1.05	<i>Adgr11</i>	adhesion G protein-coupled receptor L1	0007157 // heterophilic cell-cell adhesion via plasma membrane cell adhesion molecule
NM_001168652	//	0.05	0.033				1.10	1.06	-1.03	-1.01	<i>Gm20605</i>	predicted gene 20605//leucine-rich repeats and calponin homology (CH) domain con	0006351 // transcription, DNA-templated // inferred from electronic annotation//00063
NM_013581	//XM	0.0653	0.022	1.02	1.06	-1.03	-1.05	<i>Cog1</i>	component of oligomeric golgi complex 1//conserved oligomeric Golgi complex subu	0000301 // retrograde transport, vesicle recycling within Golgi // not recorded//0006811			
XM_357640	//XM	0.047	0.025	1.11	1.16	-1.03	-1.05	<i>Igk-V21</i>	immunoglobulin kappa chain variable 21 (V21)//immunoglobulin kappa chain variabl	0006898 // receptor-mediated endocytosis // not recorded//0006910 // phagocytosis, r			
NM_001163633	//NM_001	0.009					1.10	1.03	-1.03	-1.10	<i>Wnt7b</i>	wingless-type MMTV integration site family, member 7B	0001525 // angiogenesis // inferred from genetic interaction//0001525 // angiogenesis ,
NM_0011	0.0042						1.07	-1.10	-1.03	-1.08	<i>Zfp746</i>	zinc finger protein 746	0001122 // negative regulation of transcription from RNA polymerase II promoter // infer
NM_053126		0.006					-1.08	-1.04	-1.03	1.01	<i>Pcdhb1</i>	protocadherin beta 1	0007155 // cell adhesion // inferred from electronic annotation//0007156 // homophilic
NM_001291235	//	0.002					1.15	1.01	-1.03	-1.04	<i>Tlcd1</i>	TLC domain containing 1	
NM_026645	//XM	0.01124	0.017				-1.10	-1.08	-1.03	-1.04	<i>Iqcf3</i>	IQ motif containing F3	
NM_0109	0.0118						1.02	1.11	-1.03	-1.09	<i>Ntn3</i>	netrin 3//TBC1 domain family, member 24	0006355 // regulation of transcription, DNA-templated // not recorded//0007409 // axo
NM_001081171	//XM	0.006	0.045				1.04	1.05	-1.03	-1.07	<i>Lama5</i>	laminin, alpha 5	0001658 // branching involved in ureteric bud morphogenesis // inferred from mutant pf
NM_0079	0.0103						-1.10	1.12	-1.03	-1.14	<i>Fscn1</i>	fascin homolog 1, actin bundling protein (Strongylocentrotus purpuratus)	0007015 // actin filament organization // inferred from electronic annotation//0007043
NM_001145881	//	0.026					1.11	1.05	-1.03	1.10	<i>Zfp212</i>	Zinc finger protein 212	0006355 // regulation of transcription, DNA-templated // inferred from electronic annotz
NM_001029850	//NM_001	0.037					1.06	-1.01	-1.03	-1.12	<i>Magi1</i>	membrane associated guanylate kinase, WW and PDZ domain containing 1	0070997 // neuron death // not recorded
NM_0011	0.0278						1.06	-1.11	-1.03	-1.02	<i>Mrps2</i>	mitochondrial ribosomal protein S2	0002230 // positive regulation of defense response to virus by host // not recorded//000
NM_0205	0.0057						1.06	-1.07	-1.03	-1.02	<i>Tas2r108</i>	taste receptor, type 2, member 108	0001580 // detection of chemical stimulus involved in sensory perception of bitter taste /
NM_1448	0.0261	0.012	0.04				1.16	-1.09	-1.03	-1.06	<i>Nrbp2</i>	nuclear receptor type binding protein 2	0006468 // protein phosphorylation // inferred from electronic annotation//0007399 //
NM_001290437	//	0.04	0.043				1.07	-1.01	-1.03	-1.03	<i>Inpp5e</i>	inositol polyphosphate-5-phosphatase E	0006470 // protein dephosphorylation // inferred from direct assay//0006470 // protei
NM_145425	//XM	0.0651	0.03				-1.16	-1.05	-1.03	1.14	<i>Wdpcp</i>	WD repeat containing planar cell polarity effector	0001822 // kidney development // inferred from mutant phenotype//0002093 // audit
NM_001243762	//NM_001	0.04					-1.02	-1.02	-1.03	-1.12	<i>Cln5</i>	chloride channel 5	0006810 // transport // inferred from electronic annotation//0006811 // ion transport /
NM_008916	//XM	0.006					1.16	1.14	-1.03	1.15	<i>Inpp5k</i>	inositol polyphosphate 5-phosphatase K	0001701 // in utero embryonic development // inferred from mutant phenotype//0001
NM_0105	0.0031	0.041					-1.17	1.20	-1.03	-1.20	<i>Il1r2</i>	interleukin 1 receptor, type II	0019221 // cytokine-mediated signaling pathway // inferred from electronic annotation
NM_026490		0.013					-1.18	-1.03	-1.03	1.10	<i>Mrp19</i>	mitochondrial ribosomal protein L19	0006412 // translation // inferred from sequence or structural similarity
NM_0114	0.0291						-1.08	-1.38	-1.03	1.17	<i>Serpinh6b</i>	serine (or cysteine) peptidase inhibitor, clade B, member 6b	0008406 // gonad development // non-traceable author statement//0010951 // negativ
NM_0137	0.0084						1.11	1.41	-1.03	-1.05	<i>Dok3</i>	docking protein 3	0007265 // Ras protein signal transduction // inferred from direct assay
NM_0012	0.0029	0.008					1.21	-1.01	-1.03	1.02	<i>Bcl2l11</i>	BCL2-like 11 (apoptosis facilitator)	0001701 // in utero embryonic development // inferred from genetic interaction//0001
NM_009697	//NM	0.033					1.15	1.05	-1.03	1.06	<i>Nr2f2</i>	nuclear receptor subfamily 2, group F, member 2	0000122 // negative regulation of transcription from RNA polymerase II promoter // infer
NM_0194	0.016						-1.15	1.11	-1.03	1.01	<i>Paf1</i>	Paf1, RNA polymerase II associated factor, homolog (S. cerevisiae)	0000122 // negative regulation of transcription from RNA polymerase II promoter // infer
NM_0113	0.0078						1.08	-1.13	-1.03	1.00	<i>Slc22a5</i>	solute carrier family 22 (organic cation transporter), member 5	0006810 // transport // inferred from electronic annotation//0006811 // ion transport /
NM_0011	0.0178						1.03	-1.04	-1.03	-1.11	<i>Igf1bp7</i>	insulin-like growth factor binding protein 7	0001558 // regulation of cell growth // inferred from electronic annotation//0007155 //
NM_0080	0.0184						-1.05	1.11	-1.03	1.07	<i>Ftl1</i>	ferritin light polypeptide 1//ferritin light polypeptide 2, pseudogene//ferritin light ch	0006826 // iron ion transport // inferred from electronic annotation//0006879 // cellula
NM_0082	0.0159						-1.13	1.02	-1.03	-1.15	<i>Foxa3</i>	forkhead box A3	0001678 // cellular glucose homeostasis // inferred from mutant phenotype//0006351 /
NM_008468	//XM	0.0650	0.011				-1.05	-1.02	-1.03	1.07	<i>Kpna6</i>	karyopherin (importin) alpha 6	0006606 // protein import into nucleus // inferred from direct assay//0006607 // NLS-bi
NM_0011	#####						-1.02	-1.63	-1.03	1.09	<i>Plod2</i>	procollagen lysine, 2-oxoglutarate 5-dioxygenase 2	0001666 // response to hypoxia // inferred from electronic annotation//0032870 // celli

RefSeq	Tri.p	24h	p	48h	p	72h	FD Air	FD 24h	FD 48h	FD 72h	Gene Symbol	Gene Title	Gene Ontology Biological Process
NM_001113470	///	0.025	1.08	1.16	-1.03	1.04					<b>Ctdsp2</b>	CTD (carboxy-terminal domain, RNA polymerase II, polypeptide A) small phosphatase	0001933 // negative regulation of protein phosphorylation // inferred from direct assay//
NM_0137	0.0072		-1.01	1.16	-1.03	-1.10					<b>Txnrd2</b>	thioredoxin reductase 2	0000305 // response to oxygen radical // traceable author statement//0007507 // heart
NM_0011	0.0167	0.03	0.008	1.24	1.05	-1.03	-1.10				<b>Slc16a11</b>	solute carrier family 16 (monocarboxylic acid transporters), member 11	0006629 // lipid metabolic process // not recorded//0006810 // transport // inferred frc
NM_001164062	///	0.019	1.14	1.20	-1.03	1.10					<b>Stat5a</b>	signal transducer and activator of transcription 5A	0000255 // allantoin metabolic process // inferred from mutant phenotype//0001553 //
NM_0231	#####		-1.18	1.22	-1.03	-1.03					<b>Arpc1b</b>	actin related protein 2/3 complex, subunit 1B	0030833 // regulation of actin filament polymerization // inferred from electronic annota
NM_139236	///NM	0.004	1.08	1.05	-1.03	-1.01					<b>Nol6</b>	nucleolar protein family 6 (RNA-associated)	0006364 // rRNA processing // not recorded//0006409 // tRNA export from nucleus // n
NM_0532	0.0486		1.01	-1.05	-1.03	-1.02					<b>Erc1</b>	ELKS/RAB6-interacting/CAST family member 1	0006810 // transport // inferred from electronic annotation//0007252 // I-kappaB phos
NM_025476	///XR	0.007	1.27	1.15	-1.03	1.08					<b>Rmdn1</b>	regulator of microtubule dynamics 1	
NM_0090	0.0496		1.08	-1.10	-1.03	-1.03					<b>Rel</b>	reticuloendotheliosis oncogene	0000122 // negative regulation of transcription from RNA polymerase II promoter // not r
NM_0236	0.0143		-1.00	1.13	-1.03	-1.04					<b>Sars2</b>	seryl-aminoacyl-tRNA synthetase 2	0006412 // translation // inferred from electronic annotation//0006418 // tRNA aminoa
NM_0080	0.0301		1.13	-1.01	-1.03	1.15					<b>Fzd7</b>	frizzled homolog 7 (Drosophila)	0006355 // regulation of transcription, DNA-templated // not recorded//0007165 // sigr
NM_001301100	///NM_18	0.003	1.15	1.04	-1.03	-1.06					<b>Edc4</b>	enhancer of mRNA decapping 4	
NM_0011	0.0099		-1.03	-1.17	-1.02	1.24					<b>Cep55</b>	centrosomal protein 55	0000281 // mitotic cytokinesis // not recorded//0000920 // cell separation after cytokin
NM_001290740	///	0.031	1.28	1.07	-1.02	1.24					<b>Cwc22</b> ///Xdh	CWC22 spliceosome-associated protein homolog (S. cerevisiae)///xanthine dehydroge	0000398 // mRNA splicing, via spliceosome // not recorded//0001933 // negative regula
NM_013905		0.005	1.12	1.05	-1.02	1.24					<b>Heyl</b>	hairly/enhancer-of-split related with YRPW motif-like	0003151 // outflow tract morphogenesis // inferred from genetic interaction//0003181 .
NM_0085	0.0441	#####	1.04	-1.08	-1.02	-1.17					<b>Lor</b>	loricrin	0031424 // keratinization // inferred from electronic annotation
NM_0012	0.0201		1.03	-1.06	-1.02	-1.11					<b>Ngb</b>	neuroglobin	0006810 // transport // inferred from electronic annotation//0006915 // apoptotic proc
NM_0012	0.0031		-1.02	-1.13	-1.02	1.00					<b>Ncor1</b>	nuclear receptor co-repressor 1	0000122 // negative regulation of transcription from RNA polymerase II promoter // infer
NM_1786	0.0059		1.08	-1.10	-1.02	1.07					<b>Poldip3</b>	polymerase (DNA-directed), delta interacting protein 3	0006417 // regulation of translation // inferred from electronic annotation//0006810 //
NM_1386	0.0021		1.04	-1.03	-1.02	1.16					<b>Casc3</b>	cancer susceptibility candidate 3	000184 // nuclear-transcribed mRNA catabolic process, nonsense-mediated decay // inf
NM_199467	///XM_00653	0.043	-1.04	1.06	-1.02	1.18					<b>Mms22l</b>	MMS22-like, DNA repair protein	0000724 // double-strand break repair via homologous recombination // not recorded//
NM_0010	0.0459		1.17	-1.02	-1.02	-1.16					<b>Cracr2b</b>	calcium release activated channel regulator 2B	0002115 // store-operated calcium entry // not recorded//0034613 // cellular protein Ic
NM_0010	0.0343		-1.07	1.12	-1.02	1.05					<b>Spryd3</b>	SPRY domain containing 3	
NM_011505	///XM	0.025	0.022	-1.11	-1.14	-1.02					<b>Stxbp4</b>	syntaxin binding protein 4	0006605 // protein targeting // inferred from direct assay//0006974 // cellular response
NM_0223	0.0266	0.008	1.12	-1.03	-1.02	-1.19					<b>Slc28a3</b>	solute carrier family 28 (sodium-coupled nucleoside transporter), member 3	0001895 // retina homeostasis // not recorded//0006810 // transport // inferred from e
NM_053185	///XM_01124	0.009	-1.01	-1.05	-1.02	1.10					<b>Col4a6</b>	collagen, type IV, alpha 6	0030198 // extracellular matrix organization // inferred from direct assay//0071230 // c
NM_0117	0.0376		-1.03	-1.20	-1.02	1.02					<b>Ywhah</b>	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, eta poly	0002028 // regulation of sodium ion transport // not recorded//0002028 // regulation o
NM_0010	0.0283		-1.02	-1.09	-1.02	-1.05					<b>Purg</b>	purine-rich element binding protein G	
NM_009160		0.014	-1.04	-1.03	-1.02	1.13					<b>Sftpd</b>	surfactant associated protein D	0002376 // immune system process // inferred from electronic annotation//0007585 //
NM_0012	0.0014		1.18	-1.25	-1.02	1.30					<b>Alas1</b>	aminolevulinic acid synthase 1	0006778 // porphyrin-containing compound metabolic process // inferred from electroni
NM_011359		0.02	-1.04	-1.05	-1.02	-1.03					<b>Sftpc</b>	surfactant associated protein C	0007585 // respiratory gaseous exchange // inferred from electronic annotation//00076
NM_001252448	///NM_00	0.045	-1.03	1.03	-1.02	1.07					<b>Strada</b>	STE20-related kinase adaptor alpha	0006468 // protein phosphorylation // inferred from electronic annotation//0006611 //
NM_1387	0.0453		1.11	-1.10	-1.02	1.23					<b>Sdpr</b>	serum deprivation response	0045944 // positive regulation of transcription from RNA polymerase II promoter // not r
NM_139236	///NM_13923	0.022	1.08	1.08	-1.02	-1.01					<b>Nol6</b>	nucleolar protein family 6 (RNA-associated)	0006364 // rRNA processing // not recorded//0006409 // tRNA export from nucleus // n
NM_0199	0.0434		1.03	-1.11	-1.02	-1.03					<b>Alg2</b>	asparagine-linked glycosylation 2 (alpha-1,3-mannosyltransferase)	0006486 // protein glycosylation // inferred from electronic annotation//0006488 // dol
NM_001078649	///	0.049	1.09	1.14	-1.02	-1.06					<b>Tmem134</b>	transmembrane protein 134	
NM_001311156	///	0.025	1.09	1.10	-1.02	1.05					<b>Tcta</b>	T cell leukemia translocation altered gene	
NM_0114	0.0239		-1.14	1.47	-1.02	-1.09					<b>Sifn1</b>	schlafen 1	0000122 // negative regulation of transcription from RNA polymerase II promoter // infer
NM_0090	0.0028		-1.10	1.80	-1.02	1.04					<b>Rac2</b>	RAS-related C3 botulinum substrate 2	0006935 // chemotaxis // inferred from direct assay//0007015 // actin filament organiz
NM_0187	0.0387		-1.05	1.10	-1.02	-1.08					<b>Nme6</b>	NME/NM23 nucleoside diphosphate kinase 6	0006165 // nucleoside diphosphate phosphorylation // inferred from electronic annotati
NM_1531	0.0348		-1.04	1.18	-1.02	-1.02					<b>Phospho1</b> ///Zfp652	phosphatase, orphan 1///zinc finger protein 652	0001958 // mitochondrial ossification // inferred from mutant phenotype//0006351 // t
NM_0312	0.0199		1.04	1.35	-1.02	1.05					<b>Gimap3</b>	GTPase, IMAP family member 3	0033955 // mitochondrial DNA inheritance // inferred from mutant phenotype
NM_001291047	///NM_00	0.047	1.03	1.01	-1.02	-1.08					<b>Ypel1</b>	yippee-like 1 (Drosophila)	
NM_1990	0.0184		1.14	-1.14	-1.02	1.00					<b>Stard8</b>	START domain containing 8	0007165 // signal transduction // inferred from electronic annotation//0043547 // posit
NM_008581		0.025	1.15	1.02	-1.02	1.04					<b>Mela</b>	melanoma antigen	0006508 // proteolysis // inferred from electronic annotation//0015074 // DNA integrat
NM_0010	0.0038	0.013	0.043	1.10	-1.04	-1.02					<b>Cdc42bpa</b>	CDC42 binding protein kinase alpha	0000226 // microtubule cytoskeleton organization // inferred from mutant phenotype//
NM_0280	0.0143		1.02	1.18	-1.02	-1.22					<b>Ddx54</b>	DEAD (Asp-Glu-Ala-Asp) box polypeptide 54	0006351 // transcription, DNA-templated // inferred from electronic annotation//00063
NM_0272	0.0361	0.012	1.10	-1.03	-1.02	-1.16					<b>Ppp1r35</b>	protein phosphatase 1, regulatory subunit 35	0010923 // negative regulation of phosphatase activity // not recorded
NM_0335	0.0084		1.08	-1.11	-1.02	1.04					<b>Aff4</b>	AF4/FMR2 family, member 4	0006351 // transcription, DNA-templated // inferred from electronic annotation//00063
NM_017401	///XM_00651	0.039	1.14	1.17	-1.02	-1.05					<b>Polm</b>	polymerase (DNA directed), mu	0006281 // DNA repair // inferred from electronic annotation//0006310 // DNA recomb
NM_0231	0.0402		1.05	1.14	-1.02	-1.16					<b>Map2k2</b>	mitogen-activated protein kinase kinase 2	0000165 // MAPK cascade // not recorded//0000187 // activation of MAPK activity // tr
NM_019435	///XM_00652	0.039	1.01	-1.03	-1.02	-1.04					<b>Ndufb11</b>	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 11	0006810 // transport // inferred from electronic annotation//0055114 // oxidation-redu
NM_0011	0.0257		-1.09	-1.39	-1.02	-1.02					<b>Grlh1</b>	grainyhead-like 1 (Drosophila)	0006351 // transcription, DNA-templated // inferred from electronic annotation//00063
NM_029342		0.044	1.12	1.03	-1.02	-1.12					<b>Nhej1</b>	nonhomologous end-joining factor 1	0006281 // DNA repair // inferred from electronic annotation//0006302 // double-stran
NM_0105	0.0024		1.11	-1.10	-1.02	1.00					<b>Il17a</b>	interleukin 17A	0006954 // inflammatory response // inferred from electronic annotation//0007166 // c
NM_0012	0.0024		-1.04	1.19	-1.02	-1.20					<b>Blnrb</b>	biliverdin reductase B (flavin reductase (NADPH))	0042167 // heme catabolic process // not recorded//0055114 // oxidation-reduction pr
NM_023058	///XM_00652	0.048	1.02	1.01	-1.02	-1.09					<b>Pkmyt1</b>	protein kinase, membrane associated tyrosine/threonine 1	0006468 // protein phosphorylation // inferred from electronic annotation//0007049 //
NM_008106	///XM_00652	0.048	1.07	1.01	-1.02	-1.12					<b>Opn1mw</b>	opsin 1 (cone pigments), medium-wave-sensitive (color blindness, deutan)	0007165 // signal transduction // inferred from electronic annotation//0007186 // G-pr
NM_0011	0.0203		1.04	-1.18	-1.02	1.06					<b>Sec14l1</b>	SEC14-like lipid binding 1	0006810 // transport // inferred from electronic annotation
NM_008168	///XM_00653	0.007	1.18	-1.01	-1.02	-1.17					<b>Grik5</b>	glutamate receptor, ionotropic, kainate 5 (gamma 2)	0006621 // protein retention in ER lumen // not recorded//0006810 // transport // infer
NM_1337	0.0185	0.022	1.21	-1.02	-1.02	1.27					<b>Ctdsp1</b>	CTD (carboxy-terminal domain, RNA polymerase II, polypeptide A) small phosphatase	0001933 // negative regulation of protein phosphorylation // inferred from direct assay//
NM_1755	0.045		1.00	-1.12	-1.02	-1.02					<b>Wdfy2</b>	WD repeat and FYVE domain containing 2	0001934 // positive regulation of protein phosphorylation // not recorded//0045600 //
NM_0194	0.0167		1.05	1.31	-1.02	1.06					<b>Atf7ip</b>	activating transcription factor 7 interacting protein	0000122 // negative regulation of transcription from RNA polymerase II promoter // infer
NM_001166273	///NM_01	0.012	-1.00	-1.13	-1.02	-1.22					<b>Cspg5</b>	chondroitin sulfate proteoglycan 5	0002230 // positive regulation of defense response to virus by host // not recorded//000

RefSeq	Tri	p 24h	p 48h	p 72h	FD Air	FD 24h	FD 48h	FD 72h	Gene Symbol	Gene Title	Gene Ontology Biological Process
NM_009320	//XM	0.03			1.17	1.20	-1.02	1.12	<i>Slc6a6</i>	solute carrier family 6 (neurotransmitter transporter, taurine), member 6	0001762 // beta-alanine transport // inferred from direct assay//0006810 // transport //
NM_0010	0.0407				1.03	-1.60	-1.02	1.01	<i>Edem3</i>	ER degradation enhancer, mannosidase alpha-like 3	0006491 // N-glycan processing // not recorded//0006516 // glycoprotein catabolic pro
NM_0118	0.0351				1.00	1.09	-1.02	-1.01	<i>Lamc3</i>	laminin gamma 3	0000904 // cell morphogenesis involved in differentiation // inferred from genetic interac
NM_0010	0.0023				-1.01	-1.13	-1.02	1.14	<i>Kat6a</i>	K(lysine) acetyltransferase 6A	0003007 // heart morphogenesis // inferred from genetic interaction//0003007 // heart
NM_1336	0.0378				-1.03	1.12	-1.02	1.08	<i>Ndufv1</i>	NADH dehydrogenase (ubiquinone) flavoprotein 1	0006120 // mitochondrial electron transport, NADH to ubiquinone // --//0006810 // tr
NM_1530	0.0286				1.04	-1.10	-1.02	-1.07	<i>Gprc6a</i>	G protein-coupled receptor, family C, group 6, member A	0007165 // signal transduction // inferred from electronic annotation//0007186 // G-pr
NM_008868		0.009			1.07	1.05	-1.02	-1.15	<i>Pla2g2c</i>	phospholipase A2, group IIC	0006629 // lipid metabolic process // inferred from electronic annotation//0006644 // p
NM_0086	0.028				-1.20	1.07	-1.02	1.04	<i>Mmp8</i>	matrix metalloproteinase 8	0006508 // proteolysis // not recorded//0030574 // collagen catabolic process // inferre
NM_0085	0.0055				1.02	-1.25	-1.02	1.08	<i>Smad1</i>	SMAD family member 1	0000165 // MAPK cascade // inferred from mutant phenotype//0000165 // MAPK casca
NM_0262	0.038				1.08	-1.04	-1.02	1.01	<i>H2afy2</i>	H2A histone family, member Y2	0000122 // negative regulation of transcription from RNA polymerase II promoter // not r
NM_0010	0.0412				-1.07	-1.02	-1.02	-1.09	<i>Rpf2</i>	ribosome production factor 2 homolog (S. cerevisiae)	0000027 // ribosomal large subunit assembly // not recorded//0000463 // maturation o
NM_0010	0.046				1.04	-1.03	-1.02	1.05	<i>Strn4</i>	striatin, calmodulin binding protein 4	
		0.019			-1.06	-1.04	-1.02	-1.12	<i>C78228</i>	expressed sequence C78228	
NM_001130150	//	0.016	0.049		1.26	1.25	-1.02	1.03	<i>Arhgef1</i>	Rho guanine nucleotide exchange factor (GEF) 1	0035023 // regulation of Rho protein signal transduction // inferred from electronic anno
NM_0276	0.0086				-1.03	-1.29	-1.02	-1.06	<i>Psd3</i>	pleckstrin and Sec7 domain containing 3	0016192 // vesicle-mediated transport // --//0030182 // neuron differentiation // not r
NM_1389	0.0223				1.05	-1.07	-1.02	-1.05	<i>Wdr81</i>	WD repeat domain 81	0000132 // establishment of mitotic spindle orientation // not recorded//0007097 // nu
NM_1337	0.0357		0.046		-1.02	1.13	-1.02	1.06	<i>Ptcd1</i>	pentatricopeptide repeat domain 1	0008033 // tRNA processing // inferred from electronic annotation//0042780 // tRNA 3'
	0.0302		0.008		1.05	-1.06	-1.02	-1.10	<i>C80012</i>	expressed sequence C80012	
NM_001081065	//XM_006	0.008			1.09	1.08	-1.02	-1.03	<i>Zfp707</i>	zinc finger protein 707	0006355 // regulation of transcription, DNA-templated // not recorded
NM_0010	0.0124				1.11	1.66	-1.02	-1.02	<i>Cd22</i>	CD22 antigen	0007155 // cell adhesion // inferred from electronic annotation//0007166 // cell surface
NM_010213	//XM_00650	0.037			-1.00	1.10	-1.02	-1.28	<i>Fhl3</i>	four and a half LIM domains 3	0030036 // actin cytoskeleton organization // inferred from direct assay
NM_0010	0.0316				1.04	-1.23	-1.02	1.16	<i>Cep350</i>	centrosomal protein 350	0034453 // microtubule anchoring // inferred from electronic annotation
NM_0214	0.004	0.05			1.08	-1.12	-1.02	-1.01	<i>Rnase4</i>	ribonuclease, RNase A family 4	0001525 // angiogenesis // inferred from electronic annotation//0001525 // angiogenes
NM_018762	//XM_00650	0.038			1.00	1.06	-1.02	-1.18	<i>Gp9</i>	glycoprotein 9 (platelet)	0007155 // cell adhesion // inferred from electronic annotation//0007596 // blood coag
NM_1448	#####				1.08	-1.20	-1.02	1.04	<i>Rprd1a</i>	regulation of nuclear pre-mRNA domain containing 1A	0070940 // dephosphorylation of RNA polymerase II C-terminal domain // not recorded
NM_013876	//XM	0.043			1.12	-1.05	-1.02	-1.12	<i>Rnf11</i>	ring finger protein 11	0006511 // ubiquitin-dependent protein catabolic process // inferred from physical inter
NM_020283	//XM_00649	0.016			1.12	1.01	-1.02	-1.12	<i>B3galt1</i>	UDP-Gal:betaGlcNAc beta 1,3-galactosyltransferase, polypeptide 1	0006486 // protein glycosylation // not recorded//0009312 // oligosaccharide biosynthe
NM_0013	0.0021				1.02	-1.18	-1.02	1.22	<i>Pmp22</i>	peripheral myelin protein 22	0007049 // cell cycle // inferred from electronic annotation//0007050 // cell cycle arrest
NM_019685		0.012			-1.12	-1.06	-1.02	1.03	<i>Ruvb1</i>	RuvB-like protein 1	0006281 // DNA repair // inferred from electronic annotation//0006310 // DNA recomb
NM_0013	0.0126				-1.04	1.19	-1.02	1.02	<i>Csk</i>	c-src tyrosine kinase	0001817 // regulation of cytokine production // not recorded//0002009 // morphogene
NM_001001297	//NM_17	0.023			-1.05	1.06	-1.02	1.09	<i>Thns1</i>	threonine synthase-like 1 (bacterial)	0009088 // threonine biosynthetic process // not recorded
NM_0010	0.0114				1.00	-1.09	-1.01	1.08	<i>Hsd11b1</i>	hydroxysteroid 11-beta dehydrogenase 1	0006629 // lipid metabolic process // inferred from electronic annotation//0006704 // g
NM_018775	//XM	0.013			-1.41	-1.41	-1.01	-1.11	<i>Tbc1d8</i>	TBC1 domain family, member 8	0043547 // positive regulation of GTPase activity // inferred from electronic annotation
NM_026585	//XM_00650	0.013			-1.01	1.02	-1.01	1.13	<i>Fam21</i>	family with sequence similarity 21	0006810 // transport // inferred from electronic annotation//0015031 // protein transp
NM_029645		0.023			1.06	-1.01	-1.01	-1.07	<i>Gatc</i>	glutamyl-tRNA(Gln) amidotransferase, subunit C	0006412 // translation // inferred from electronic annotation//0006450 // regulation of
NM_0086	0.0439				-1.02	1.41	-1.01	-1.04	<i>Ncf4</i>	neutrophil cytosolic factor 4	0043085 // positive regulation of catalytic activity // not recorded
NM_1336	0.0211				-1.00	-1.14	-1.01	1.06	<i>Arhgef5</i>	Rho guanine nucleotide exchange factor (GEF) 5	0002408 // myeloid dendritic cell chemotaxis // inferred from mutant phenotype//0030
NM_0075	0.003				-1.05	1.20	-1.01	1.00	<i>Bid</i>	BH3 interacting domain death agonist	0001836 // release of cytochrome c from mitochondria // inferred from direct assay//0C
NM_0238	0.0408	0.008			-1.14	1.04	-1.01	-1.06	<i>Retnlb</i>	resistin like beta	
NM_0010	0.009				1.01	-1.24	-1.01	1.00	<i>Brd1</i>	bromodomain containing 1	0035902 // response to immobilization stress // inferred from electronic annotation//0C
NM_1337	0.0456		0.035		1.13	-1.01	-1.01	-1.07	<i>Fam131a</i>	family with sequence similarity 131, member A	
NM_001205043	//	0.04			1.14	1.09	-1.01	1.05	<i>Jarid2</i>	jumonji, AT rich interactive domain 2	0000122 // negative regulation of transcription from RNA polymerase II promoter // infer
NM_0099	0.0366				-1.00	1.10	-1.01	1.05	<i>Dpysl2</i>	dihydropyrimidinase-like 2	0001975 // response to amphetamine // inferred from electronic annotation//0006897
NM_008553		0.048			1.06	-1.11	-1.01	-1.15	<i>Ascl1</i>	achaete-scute complex homolog 1 (Drosophila)	0000122 // negative regulation of transcription from RNA polymerase II promoter // not r
NM_0253	0.0397				1.01	1.18	-1.01	-1.07	<i>Sharpin</i>	SHANK-associated RH domain interacting protein	0007005 // mitochondrion organization // inferred from mutant phenotype//0007420 //
NM_0011	0.0309				1.03	-1.10	-1.01	1.02	<i>Aamd1c</i>	adipogenesis associated Mth938 domain containing	0043066 // negative regulation of apoptotic process // inferred from mutant phenotype//
NM_0012	0.0059				1.03	-1.10	-1.01	1.01	<i>Thsd1</i>	thrombospondin, type I, domain 1	0002244 // hematopoietic progenitor cell differentiation // inferred from genetic interact
NM_028354	//XM_00651	0.035			1.01	1.02	-1.01	1.07	<i>Tdp1</i>	tyrosyl-DNA phosphodiesterase 1	0000012 // single strand break repair // inferred from mutant phenotype//0000012 // si
NM_026058	//XM	0.011			1.22	1.18	-1.01	1.17	<i>Cers4</i>	ceramide synthase 4	0006629 // lipid metabolic process // inferred from electronic annotation//00030148 // s
NM_022031	//XM_00650	0.047			1.04	1.01	-1.01	-1.14	<i>Hapln2</i>	hyaluronan and proteoglycan link protein 2	0001501 // skeletal system development // not recorded//0007155 // cell adhesion // n
NM_0013	0.0199				1.04	1.41	-1.01	-1.03	<i>Cyba</i>	cytochrome b-245, alpha polypeptide	0001938 // positive regulation of endothelial cell proliferation // not recorded//000310
NM_001161428	//	0.036	0.044		1.10	1.17	-1.01	-1.10	<i>Unc93b1</i>	unc-93 homolog B1 (C. elegans)	0002224 // toll-like receptor signaling pathway // inferred from mutant phenotype//00C
NM_001313888	//NM_00	0.028			-1.07	1.00	-1.01	1.04	<i>Ii7</i>	interleukin 7	0002360 // T cell lineage commitment // inferred from mutant phenotype//0006955 // i
NM_0012	0.0398				1.02	-1.04	-1.01	1.20	<i>Kif1b</i>	kinesin family member 1B	0007018 // microtubule-based movement // inferred from direct assay//0007270 // neu
NM_0107	0.0283				-1.02	-1.29	-1.01	-1.15	<i>Mxd4</i>	Max dimerization protein 4	0006351 // transcription, DNA-templated // inferred from electronic annotation//00063
NM_001033175		0.031			1.12	1.07	-1.01	1.16	<i>Cln6</i>	ceroid-lipofuscinosis, neuronal 6	0001573 // ganglioside metabolic process // not recorded//0001573 // ganglioside met
NM_0197	0.0378				1.01	-1.09	-1.01	-1.09	<i>Nme4</i>	NME/NM23 nucleoside diphosphate kinase 4	0006163 // purine nucleotide metabolic process // not recorded//0006165 // nucleosid
NM_008572	//XM_00651	0.024			-1.14	1.10	-1.01	-1.14	<i>Mcpt8</i>	mast cell protease 8	0006508 // proteolysis // inferred from electronic annotation//0006955 // immune resp
NM_027493	//XM_00651	0.045			1.03	1.07	-1.01	1.14	<i>Actr8</i>	ARPB actin-related protein 8	0006281 // DNA repair // inferred from electronic annotation//0006310 // DNA recomb
NM_008052	//XM_01124	0.049			1.04	1.07	-1.01	-1.18	<i>Dtx1</i>	deltex 1 homolog (Drosophila)	0007219 // Notch signaling pathway // inferred from direct assay//0007219 // Notch sig
NM_0010	0.0056				1.02	-1.12	-1.01	1.05	<i>Fhl1</i>	four and a half LIM domains 1	0003254 // regulation of membrane depolarization // not recorded//0007275 // multic
NM_0012	0.0092				1.13	1.03	-1.01	1.19	<i>Jund</i>	jun D proto-oncogene	0000122 // negative regulation of transcription from RNA polymerase II promoter // not r
NM_133823	//XM_00653	0.027			1.02	-1.15	-1.01	1.26	<i>Mmaa</i>	methylmalonic aciduria (cobalamin deficiency) type A	0009236 // cobalamin biosynthetic process // inferred from electronic annotation
NM_0011	0.0057				1.01	1.32	-1.01	1.07	<i>Meis1</i>	Meis homeobox 1	0001525 // angiogenesis // inferred from mutant phenotype//0002089 // lens morphog

RefSeq	Tri	p 24h	p 48h	p 72h	FD Air	FD 24h	FD 48h	FD 72h	Gene Symbol	Gene Title	Gene Ontology Biological Process
NM_0265		0.0382			1.24	-1.14	-1.01	1.10	<i>Upf3b</i>	UPF3 regulator of nonsense transcripts homolog B (yeast)	0000184 // nuclear-transcribed mRNA catabolic process, nonsense-mediated decay // no
NM_0010		0.0343			1.03	1.35	-1.01	1.07	<i>Pgd</i>	phosphogluconate dehydrogenase	0005975 // carbohydrate metabolic process // not recorded//0006098 // pentose-phos
NM_0010		0.0214			1.06	-1.10	-1.01	1.03	<i>Mecp2</i>	methyl CpG binding protein 2	0000122 // negative regulation of transcription from RNA polymerase II promoter // not r
NM_0110		0.036			1.13	-1.08	-1.01	-1.08	<i>Phex</i>	phosphate regulating endopeptidase homolog, X-linked	0006508 // proteolysis // not recorded//0019637 // organophosphate metabolic proces
NM_010108	//XM_00650	0.015			1.07	1.03	-1.01	1.15	<i>Efna3</i>	ephrin A3	0007411 // axon guidance // not recorded//0045664 // regulation of neuron differentia
NM_0011		0.012			1.09	-1.11	-1.01	1.11	<i>Rnf146</i>	ring finger protein 146	0016055 // Wnt signaling pathway // inferred from electronic annotation//0016567 // p
NM_0200		0.0249			-1.04	1.06	-1.01	-1.07	<i>Dhodh</i>	dihydroorotate dehydrogenase	0006207 // 'de novo' pyrimidine nucleobase biosynthetic process // not recorded//0006
NM_145540	//NM_17887	0.046			-1.17	-1.13	-1.01	1.05	<i>Ints3</i>	integrator complex subunit 3	0006281 // DNA repair // not recorded//0006974 // cellular response to DNA damage st
NM_0100		0.0348			1.12	-1.10	-1.01	1.04	<i>Dapk2</i>	death-associated protein kinase 2	0006468 // protein phosphorylation // not recorded//0006468 // protein phosphorylati
NM_007376		0.022			-1.15	-1.07	-1.01	-1.13	<i>Pzp</i>	pregnancy zone protein	0007566 // embryo implantation // inferred from genetic interaction//0010466 // negat
NM_025912	//XM_0021				1.06	1.02	-1.01	-1.09	<i>Fam210b</i>	family with sequence similarity 210, member B	
NM_001205330	//NM_00	0.042			-1.07	-1.19	-1.01	1.10	<i>Map4</i>	microtubule-associated protein 4	0007052 // mitotic spindle organization // inferred from direct assay//0007052 // mitoti
NM_1725		0.0353			1.07	-1.05	-1.01	-1.02	<i>Boc</i>	biregional cell adhesion molecule-related/down-regulated by oncogenes (Cdon) bindin	0007155 // cell adhesion // inferred from electronic annotation//0007224 // smoothne
NM_0335	#####				1.09	-1.33	-1.01	1.08	<i>Klf7</i>	Kruppel-like factor 7 (ubiquitous)	0006351 // transcription, DNA-templated // inferred from electronic annotation//00063
NM_001081650	//NM_00	0.023			1.09	1.18	-1.01	-1.04	<i>Rgs3</i>	regulator of G-protein signaling 3	0007165 // signal transduction // not recorded//0007186 // G-protein coupled receptor
NM_0262		0.0381			1.27	-1.10	-1.01	1.06	<i>Fibin</i>	fin bud initiation factor homolog (zebrafish)	
NM_0112		0.0264		0.021	1.14	1.02	-1.01	1.05	<i>Rad9a</i>	RAD9 homolog A	0000075 // cell cycle checkpoint // inferred from electronic annotation//0000076 // DN,
NM_0011		0.0426			-1.20	-1.60	-1.01	-1.06	<i>Fxr1</i>	fragile X mental retardation gene 1, autosomal homolog	0007275 // multicellular organismal development // inferred from electronic annotation/
NM_010098	//XM_0047				-1.09	-1.03	-1.01	-1.14	<i>Opn3</i>	opsin 3	0007165 // signal transduction // inferred from electronic annotation//0007186 // G-pr
NM_0089		0.0124			1.04	-1.24	-1.01	-1.03	<i>Ptger2</i>	prostaglandin E receptor 2 (subtype EP2)	0007165 // signal transduction // inferred from electronic annotation//0007186 // G-pr
NM_001290299	//NM_14	0.037			1.04	1.02	-1.01	-1.16	<i>Plppr2</i>	phospholipid phosphatase related 2	0006470 // protein dephosphorylation // inferred from electronic annotation//0006644
NM_134097		0.038			-1.02	1.07	-1.01	1.18	<i>Topors</i>	topoisomerase I binding, arginine/serine-rich	0006511 // ubiquitin-dependent protein catabolic process // not recorded//0006513 //
NM_0011		0.0328			1.16	-1.03	-1.01	1.11	<i>Isir</i>	immunoglobulin superfamily containing leucine-rich repeat	
NM_0012		0.0147			1.02	1.18	-1.01	-1.12	<i>Arhgap9</i>	Rho GTPase activating protein 9	0007165 // signal transduction // inferred from electronic annotation//0043547 // posi
NM_001305185	//NM_00	0.009			1.08	-1.02	-1.01	-1.07	<i>Plekha7</i>	pleckstrin homology domain containing, family A member 7	0045218 // zonula adherens maintenance // not recorded//0090136 // epithelial cell-ce
NM_0205		0.0125			-1.02	1.07	-1.01	-1.01	<i>Flad1//Lenep</i>	RFad1, flavin adenine dinucleotide synthetase, homolog (yeast)//lens epithelial prote	0006747 // FAD biosynthetic process // inferred from electronic annotation//0007275 //,
NM_026639		0.017	0.002		-1.13	-1.07	-1.01	1.16	<i>Art4</i>	ADP-ribosyltransferase 4	0006471 // protein ADP-ribosylation // inferred from electronic annotation
NM_0013		0.0226			-1.15	-1.00	-1.01	-1.03	<i>Ahcy//Gm4737</i>	S-adenosylhomocysteine hydrolase//predicted gene 4737	0002439 // chronic inflammatory response to antigenic stimulus // not recorded//00067
NM_0098		0.0298			1.12	1.70	-1.01	-1.04	<i>Cd19</i>	CD19 antigen	0006968 // cellular defense response // not recorded//0007173 // epidermal growth fac
NM_0074		0.0393			1.09	-1.45	-1.01	1.06	<i>Adrb2</i>	adrenergic receptor, beta 2	0001666 // response to hypoxia // inferred from electronic annotation//0001889 // livei
NM_0206		0.0151			-1.03	-1.17	-1.01	-1.01	<i>Cramp1</i>	Crn, cramped-like (Drosophila)	
NM_0110		0.0317			-1.09	1.05	-1.01	1.14	<i>Pfdn2</i>	prefoldin 2	0006457 // protein folding // inferred from direct assay//0051495 // positive regulation
NM_0011		0.0186			-1.04	1.25	-1.01	1.01	<i>Mical1</i>	microtubule associated monooxygenase, calponin and LIM domain containing 1	0001933 // negative regulation of protein phosphorylation // inferred from mutant phen
NM_1460		0.0061			1.05	1.31	-1.01	-1.04	<i>Nrras</i>	negative regulator of reactive oxygen species	0002376 // immune system process // inferred from electronic annotation//0006801 //
NM_0187		0.0072			1.06	-1.09	-1.01	1.10	<i>Atp6ap1</i>	ATPase, H+ transporting, lysosomal accessory protein 1	0006810 // transport // inferred from electronic annotation//0006811 // ion transport/
NM_011693		0.047			-1.19	-1.23	-1.01	1.11	<i>Vcam1</i>	vascular cell adhesion molecule 1	0007155 // cell adhesion // inferred from direct assay//0007155 // cell adhesion // not r
NM_0013		0.0162			1.02	1.25	-1.01	1.01	<i>Cnr2</i>	cannabinoid receptor 2 (macrophage)	0001975 // response to amphetamine // inferred from electronic annotation//0006954.
NM_007650	//XM_00652	0.015			1.06	1.16	-1.01	-1.28	<i>Cd5</i>	CD5 antigen	0006898 // receptor-mediated endocytosis // inferred from electronic annotation//0031
NM_001105066	// 0.05				-1.02	1.04	-1.01	-1.04	<i>Vmn2r34//Vmn2r42//Vmn2r45</i>	vomeronal 2, receptor 34//vomeronal 2, receptor 42//vomeronal 2, receptor	0007165 // signal transduction // inferred from electronic annotation//0007186 // G-pr
NM_001004150	//NM_00	0.04			-1.18	-1.13	-1.01	1.27	<i>A4galt</i>	alpha 1,4-galactosyltransferase	0001576 // globoside biosynthetic process // inferred from direct assay//0001576 // glo
NM_0011		0.0011			1.15	-1.24	-1.01	1.12	<i>Slc4a5</i>	solute carrier family 4, sodium bicarbonate cotransporter, member 5	0002064 // epithelial cell development // inferred from mutant phenotype//0003014 //
NM_0091		0.0478			-1.09	1.21	-1.01	-1.06	<i>Selplg</i>	selectin, platelet (p-selectin) ligand	0007155 // cell adhesion // inferred from electronic annotation//0050901 // leukocyte t
NM_008962	//XR_383147	0.006			1.00	1.01	-1.01	-1.18	<i>Ptgdr</i>	prostaglandin D receptor	0006954 // inflammatory response // inferred from mutant phenotype//0007165 // sigr
NM_001033231	//XM_01	0.006			1.09	1.02	-1.01	-1.11	<i>Fam195b</i>	family with sequence similarity 195, member B	0010717 // regulation of epithelial to mesenchymal transition // not recorded
NM_009630	//XM_00651	0.024			1.01	1.08	-1.01	-1.11	<i>Adora2a</i>	adenosine A2a receptor	0001963 // synaptic transmission, dopaminergic // inferred from genetic interaction//OC
NM_0011		0.0082		0.035	1.17	-1.02	-1.01	1.04	<i>Tmem80</i>	transmembrane protein 80	
NM_001146023	//NM_02	0.018			1.13	1.16	-1.00	-1.02	<i>Fam98c</i>	family with sequence similarity 98, member C	
NM_1393		0.0136			1.05	-1.14	-1.00	1.08	<i>Vasn</i>	vasorin	0010719 // negative regulation of epithelial to mesenchymal transition // not recorded//,
NM_016854		0.049			-1.18	-1.08	-1.00	-1.09	<i>Ppp1r3c</i>	protein phosphatase 1, regulatory (inhibitor) subunit 3C	0005975 // carbohydrate metabolic process // inferred from electronic annotation//000
NM_001291442	// 0.024				1.05	1.00	-1.00	1.14	<i>Micu1</i>	mitochondrial calcium uptake 1	0006810 // transport // inferred from electronic annotation//0006811 // ion transport/
NM_0011		0.0211			1.09	-1.06	-1.00	1.04	<i>Enpp2</i>	ectonucleotide pyrophosphatase/phosphodiesterase 2	0001953 // negative regulation of cell-matrix adhesion // not recorded//0006629 // lipic
NM_001047158	//NM_19	0.026			1.04	1.01	-1.00	-1.06	<i>Uqcrl2</i>	ubiquinol-cytochrome c reductase, complex III subunit X	0006122 // mitochondrial electron transport, ubiquinol to cytochrome c // inferred from
NM_0199		0.0288			1.06	-1.14	-1.00	-1.13	<i>Zfp235</i>	zinc finger protein 235	0006355 // regulation of transcription, DNA-templated // inferred from electronic annot
NM_0214		0.0191			1.14	-1.17	-1.00	-1.17	<i>Shank3</i>	SH3/ankyrin domain gene 3	0000165 // MAPK cascade // inferred from genetic interaction//0001838 // embryonic e
NM_0010		0.0404			-1.94	-5.56	-1.00	-1.16	<i>Zbtb16</i>	zinc finger and BTB domain containing 16	0000122 // negative regulation of transcription from RNA polymerase II promoter // not r
NM_130892	//XR_0019				1.06	1.02	-1.00	-1.01	<i>Rtn4ip1</i>	reticulin 4 interacting protein 1	0055114 // oxidation-reduction process // inferred from electronic annotation
NM_0010	#####	0.039			1.10	-1.13	-1.00	-1.07	<i>Zbtb2</i>	zinc finger and BTB domain containing 2	
NM_0013		0.0316			1.20	-1.08	-1.00	1.01	<i>Spry7</i>	SPRY domain containing 7	
NM_023463		0.008			1.02	1.09	-1.00	1.21	<i>Ly6g6c</i>	lymphocyte antigen 6 complex, locus G6C	
NM_0213		0.0272		0.027	1.17	-1.06	-1.00	-1.19	<i>Slc26a3</i>	solute carrier family 26, member 3	0006810 // transport // inferred from electronic annotation//0006821 // chloride trans
NM_0091	#####				1.00	-1.13	-1.00	1.00	<i>Slc16a2</i>	solute carrier family 16 (monocarboxylic acid transporters), member 2	0006810 // transport // inferred from electronic annotation//0009914 // hormone trans
NM_025963	//XM_01124	0.011			1.03	1.13	-1.00	-1.04	<i>Rps10//Rps10-ps2</i>	ribosomal protein S10//ribosomal protein S10, pseudogene 2	0000028 // ribosomal small subunit assembly // ---
NM_0010		0.009			1.10	-1.12	-1.00	1.06	<i>Syne1</i>	spectrin repeat containing, nuclear envelope 1	0007030 // Golgi organization // not recorded//0040023 // establishment of nucleus loc
NM_0013		0.0139			1.06	-1.23	-1.00	1.03	<i>Tpk1</i>	thiamine pyrophosphokinase	0006772 // thiamine metabolic process // inferred from direct assay//0009229 // thiami

RefSeq	Tri.p	24h	p	48h	p	72h	FD Air	FD 24h	FD 48h	FD 72h	Gene Symbol	Gene Title	Gene Ontology Biological Process
NM_001172112	0.024	0.035	-1.12	-1.01	-1.00	1.08					<i>Dhrs7b</i>	dehydrogenase/reductase (SDR family) member 7B	0008152 // metabolic process // inferred from electronic annotation//00055114 // oxidal
NM_0010	0.0394		-1.05	1.07	1.00	-1.13					<i>Tnfrsf9</i>	tumor necrosis factor receptor superfamily, member 9	0006954 // inflammatory response // not recorded//0006955 // immune response // nc
NM_0086	0.0471		-1.07	1.07	1.00	-1.11					<i>Msh2</i>	mutS homolog 2 (E. coli)	0000710 // meiotic mismatch repair // not recorded//0001701 // in utero embryonic de
NM_0011	0.045		1.00	1.26	1.00	1.03					<i>Sh3bp2</i>	SH3-domain binding protein 2	
NM_0011	0.0035		-1.05	1.12	1.00	1.10					<i>Ptpra</i>	protein tyrosine phosphatase, receptor type, A	0006468 // protein phosphorylation // inferred from direct assay//0006470 // protein d
NM_0194	0.0209		1.03	1.49	1.00	1.15					<i>Tmem37</i>	transmembrane protein 37	0006810 // transport // inferred from electronic annotation//0006811 // ion transport /
NM_0011	0.0131	0.003	1.22	1.09	1.00	1.04					<i>Prrc2a</i>	proline-rich coiled-coil 2A	
NM_0166	0.0374		1.01	1.14	1.00	-1.01					<i>Cldn2</i>	claudin 2	0016338 // calcium-independent cell-cell adhesion via plasma membrane cell-adhesion n
NM_1722	0.0203		1.05	1.31	1.00	-1.01					<i>Plcg2</i>	phospholipase C, gamma 2	0002092 // positive regulation of receptor internalization // inferred from mutant phenol
NM_0074	0.0357		-1.08	1.02	1.00	-1.14					<i>Adra2a</i>	adrenergic receptor, alpha 2a	0001819 // positive regulation of cytokine production // not recorded//0002526 // acut
NM_0117	0.045		-1.08	1.19	1.00	-1.23					<i>Wnt9b</i>	wingless-type MMTV integration site family, member 9B	0001658 // branching involved in ureteric bud morphogenesis // inferred from genetic in
NM_001045525	0.044	0.044	1.00	1.04	1.00	1.17					<i>Cybd1</i>	cytochrome b5 domain containing 1	
NM_1454	0.0134		-1.01	1.14	1.00	1.09					<i>Stk24</i>	serine/threonine kinase 24	0006468 // protein phosphorylation // not recorded//0006915 // apoptotic process // tr
NM_024288	0.013	0.013	1.02	-1.04	1.00	1.25					<i>Rmnd5a</i>	required for meiotic nuclear division 5 homolog A (S. cerevisiae)	
NM_146168	0.021	0.021	-1.14	-1.23	1.00	1.08					<i>Vopp1</i>	vesicular, overexpressed in cancer, prosurvival protein 1	0006351 // transcription, DNA-templated // inferred from electronic annotation//00063
NM_175324	0.004	0.004	1.01	-1.04	1.00	1.18					<i>Acad11</i>	acyl-Coenzyme A dehydrogenase family, member 11	0008152 // metabolic process // inferred from electronic annotation//0003539 // fatty a
NM_0010	0.0478		-1.12	1.03	1.00	-1.01					<i>St3gal5</i>	ST3 beta-galactoside alpha-2,3-sialyltransferase 5	0001574 // ganglioside biosynthetic process // not recorded//0006486 // protein glyco
NM_1725	0.042		-1.02	1.14	1.00	1.03					<i>Rufy1</i>	RUN and FYVE domain containing 1	0006810 // transport // inferred from electronic annotation//0006897 // endocytosis //
NM_025914	0.031	0.031	-1.05	-1.14	1.00	1.06					<i>Actr6</i>	ARP6 actin-related protein 6	0006338 // chromatin remodeling // inferred from electronic annotation
NM_0074	0.0027		-1.08	1.15	1.00	-1.01					<i>Adora2b</i>	adenosine A2b receptor	0001973 // adenosine receptor signaling pathway // inferred from electronic annotation/
NM_001033908	0.045	0.03	1.14	1.00	1.00	-1.08					<i>Med22</i>	mediator complex subunit 22	0006351 // transcription, DNA-templated // inferred from electronic annotation//00063
NM_0010	0.0387		-1.04	1.30	1.00	1.20					<i>Eno1</i>	enolase 1, alpha non-neuron//enolase 1B, retrotransposed	0001701 // in utero embryonic development // inferred from mutant phenotype//00060
NM_0010	0.0387		1.07	-1.08	1.00	1.07					<i>Adam28</i>	a disintegrin and metalloproteinase domain 28	0006508 // proteolysis // inferred from electronic annotation//0007229 // integrin-med
NM_134133	0.015	0.015	-1.17	-1.23	1.00	-1.03					<i>Smim3</i>	small integral membrane protein 3	
NM_0012	0.0014		-1.02	1.31	1.00	-1.14					<i>B4galnt1</i>	beta-1,4-N-acetyl-galactosaminyl transferase 1	0001574 // ganglioside biosynthetic process // inferred from genetic interaction//00015
NM_1339	0.0025		1.01	1.27	1.00	-1.13					<i>Chpf2</i>	chondroitin polymerizing factor 2	0008152 // metabolic process // inferred from electronic annotation
NM_027909	0.034	0.034	1.05	1.06	1.00	-1.00					<i>C2cd2l</i>	C2 calcium-dependent domain containing 2-like	0035774 // positive regulation of insulin secretion involved in cellular response to glucos
NM_0198	0.0207		-1.02	-1.24	1.00	-1.08					<i>Gkap1</i>	G kinase anchoring protein 1	0007165 // signal transduction // inferred from direct assay//0007199 // G-protein cou
NM_025989	0.03	0.03	-1.17	-1.11	1.00	1.06					<i>Gp2</i>	glycoprotein 2 (zymogen granule membrane)	0002412 // antigen transcytosis by M cells in mucosal-associated lymphoid tissue // infer
NM_008598	0.023	0.023	1.05	1.00	1.00	-1.18					<i>Mgmt</i>	O-6-methylguanine-DNA methyltransferase	0006281 // DNA repair // inferred from mutant phenotype//0006307 // DNA dealkylat
NM_031406	0.017	0.017	1.12	1.06	1.00	-1.03					<i>Slc12a9</i>	solute carrier family 12 (potassium/chloride transporters), member 9	0006810 // transport // inferred from electronic annotation//0006811 // ion transport /
NM_0260	0.0079		1.04	1.18	1.00	1.11					<i>Ikbkap</i>	inhibitor of kappa light polypeptide enhancer in B cells, kinase complex-associated pro	0006351 // transcription, DNA-templated // inferred from electronic annotation//00063
NM_0075	0.0087		1.02	1.19	1.00	-1.15					<i>Phb2</i>	prohibitin 2	0000060 // protein import into nucleus, translocation // not recorded//0006351 // tran
NM_0532	0.0446		-1.10	1.11	1.00	-1.06					<i>Myo1f</i>	myosin IF	0002446 // neutrophil mediated immunity // inferred from mutant phenotype//000716:
NM_0012	0.0207	0.048	1.07	-1.29	1.00	1.33					<i>Cipc</i>	CLOCK interacting protein, circadian	0006351 // transcription, DNA-templated // inferred from electronic annotation//00063
NM_0090	0.0324		-1.07	1.06	1.00	1.04					<i>Rasgrf2</i>	RAS protein-specific guanine nucleotide-releasing factor 2	0007264 // small GTPase mediated signal transduction // inferred from electronic annota
NM_145416	0.016	0.016	1.07	-1.04	1.00	-1.09					<i>Kri1</i>	KRI1 homolog (S. cerevisiae)	
NM_0010	0.0223		1.07	-1.00	1.00	1.02					<i>Atxn7l3b</i>	ataxin 7-like 3B	
NM_001185083	0.022	0.022	1.07	1.02	1.00	-1.09					<i>Ins2</i>	insulin II	0000122 // negative regulation of transcription from RNA polymerase II promoter // infer
NM_0013	0.0451	0.002	1.09	-1.02	1.00	1.02					<i>Tmub2</i>	transmembrane and ubiquitin-like domain containing 2	
NM_001081339	0.034	0.034	-1.11	-1.15	1.00	-1.19					<i>Xirp1</i>	xin actin-binding repeat containing 1	0003007 // heart morphogenesis // not recorded//0007219 // Notch signaling pathway
NM_0011	0.003		1.11	-1.33	1.00	-1.04					<i>Gjc1</i>	gap junction protein, gamma 1	0001570 // vasculogenesis // inferred from mutant phenotype//0007154 // cell commu
NM_0011	0.0038		-1.05	1.18	1.01	-1.14					<i>Psmg4</i>	proteasome (prosome, macropain) assembly chaperone 4	0043248 // proteasome assembly // inferred from electronic annotation
NM_001290011	0.047	0.047	1.06	-1.04	1.01	-1.10					<i>Pemt</i>	phosphatidylethanolamine N-methyltransferase	0006629 // lipid metabolic process // inferred from electronic annotation//0006644 // p
NM_1988	0.0321		1.12	-1.04	1.01	-1.07					<i>Scx</i>	scleraxis	0001707 // mesoderm formation // inferred from mutant phenotype//0001894 // tissue
NM_001122958	0.014	0.014	-1.12	-1.04	1.01	-1.01					<i>Rad54l</i>	RAD54 like (S. cerevisiae)	0000724 // double-strand break repair via homologous recombination // inferred from g
NM_0012	0.0226	0.04	-1.07	1.03	1.01	-1.08					<i>D16Erd472e</i>	DNA segment, Chr 16, ERATO Doi 472, expressed	
NM_0013	0.0417		-1.01	1.11	1.01	1.10					<i>Psmf1</i>	proteasome (prosome, macropain) inhibitor subunit 1	0006511 // ubiquitin-dependent protein catabolic process // not recorded//1901799 //
NM_177876	0.047	0.047	1.03	1.12	1.01	-1.19					<i>Vps37b</i>	vacuolar protein sorting 37B (yeast)	0006810 // transport // inferred from electronic annotation//0015031 // protein transp
NM_0013	0.0373		1.01	1.32	1.01	-1.13					<i>Unc119</i>	unc-119 homolog (C. elegans)	0006810 // transport // inferred from electronic annotation//0006897 // endocytosis //
NM_001164082	0.033	0.033	-1.01	1.06	1.01	-1.11					<i>Polr3d</i>	polymerase (RNA) III (DNA directed) polypeptide D	0002376 // immune system process // inferred from electronic annotation//0006351 //
NM_0011	0.0089		-1.16	1.11	1.01	-1.11					<i>Lmo4</i>	LIM domain only 4	0001843 // neural tube closure // inferred from mutant phenotype//0003281 // ventric
NM_1454	0.0181		-1.01	1.09	1.01	-1.02					<i>Heatr6</i>	HEAT repeat containing 6	
NM_0011	0.0089		1.02	-1.24	1.01	1.10					<i>Tsc22d1</i>	TSC22 domain family, member 1	0006351 // transcription, DNA-templated // inferred from electronic annotation//00063
NM_009076	0.007	0.007	1.02	1.22	1.01	-1.15					<i>LOC102635048</i>	60S ribosomal protein L12 pseudogene//ribosomal protein L12//ribosomal protein L	0000027 // ribosomal large subunit assembly // ---//0006412 // translation // inferred fr
NM_0195	0.0295		1.01	-1.27	1.01	1.00					<i>Pfce1</i>	phospholipase C, epsilon 1	0000187 // activation of MAPK activity // not recorded//0006629 // lipid metabolic pro
NM_0011	0.0441		1.13	-1.02	1.01	1.05					<i>Sprtn</i>	SprT-like N-terminal domain	0006281 // DNA repair // inferred from electronic annotation//0006974 // cellular resp
NM_0010	0.0376		1.01	-1.12	1.01	1.09					<i>Myrf</i>	myelin regulatory factor	0006351 // transcription, DNA-templated // inferred from electronic annotation//00063
NM_025857	0.006	0.006	-1.02	1.02	1.01	1.11					<i>Aagab</i>	alpha- and gamma-adaptin binding protein	0006810 // transport // inferred from electronic annotation//0015031 // protein transp
NM_0540	0.0438	0.047	1.14	-1.03	1.01	1.13					<i>Pip4k2c</i>	phosphatidylinositol-5-phosphate 4-kinase, type II, gamma	0010506 // regulation of autophagy // not recorded//0016310 // phosphorylation // inf
NM_025465	0.036	0.036	-1.12	1.01	1.01	-1.02					<i>Tma16</i>	translation machinery associated 16 homolog (S. cerevisiae)	
NM_0111	0.0356		-1.01	1.08	1.01	1.17					<i>Pa2g4</i>	proliferation-associated 2G4	0006351 // transcription, DNA-templated // inferred from electronic annotation//00063
NM_030168	0.016	0.016	-1.06	-1.01	1.01	1.01					<i>Rictor</i>	RPTOR independent companion of MTOR, complex 2	0001932 // regulation of protein phosphorylation // inferred from mutant phenotype//C
NM_0306	0.0329		1.07	-1.26	1.01	1.02					<i>Kank3</i>	KN motif and ankyrin repeat domains 3	0051497 // negative regulation of stress fiber assembly // not recorded



RefSeq	Tri	p 24h	p 48h	p 72h	FD Air	FD 24h	FD 48h	FD 72h	Gene Symbol	Gene Title	Gene Ontology Biological Process
NM_0092	0.003	0.046	1.13	-1.05	1.02	1.10	1.10	1.10	<i>Sptbn1</i>	spectrin beta, non-erythrocytic 1	0000281 // mitotic cytokinesis // not recorded//0007009 // plasma membrane organiza
NM_0012	0.0055		1.07	-1.04	1.02	1.05	1.05	1.05	<i>Foxj3</i>	forkhead box J3	0006351 // transcription, DNA-templated // inferred from electronic annotation//000063
NM_001038608	///NM_00	0.03	1.04	1.08	1.02	-1.04	-1.04	-1.04	<i>Txn14a</i>	thioredoxin-like 4A	0000245 // spliceosomal complex assembly // not recorded//0000398 // mRNA splicing,
NM_0099	0.0137		-1.30	1.06	1.02	1.03	1.03	1.03	<i>Ccr1</i>	chemokine (C-C motif) receptor 1	0006816 // calcium ion transport // not recorded//0006874 // cellular calcium ion home
NM_0012	0.0019		1.11	1.73	1.02	-1.01	-1.01	-1.01	<i>Fcer2a</i>	Fc receptor, IgE, low affinity II, alpha polypeptide	0002925 // positive regulation of humoral immune response mediated by circulating immr
NM_1341	0.013		1.09	1.35	1.02	1.25	1.25	1.25	<i>Gpsm3</i>	G-protein signalling modulator 3 (AGS3-like, C. elegans)	0002690 // positive regulation of leukocyte chemotaxis // inferred from mutant phenoty
NM_001290817	///	0.047	-1.19	-1.15	1.02	1.00	1.00	1.00	<i>Sparc</i>	secreted acidic cysteine rich glycoprotein	0001503 // ossification // inferred from electronic annotation//0001937 // negative reg
NM_0010	0.0148		1.03	-1.12	1.02	1.18	1.18	1.18	<i>Hnrnpul2</i>	heterogeneous nuclear ribonucleoprotein U-like 2	
NM_023732	///XM	0.012	-1.04	1.13	1.02	-1.01	-1.01	-1.01	<i>Abcb6</i>	ATP-binding cassette, sub-family B (MDR/TAP), member 6	0006779 // porphyrin-containing compound biosynthetic process // not recorded//0006
NM_0298	0.0161		-1.07	-1.28	1.02	1.17	1.17	1.17	<i>Chmp5</i>	charged multivesicular body protein 5	0000920 // cell separation after cytokinesis // not recorded//0001919 // regulation of re
NM_0010	0.0223	0.017	1.01	-1.13	1.02	-1.20	-1.20	-1.20	<i>Glyctk</i>	glycerate kinase	0006468 // protein phosphorylation // not recorded//0016310 // phosphorylation // inf
NM_172710	///XM_01124	0.017	-1.14	1.07	1.02	1.07	1.07	1.07	<i>Sel1l3</i>	sel-1 suppressor of lin-12-like 3 (C. elegans)	
NM_0013	0.0039		1.14	2.54	1.02	-1.02	-1.02	-1.02	<i>Cd79b</i>	CD79B antigen	0002250 // adaptive immune response // inferred from electronic annotation//0002376
NM_001304773	///NM_00	0.03	-1.04	-1.13	1.02	1.07	1.07	1.07	<i>Pex26</i>	peroxisomal biogenesis factor 26	0006810 // transport // inferred from electronic annotation//0015031 // protein transp
NM_011295	///XR	0.016	1.02	1.15	1.02	-1.00	-1.00	-1.00	<i>Rps12</i> ///Rps12-ps10//Rps12-ps11//Rps1	ribosomal protein S12//ribosomal protein S12, pseudogene 10//ribosomal protein S	0006412 // translation // inferred from electronic annotation
NM_0287	#####		1.05	-1.05	1.02	-1.03	-1.03	-1.03	<i>Gm10651</i> ///Josl61	predicted pseudogene 10651//Josephin domain containing 1	0006508 // proteolysis // inferred from electronic annotation
NM_0261	0.0329		1.12	-1.22	1.02	-1.22	-1.22	-1.22	<i>Dedd2</i>	death effector domain-containing DNA binding protein 2	0006351 // transcription, DNA-templated // inferred from electronic annotation//00063
NM_0263	0.0368		-1.15	1.25	1.02	-1.18	-1.18	-1.18	<i>Cdk2ap2</i>	CDK2-associated protein 2	
NM_0010	0.011		1.11	-1.01	1.02	1.17	1.17	1.17	<i>Arid1a</i>	AT rich interactive domain 1A (SWI-like)	0000122 // negative regulation of transcription from RNA polymerase II promoter // infer
NM_0294	0.0458		1.05	1.26	1.02	-1.08	-1.08	-1.08	<i>Ms4a4c</i>	membrane-spanning 4-domains, subfamily A, member 4C	
NM_0200	0.0109		1.04	1.29	1.02	1.10	1.10	1.10	<i>Tacstd2</i>	tumor-associated calcium signal transducer 2	0010633 // negative regulation of epithelial cell migration // inferred from direct assay//
NM_001286005	///NM_02	0.019	1.03	-1.03	1.02	-1.15	-1.15	-1.15	<i>Abcg8</i>	ATP-binding cassette, sub-family G (WHITE), member 8	0006810 // transport // inferred from electronic annotation//0007584 // response to nu
NM_0010	0.0014		1.02	1.28	1.02	-1.18	-1.18	-1.18	<i>Akna</i>	AT-hook transcription factor	0006351 // transcription, DNA-templated // inferred from electronic annotation//00063
NM_0011	0.0099		1.14	-1.03	1.02	1.08	1.08	1.08	<i>Cntn1</i>	contactin 1	0007155 // cell adhesion // inferred from electronic annotation//0007219 // Notch sign:
NM_0194	0.0296		1.15	1.01	1.02	-1.03	-1.03	-1.03	<i>Hes6</i>	hairy and enhancer of split 6	0000122 // negative regulation of transcription from RNA polymerase II promoter // infer
NM_024465	///XM_00650	0.043	1.12	1.16	1.02	1.01	1.01	1.01	<i>Abhd12</i>	abhydrolase domain containing 12	0006660 // phosphatidylserine catabolic process // inferred from mutant phenotype//00
NM_0011	0.0028		1.07	-1.06	1.02	1.04	1.04	1.04	<i>Senp3</i>	SUMO/sentrin specific peptidase 3	0006508 // proteolysis // inferred from electronic annotation//0016926 // protein desu
NM_001289848	///NM_00	0.034	-1.01	1.11	1.02	1.15	1.15	1.15	<i>Cox6b2</i>	cytochrome c oxidase subunit VIb polypeptide 2	1902600 // hydrogen ion transmembrane transport // inferred from electronic annotat
NM_0010	0.0088		-1.04	1.23	1.02	-1.05	-1.05	-1.05	<i>Ptpn6</i>	protein tyrosine phosphatase, non-receptor type 6	0002244 // hematopoietic progenitor cell differentiation // inferred from mutant phenot
NM_0074	#####		1.01	1.24	1.02	1.14	1.14	1.14	<i>Rplp0</i>	ribosomal protein, large, P0	0042254 // ribosome biogenesis // inferred from electronic annotation//0071353 // cell
NM_018779	///XM_00650	0.02	1.03	-1.10	1.02	-1.20	-1.20	-1.20	<i>Pde3a</i>	phosphodiesterase 3A, cGMP inhibited	0001556 // oocyte maturation // inferred from direct assay//0006198 // cAMP catabolic
NM_0011	0.0123		-1.04	1.11	1.02	-1.07	-1.07	-1.07	<i>LOC102641289</i> ///Tbc1d14	TBC1 domain family member 14//TBC1 domain family, member 14	0010507 // negative regulation of autophagy // not recorded//0043547 // positive regul
NM_0119	0.0495		-1.02	1.20	1.02	1.11	1.11	1.11	<i>Nubp2</i>	nucleotide binding protein 2	0016226 // iron-sulfur cluster assembly // inferred from electronic annotation//003003
NM_0010	0.0313		1.06	-1.15	1.02	1.06	1.06	1.06	<i>Phactr1</i>	phosphatase and actin regulator 1	0031032 // actomyosin structure organization // inferred from mutant phenotype//003:
NM_0012	0.0428		1.15	-1.04	1.02	1.08	1.08	1.08	<i>Wdr13</i>	WD repeat domain 13	
NM_0256	0.0273	0.008	1.08	1.03	1.03	1.16	1.16	1.16	<i>Rnf181</i>	ring finger protein 181	0000209 // protein polyubiquitination // --//0016567 // protein ubiquitination // infer
NM_177638	///XM_00652	0.027	1.11	1.08	1.03	-1.09	-1.09	-1.09	<i>Crb3</i>	crumbs family member 3	0045198 // establishment of epithelial cell apical/basal polarity // not recorded//00452
NM_1447	0.0074		1.11	1.39	1.03	-1.13	-1.13	-1.13	<i>Metrn1</i>	meteorin, glial cell differentiation regulator-like	0009409 // response to cold // inferred from direct assay//0014850 // response to musc
NM_033324	///XM	0.032	-1.06	1.10	1.03	-1.05	-1.05	-1.05	<i>Dgcr8</i>	DiGeorge syndrome critical region gene 8	0031053 // primary miRNA processing // not recorded//0072091 // regulation of stem c
NM_012017	///XM	0.003	1.20	1.11	1.03	1.11	1.11	1.11	<i>Zfp346</i>	zinc finger protein 346	0043065 // positive regulation of apoptotic process // inferred from mutant phenotype//
NM_0242	0.0389		1.00	1.10	1.03	1.04	1.04	1.04	<i>Ipo4</i> ///Tms9sf1	importin 4//transmembrane 9 superfamily member 1	0000059 // protein import into nucleus, docking // not recorded//0000060 // protein im
NM_001277265	///NM_00	0.004	1.13	1.03	1.03	-1.18	-1.18	-1.18	<i>Tbxa2r</i>	thromboxane A2 receptor	0006954 // inflammatory response // inferred from mutant phenotype//0007165 // sigr
NM_0011	0.0291		-1.03	-1.17	1.03	1.03	1.03	1.03	<i>Bub1</i>	budding uninhibited by benzimidazoles 1 homolog (S. cerevisiae)	0006468 // protein phosphorylation // inferred from electronic annotation//0006915 //
NM_0091	0.0346	0.036	1.06	1.00	1.03	1.21	1.21	1.21	<i>Sepw1</i>	selenoprotein W, muscle 1	0045454 // cell redox homeostasis // inferred from electronic annotation//0055114 // o
NM_0087	0.0074		1.02	-1.19	1.03	1.00	1.00	1.00	<i>Notch1</i>	notch 1	0000122 // negative regulation of transcription from RNA polymerase II promoter // infer
NM_0137	0.0122		-1.18	1.65	1.03	-1.23	-1.23	-1.23	<i>Cd52</i>	CD52 antigen	
NM_0011	0.011		1.14	1.38	1.03	1.02	1.02	1.02	<i>Myc</i>	myelocytomatosis oncogene	0000122 // negative regulation of transcription from RNA polymerase II promoter // infer
NM_145134		0.007	1.03	1.03	1.03	-1.17	-1.17	-1.17	<i>Spsb4</i>	splA/ryanodine receptor domain and SOCS box containing 4	0016567 // protein ubiquitination // inferred from electronic annotation//0035556 // in
NM_0113	0.0273		1.08	-1.08	1.03	1.16	1.16	1.16	<i>Scnn1g</i>	sodium channel, nonvoltage-gated 1 gamma	0006810 // transport // inferred from electronic annotation//0006811 // ion transport /
NM_0010	0.0046		-1.08	1.58	1.03	1.00	1.00	1.00	<i>Evi2a</i>	ecotropic viral integration site 2a	
NM_0260	#####		-1.06	1.12	1.03	-1.01	-1.01	-1.01	<i>Rrp15</i>	ribosomal RNA processing 15 homolog (S. cerevisiae)	
NM_001128609	///	0.044	-1.01	1.01	1.03	1.04	1.04	1.04	<i>Dedd</i>	death effector domain-containing	0006351 // transcription, DNA-templated // inferred from electronic annotation//00063
NM_0013	0.0304		-1.10	1.10	1.03	1.23	1.23	1.23	<i>Rab5c</i>	RAB5C, member RAS oncogene family	0006810 // transport // inferred from electronic annotation//0006886 // intracellular pr
NM_0010	#####		1.12	-1.03	1.03	1.34	1.34	1.34	<i>Rere</i>	arginine glutamic acid dipeptide (RE) repeats	0000122 // negative regulation of transcription from RNA polymerase II promoter // infer
NM_009201	///XM	0.048	1.24	1.24	1.03	1.09	1.09	1.09	<i>Slc1a5</i>	solute carrier family 1 (neutral amino acid transporter), member 5	0003333 // amino acid transmembrane transport // not recorded//0006810 // transpor
NM_1769	0.0166		-1.01	-1.08	1.03	1.00	1.00	1.00	<i>Galm</i>	galactose mutarotase	0005975 // carbohydrate metabolic process // not recorded//0006006 // glucose metab
NM_0012	0.0046		-1.03	1.23	1.03	1.01	1.01	1.01	<i>Sulf2</i>	sulfatase 2	0001822 // kidney development // inferred from genetic interaction//0002063 // chond
NM_0011	0.0456		-1.07	-1.34	1.03	1.01	1.01	1.01	<i>Atp7a</i>	ATPase, Cu++ transporting, alpha polypeptide	0001568 // blood vessel development // inferred from mutant phenotype//0001701 // i
NM_027898	///XM_00654	0.024	1.03	1.00	1.03	-1.28	-1.28	-1.28	<i>Gramd1a</i>	GRAM domain containing 1A	
NM_054094	///XM	0.046	-1.17	-1.08	1.03	1.10	1.10	1.10	<i>Acsm1</i>	acyl-CoA synthetase medium-chain family member 1	0006629 // lipid metabolic process // inferred from electronic annotation//0006631 // f.
NM_0010	0.0261		1.11	-1.10	1.03	-1.06	-1.06	-1.06	<i>Arl4a</i>	ADP-ribosylation factor-like 4A	0007264 // small GTPase mediated signal transduction // inferred from electronic annota
NM_011657	///XM_00650	0.009	-1.04	-1.02	1.03	1.08	1.08	1.08	<i>Tulp3</i>	tubby-like protein 3	0001841 // neural tube formation // inferred from mutant phenotype//0001843 // neur
NM_0101	0.0018		1.08	-1.20	1.03	-1.11	-1.11	-1.11	<i>Efnb1</i>	ephrin B1	0001755 // neural crest cell migration // inferred from mutant phenotype//0007275 // r
NM_008172	///XM_00654	0.007	1.04	1.04	1.03	-1.24	-1.24	-1.24	<i>Grin2d</i>	glutamate receptor, ionotropic, NMDA2D (epsilon 4)	0001964 // startle response // inferred from mutant phenotype//0006810 // transport /



RefSeq	Tri	p 24h	p 48h	p 72h	FD Air	FD 24h	FD 48h	FD 72h	Gene Symbol	Gene Title	Gene Ontology Biological Process
NM_0012		0.016			-1.03	1.11	1.03	1.05	<i>Pex5</i>	peroxisomal biogenesis factor 5	0000038 // very long-chain fatty acid metabolic process // inferred from mutant phenoty
NM_0083		0.0456			-1.01	1.11	1.03	-1.33	<i>Il3ra</i>	interleukin 3 receptor, alpha chain	00191221 // cytokine-mediated signaling pathway // inferred from electronic annotation
NM_198604	///XM_006505		0.017		1.03	-1.01	1.03	-1.12	<i>Plekhhg6</i>	pleckstrin homology domain containing, family G (with RhoGef domain) member 6	0035023 // regulation of Rho protein signal transduction // inferred from electronic anno
NM_0333		0.0343			1.00	1.39	1.03	-1.01	<i>Dock2</i>	dedicator of cyto-kinesis 2	0001766 // membrane raft polarization // inferred from mutant phenotype//0001768 //
NM_0010		0.0341			1.04	-1.10	1.03	1.16	<i>Tulp4</i>	tubby like protein 4	0016567 // protein ubiquitination // inferred from electronic annotation//0035556 // i
NM_0265		0.0358			1.08	-1.06	1.03	-1.15	<i>Cog8///Pdf</i>	component of oligomeric golgi complex 8//peptide deformylase (mitochondrial)	0006412 // translation // inferred from electronic annotation//0006810 // transport // in
NM_0011		0.0084		0.042	-1.03	1.15	1.03	1.15	<i>Lonp2</i>	lon peptidase 2, peroxisomal	0006508 // proteolysis // inferred from electronic annotation//0006515 // misfolded or
NM_029619	///XM_006495		0.013		1.01	1.06	1.03	-1.21	<i>Msrb2</i>	methionine sulfoxide reductase B2	0006979 // response to oxidative stress // inferred from electronic annotation//003004:
NM_0086		0.0307			1.02	1.23	1.03	1.07	<i>Mmp14</i>	matrix metallopeptidase 14 (membrane-inserted)	0001503 // ossification // inferred from genetic interaction//0001525 // angiogenesis //
NM_001190449	///NM_01		0.007		1.10	1.12	1.03	-1.03	<i>Ddah2</i>	dimethylarginine dimethylaminohydrolase 2	0000052 // citrulline metabolic process // not recorded//0006525 // arginine metabolic
NM_001163754	///	0.015	0.045		-1.08	-1.04	1.03	1.08	<i>Rab3gap2</i>	RAB3 GTPase activating protein subunit 2	0043087 // regulation of GTPase activity // not recorded//0043547 // positive regulator
NM_0098		0.0018			-1.02	-1.10	1.03	1.09	<i>Ctnna1</i>	catenin (cadherin associated protein), alpha 1	0001541 // ovarian follicle development // inferred from electronic annotation//000701
NM_0197		0.0031			-1.00	1.08	1.03	-1.07	<i>Ikbke</i>	inhibitor of kappaB kinase epsilon	0006468 // protein phosphorylation // not recorded//0006974 // cellular response to DI
NM_0805		0.0197			1.06	-1.25	1.03	1.05	<i>Ssfa2</i>	sperm specific antigen 2	
NM_0012		0.0172			1.11	-1.06	1.03	1.14	<i>Gtf2h1</i>	general transcription factor II H, polypeptide 1	0006281 // DNA repair // inferred from electronic annotation//0006289 // nucleotide-e-
NM_0011		0.0462			-1.06	1.07	1.03	1.10	<i>Ptprj///Gm38718///Gm39869</i>	protein tyrosine phosphatase, receptor type, 3//predicted gene, 38718//predicted ge	0001570 // vasculogenesis // inferred from mutant phenotype//0001954 // positive regu
NM_0011		0.0349			-1.01	1.39	1.03	1.05	<i>Evl</i>	Ena-vasodilator stimulated phosphoprotein	0007411 // axon guidance // non-traceable author statement//0008154 // intrac polym
NM_0011		0.027			-1.08	1.07	1.03	1.09	<i>Snx10</i>	sorting nexin 10	0006810 // transport // inferred from electronic annotation//0006897 // endocytosis //
NM_0257		0.0094			-1.13	1.12	1.03	1.13	<i>Pgmp1</i>	phosphoglucomutase 1	0005975 // carbohydrate metabolic process // inferred from electronic annotation//000
NM_011890			0.023		-1.00	-1.05	1.03	1.18	<i>Sgcb</i>	sarcoglycan, beta (dystrophin-associated glycoprotein)	0007517 // muscle organ development // inferred from electronic annotation//0048747
NM_0169		0.03		0.03	-1.14	1.30	1.03	1.36	<i>Gm8096///Phgdh</i>	3-phosphoglycerate dehydrogenase pseudogene//3-phosphoglycerate dehydrogenas	0006541 // glutamine metabolic process // inferred from mutant phenotype//0006544 ,
NM_1534		0.0138			1.21	-1.06	1.03	1.26	<i>Dusp7</i>	dual specificity phosphatase 7	0000188 // inactivation of MAPK activity // not recorded//0006470 // protein dephosp
NM_0011		0.044			-1.03	-1.11	1.03	1.07	<i>Nucb1</i>	nucleobindin 1	0007218 // response to cisplatin // inferred from electronic annotation//1903533 // reg
NM_145610			0.035		1.14	1.16	1.03	-1.16	<i>Ppan</i>	petar pan homolog (Drosophila)	0000027 // ribosomal large subunit assembly // ---//0001560 // regulation of cell growt
NM_0263		0.035			1.12	-1.06	1.03	1.17	<i>Ahctf1</i>	AT hook containing transcription factor 1	0000910 // cytokinesis // not recorded//0006351 // transcription, DNA-templated // inf
NM_1454		0.027			-1.01	1.08	1.03	-1.04	<i>Prmt7</i>	protein arginine N-methyltransferase 7	0000387 // spliceosomal snRNP assembly // not recorded//0006349 // regulation of ger
NM_0280		0.0231			1.02	1.12	1.03	1.07	<i>Rpusd4</i>	RNA pseudouridylylase domain containing 4	0001522 // pseudouridine synthesis // inferred from electronic annotation//0009451 //
NM_001252218	///	0.041			-1.09	1.02	1.03	-1.02	<i>LOC102641215///Rpl31///Rpl31-ps12///R</i>	60S ribosomal protein L31 pseudogene//ribosomal protein L31//ribosomal protein L	0002181 // cytoplasmic translation // ---//0006412 // translation // inferred from electr
NM_033270	///NR	0.041			-1.14	-1.16	1.03	-1.02	<i>E2f6</i>	E2F transcription factor 6	0000083 // regulation of transcription involved in G1/S transition of mitotic cell cycle // ir
NM_0196		0.0115	0.014		-1.40	1.00	1.03	-1.21	<i>Cpxm1</i>	carboxypeptidase X1 (M14 family)	0006508 // proteolysis // inferred from direct assay//0006518 // peptide metabolic proc
NM_0115		0.0444			-1.02	1.12	1.03	1.04	<i>Gm9855///Tdg///Tdg-ps</i>	thymine DNA glycosylase pseudogene//thymine DNA glycosylase//thymine DNA glyco	0000122 // negative regulation of transcription from RNA polymerase II promoter // infer
NM_001289782	///	0.003	0.026		-1.26	-1.25	1.03	-1.00	<i>Cryab</i>	crystallin, alpha B	0001666 // response to hypoxia // inferred from mutant phenotype//0002088 // lens de
NM_010809			0.012	0.027	-1.56	-1.37	1.03	-1.19	<i>Mmp3</i>	matrix metallopeptidase 3	0006508 // proteolysis // inferred from mutant phenotype//0006508 // proteolysis // nc
NM_0094		0.0162			1.16	-1.46	1.03	1.16	<i>Top1</i>	topoisomerase (DNA) I	0006260 // DNA replication // inferred from mutant phenotype//0006265 // DNA topok
NM_0013		0.0418			-1.03	1.18	1.03	1.06	<i>Ube2v1</i>	ubiquitin-conjugating enzyme E2 variant 1	0006301 // postreplication repair // ---//0042275 // error-free postreplication DNA rep
NM_009517	///XM	0.047	0.03		-1.07	-1.02	1.03	1.07	<i>Zmat3</i>	zinc finger matrix type 3	0006810 // transport // inferred from electronic annotation//0006915 // apoptotic proc
NM_0256		0.0021			1.08	-1.06	1.03	1.01	<i>Mad211bp</i>	MAD2L1 binding protein	0007093 // mitotic cell cycle checkpoint // not recorded//0007094 // mitotic spindle ass
NM_207531	///XM	0.034	0.045		-1.03	-1.09	1.04	1.03	<i>Agr3</i>	anterior gradient 3	
NM_0091	#####				-1.00	-1.14	1.04	1.04	<i>Sdf2</i>	stromal cell derived factor 2	0000032 // cell wall mannoprotein biosynthetic process // not recorded//0007275 // m
NM_001005605	///NM_00	0.047			-1.03	-1.07	1.04	1.07	<i>Aebp2</i>	AE binding protein 2	0000122 // negative regulation of transcription from RNA polymerase II promoter // infer
NM_0287		0.005			-1.01	1.26	1.04	1.17	<i>Gga2</i>	golgi associated, gamma adaptin ear containing, ARF binding protein 2	0006810 // transport // inferred from electronic annotation//0006886 // intracellular pr
NM_001159329	///	0.038			-1.11	1.01	1.04	1.02	<i>Gtpbp8</i>	GTP-binding protein 8 (putative)	0000917 // barrier septum assembly // inferred from electronic annotation
NM_0010		0.0094			-1.02	1.43	1.04	-1.03	<i>Evi2b///Gm21975</i>	ecotropic viral integration site 2b//predicted gene 21975	
NM_001277932	///	0.029			-1.02	1.07	1.04	-1.02	<i>Casp9</i>	caspace 9	0006508 // proteolysis // not recorded//0006508 // proteolysis // inferred from review
NM_001291105	///NM_00	0.021			-1.06	-1.10	1.04	1.05	<i>E2f1</i>	E2F transcription factor 1	0000077 // DNA damage checkpoint // not recorded//0000122 // negative regulation of
NM_013770			0.013		1.26	1.27	1.04	1.04	<i>Slc25a10</i>	solute carrier family 25 (mitochondrial carrier, dicarboxylate transporter), member 10	0006810 // transport // inferred from electronic annotation//0006817 // phosphate ion
NM_0213		0.0151	0.043	1.32	1.87	1.04	-1.07	<i>Tnfrsf13b</i>	tumor necrosis factor receptor superfamily, member 13b	0001782 // B cell homeostasis // inferred from direct assay//0001782 // B cell homeost	
NM_138668	///XM_006505		0.009		-1.04	1.02	1.04	1.13	<i>Ufsp2</i>	UFM1-specific peptidase 2	0006508 // proteolysis // not recorded//0006508 // proteolysis // inferred from direct
NM_0305		0.0208	0.05		-1.16	1.03	1.04	-1.06	<i>Slc19a3</i>	solute carrier family 19, member 3	0006810 // transport // inferred from electronic annotation//0015884 // folic acid trans
NM_001111274	///	0.044			-1.32	-1.17	1.04	-1.11	<i>Igf1</i>	insulin-like growth factor 1	0001649 // osteoblast differentiation // inferred from expression pattern//0001775 // c
NM_1831		0.01			1.03	1.17	1.04	1.03	<i>Pyroxd1</i>	pyridine nucleotide-disulphide oxidoreductase domain 1	0005114 // oxidation-reduction process // inferred from electronic annotation
NM_001291104	///	0.017			-1.07	-1.05	1.04	-1.08	<i>Fgf11</i>	fibroblast growth factor 11	
NM_0010		0.0475			-1.15	1.19	1.04	-1.06	<i>Clec5a</i>	C-type lectin domain family 5, member a	0002076 // osteoblast development // inferred from direct assay//0002376 // immune s
NM_0010		0.0477			-1.01	1.07	1.04	1.01	<i>Erbp2</i>	v-erb-b2 erythroblastic leukemia viral oncogene homolog 2, neuro/glioblastoma deriv	0001889 // liver development // inferred from electronic annotation//0001934 // posit
NM_016680	///NR_125832		0.026		1.00	1.04	1.04	-1.27	<i>Clasrp</i>	CLK4-associating serine/arginine rich protein	0006397 // mRNA processing // inferred from electronic annotation//0008380 // RNA sp
NM_001290658	///NM_02		0.044		1.04	-1.03	1.04	-1.04	<i>Pomgnt1</i>	protein O-linked mannose beta 1,2-N-acetylglucosaminyltransferase	0006486 // protein glycosylation // inferred from electronic annotation//0006493 // prc
NM_0281		0.021			-1.15	1.02	1.04	1.05	<i>Tram1</i>	translocating chain-associating membrane protein 1	0006810 // transport // inferred from electronic annotation//0015031 // protein transp
NM_0270		0.0351			1.00	-1.10	1.04	1.09	<i>Sec62</i>	SEC62 homolog (S. cerevisiae)	0006620 // posttranslational protein targeting to membrane // not recorded//0006810 ,
NM_001048206	///NM_00	0.032			1.00	-1.01	1.04	1.10	<i>Traf3</i>	TNF receptor-associated factor 3	0001817 // regulation of cytokine production // inferred from mutant phenotype//0002
NM_001290430	///NM_13		0.032		-1.04	1.10	1.04	1.11	<i>Ftsj1</i>	FtsJ homolog 1 (E. coli)	0001510 // RNA methylation // inferred from electronic annotation//0002128 // tRNA N
NM_001122822	///	0.02			-1.02	1.01	1.04	1.02	<i>LOC105242468///Wrn</i>	Werner syndrome ATP-dependent helicase homolog//Werner syndrome homolog (hu	0000723 // telomere maintenance // inferred from genetic interaction//0000723 // telo
NM_1336		0.0166			1.05	-1.12	1.04	1.07	<i>Ces1e</i>	carboxylesterase 1E	0008152 // metabolic process // inferred from electronic annotation//0016042 // lipid c
NM_1332		0.0189			-1.08	1.15	1.04	-1.12	<i>Pilrb1</i>	paired immunoglobulin-like type 2 receptor beta 1	0001773 // myeloid dendritic cell activation // inferred from direct assay//0007169 // tr
NM_0231	#####				-1.05	-2.56	1.04	-1.18	<i>Klf15</i>	Kruppel-like factor 15	0006351 // transcription, DNA-templated // inferred from electronic annotation//00063

RefSeq	Tri	p 24h	p 48h	p 72h	FD Air	FD 24h	FD 48h	FD 72h	Gene Symbol	Gene Title	Gene Ontology Biological Process
NM_1455		0.0471			1.04	-1.07	1.04	1.12	<i>Tipr1</i>	TIP41, TOR signalling pathway regulator-like (S. cerevisiae)	0000077 // DNA damage checkpoint // not recorded//0034048 // negative regulation of
NM_1785		0.0442			-1.05	1.10	1.04	-1.10	<i>Ptrh1</i>	peptidyl-tRNA hydrolase 1 homolog (S. cerevisiae)	0008152 // metabolic process // inferred from electronic annotation
NM_0013		0.017			1.03	1.17	1.04	-1.02	<i>Ints7</i>	integrator complex subunit 7	0000077 // DNA damage checkpoint // not recorded//0006974 // cellular response to D
NM_001033293	///XR_374	0.039			1.05	1.31	1.04	-1.01	<i>Uap11</i>	UDP-N-acetylglucosamine pyrophosphorylase 1-like 1	0006048 // UDP-N-acetylglucosamine biosynthetic process // ---//0008152 // metabolic
NM_001033136	///	0.047			-1.04	-1.15	1.04	1.03	<i>Rmdn3</i>	regulator of microtubule dynamics 3	0006874 // cellular calcium ion homeostasis // not recorded//0006915 // apoptotic proc
NM_001044720	///NM_00	0.021			-1.17	-1.11	1.04	1.17	<i>Abcc9</i>	ATP-binding cassette, sub-family C (CFTR/MRP), member 9	0006810 // transport // inferred from electronic annotation//0006813 // potassium ion
NM_0011		0.0425			1.01	1.11	1.04	-1.11	<i>Emc6</i>	ER membrane protein complex subunit 6	0000045 // autophagosome assembly // not recorded//0034975 // protein folding in p
NM_201407	///XM_00650	0.046			1.05	1.08	1.04	-1.10	<i>Dennd4b</i>	DENN/MADD domain containing 4B	0032483 // regulation of Rab protein signal transduction // not recorded//0043547 // in pi
NM_009431			0.043		1.12	1.06	1.04	-1.09	<i>Ctr9</i>	Ctr9, Paf1/RNA polymerase II complex component, homolog (S. cerevisiae)	0000122 // negative regulation of transcription from RNA polymerase II promoter // infer
NM_1341		0.0155	0.012		-1.11	1.04	1.04	-1.07	<i>Yars</i>	tyrosyl-tRNA synthetase	0006412 // translation // inferred from electronic annotation//0006418 // tRNA aminoa
NM_028431			0.015		-1.03	1.00	1.04	1.12	<i>Pmpcb</i>	peptidase (mitochondrial processing) beta	0006122 // mitochondrial electron transport, ubiquinol to cytochrome c // not recorded//
NM_178589		0.026			-1.09	-1.13	1.04	1.18	<i>Tnfrsf21</i>	tumor necrosis factor receptor superfamily, member 21	0001783 // B cell apoptotic process // inferred from mutant phenotype//0002250 // ad
NM_0010	#####	#####			-1.19	1.35	1.04	-1.13	<i>Mcoln2</i>	mucopolin 2	0006810 // transport // inferred from electronic annotation//0006811 // ion transport /
NM_0137		0.0393			-1.14	1.05	1.04	-1.03	<i>Nbn</i>	nibrin	0000077 // DNA damage checkpoint // not recorded//0000723 // telomere maintenanc
NM_0010		0.0456			1.01	-1.02	1.04	1.17	<i>Rap1gds1</i>	RAP1, GTP-GDP dissociation stimulator 1	0007264 // small GTPase mediated signal transduction // not recorded//0014829 // vas
NM_0013		0.0316			1.21	-1.03	1.04	1.24	<i>Porcn</i>	porcupine homolog (Drosophila)	0006497 // protein lipidation // inferred from direct assay//0009100 // glycoprotein me
NM_025834	///XM_0024				-1.13	1.02	1.04	-1.14	<i>Proz</i>	protein Z, vitamin K-dependent plasma glycoprotein	0006508 // proteolysis // inferred from electronic annotation//0007596 // blood coagul
NM_1459		0.0495	0.025		-1.09	1.00	1.04	1.10	<i>Alg3</i>	asparagine-linked glycosylation 3 (alpha-1,3-mannosyltransferase)	0006486 // protein glycosylation // inferred from electronic annotation//0097502 // ma
NM_009261	///NM_0003				-1.12	1.01	1.04	-1.00	<i>Strbp</i>	spermatid perinuclear RNA binding protein	0006928 // movement of cell or subcellular component // inferred from mutant phenoty
NM_0012		0.0263			1.02	1.11	1.04	1.02	<i>Rad51d</i>	RAD51 homolog D	0000707 // meiotic DNA recombinase assembly // not recorded//0000723 // telomere n
NM_001290495	///NM_00	0.018			1.04	1.13	1.04	1.12	<i>Trub2</i>	TruB pseudouridine (psi) synthase homolog 2 (E. coli)	0001522 // pseudouridine synthesis // inferred from electronic annotation//0006396 //
NM_0197		0.0058			-1.13	-1.63	1.04	1.09	<i>Foxo3</i>	forkhead box O3	0000122 // negative regulation of transcription from RNA polymerase II promoter // not i
NM_0091		0.0333	0.039		1.07	-1.04	1.04	1.16	<i>Slc1a1</i>	solute carrier family 1 (neuronal/epithelial high affinity glutamate transporter, system	0006810 // transport // inferred from electronic annotation//0006835 // dicarboxylic ac
NM_0198		0.0237			-1.04	-1.25	1.04	-1.02	<i>Ube2g2</i>	ubiquitin-conjugating enzyme E2G 2	0000209 // protein polyubiquitination // not recorded//0016567 // protein ubiquitinat
NM_030153	///XM_00651	0.021			-1.01	-1.12	1.04	1.14	<i>Naa35</i>	N(alpha)-acetyltransferase 35, NatC auxiliary subunit	0043066 // negative regulation of apoptotic process // not recorded//0048659 // smoo
NM_001134465	///	0.043			-1.02	-1.05	1.04	1.01	<i>Dennd6a</i>	DENN/MADD domain containing 6A	0043547 // positive regulation of GTPase activity // not recorded//2000049 // positive r
NM_0268		0.0251	0.04		-1.05	1.10	1.04	-1.06	<i>Dus1</i>	dihydrouridine synthase 1-like (S. cerevisiae)	0002943 // tRNA dihydrouridine synthesis // not recorded//0008033 // tRNA processin
NM_001038625	///	0.018	0.035		1.23	1.26	1.04	1.08	<i>Sertad2</i>	SERTA domain containing 2	0006351 // transcription, DNA-templated // inferred from electronic annotation//00063
NM_138589	///XM_0025				-1.07	-1.12	1.04	-1.02	<i>Ubf1d</i>	ubiquitin family domain containing 1	
NM_0012		0.0267			-1.05	1.11	1.04	-1.06	<i>Ndufs8</i>	NADH dehydrogenase (ubiquinone) Fe-S protein 8	0006810 // transport // inferred from electronic annotation//0006979 // response to ox
NM_146247	///XM_00652	0.007			1.03	1.06	1.04	-1.19	<i>Mettl22</i>	methyltransferase like 22	0032259 // methylation // inferred from electronic annotation
NM_0257		0.0113			-1.17	1.00	1.04	-1.07	<i>Acot13</i>	acyl-CoA thioesterase 13	0008152 // metabolic process // inferred from electronic annotation//0051289 // protei
NM_0012		0.0033	0.034		1.09	-1.04	1.04	-1.03	<i>Dpf2</i>	D4, zinc and double PHD fingers family 2	0006351 // transcription, DNA-templated // inferred from electronic annotation//00063
NM_020594	///XM_0023				-1.07	-1.02	1.04	-1.02	<i>Zc3h8</i>	zinc finger CCHC type containing 8	0000122 // negative regulation of transcription from RNA polymerase II promoter // infer
NM_001310837	///NM_01	0.022			1.03	-1.11	1.04	1.21	<i>Sspn</i>	sarcospan	
NM_011914			0.039		1.01	1.05	1.04	-1.14	<i>Nelfa</i>	negative elongation factor complex member A, Whsc2	0006351 // transcription, DNA-templated // inferred from electronic annotation//00063
NM_0010		0.0187			1.01	-1.05	1.04	1.00	<i>Rtn3</i>	reticulon 3	0006810 // transport // inferred from electronic annotation//0006915 // apoptotic proc
NM_0080		0.0252			1.05	1.23	1.05	1.14	<i>G6pdx</i> ///G6pd2	glucose-6-phosphate dehydrogenase X-linked//glucose-6-phosphate dehydrogenase	0001816 // cytokine production // inferred from mutant phenotype//0001998 // angiot
NM_1340		0.0462			1.08	-1.07	1.05	1.13	<i>Tmed4</i>	transmembrane emp24 protein transport domain containing 4	0006810 // transport // inferred from electronic annotation//0007165 // signal transduc
NM_0114		0.0497			-1.12	1.04	1.05	-1.16	<i>Strap</i>	serine/threonine kinase receptor associated protein	0000122 // negative regulation of transcription from RNA polymerase II promoter // infer
NM_0012		0.0378			1.08	-1.19	1.05	1.38	<i>Cldnd1</i>	claudin domain containing 1	
NM_145460	///XR_0006				-1.08	-1.05	1.05	-1.08	<i>Oxnad1</i>	oxidoreductase NAD-binding domain containing 1	0055114 // oxidation-reduction process // inferred from electronic annotation
NM_001198823	///NM_00	0.018			1.01	1.03	1.05	1.14	<i>App</i>	amyloid beta (A4) precursor protein	0001878 // response to yeast // not recorded//0001967 // suckling behavior // inferred
NM_133223			0.026		1.18	1.40	1.05	1.04	<i>Rac3</i>	RAS-related C3 botulinum substrate 3	0007264 // small GTPase mediated signal transduction // inferred from electronic annota
NM_016918	///XM_0041				-1.03	-1.04	1.04	1.02	<i>Nudt5</i>	nudix (nucleoside diphosphate linked moiety X)-type motif 5	0006139 // nucleobase-containing compound metabolic process // inferred from direct a
NM_001123327	///XM_00	0.003			-1.11	-1.10	1.05	1.11	<i>Qser1</i>	glutamine and serine rich 1	
NM_0168		0.0194			1.01	1.17	1.05	1.24	<i>Rab25</i>	RAB25, member RAS oncogene family	0003382 // epithelial cell morphogenesis // inferred from mutant phenotype//0006810
NM_025901			0.027		-1.10	-1.04	1.05	-1.07	<i>Polr3k</i>	polymerase (RNA) III (DNA directed) polypeptide K	0002376 // immune system process // inferred from electronic annotation//0006351 //
NM_1455		0.0291			1.02	1.14	1.05	1.05	<i>Rabepk</i>	Rab9 effector protein with kelch motifs	
NM_001099298	///	0.016			-1.05	-1.04	1.05	-1.14	<i>Scn2a1</i>	sodium channel, voltage-gated, type II, alpha 1	0006810 // transport // inferred from electronic annotation//0006811 // ion transport /
NM_1342		0.011			-1.03	-1.32	1.05	1.19	<i>Elov15</i>	ELOVL family member 5, elongation of long chain fatty acids (yeast)	0006629 // lipid metabolic process // inferred from electronic annotation//0006631 // f
NM_028394	///XM_0027	0.034			-1.22	-1.15	1.05	-1.04	<i>Hspb11</i>	heat shock protein family B (small), member 11	0001501 // skeletal system development // inferred from mutant phenotype//0006810 ,
NM_0253		0.0323			1.04	1.16	1.05	1.04	<i>Dnajc15</i>	Dnaj (Hsp40) homolog, subfamily C, member 15	0006810 // transport // inferred from electronic annotation//0009267 // cellular respon
NM_0013		0.0378			-1.06	1.07	1.05	1.00	<i>Cox16</i>	cytochrome c oxidase assembly protein 16	
NM_0012		0.032			1.07	1.25	1.05	1.19	<i>Slc10a3</i>	solute carrier family 10 (sodium/bile acid cotransporter family), member 3	0006810 // transport // inferred from electronic annotation//0010033 // response to or
NM_0120		0.0014			-1.04	1.13	1.05	-1.06	<i>Srp9</i>	signal recognition particle 9	0006814 // SRP-dependent cotranslational protein targeting to membrane // inferred fr
NM_0271		0.0037			1.03	-1.06	1.05	1.13	<i>Esam</i>	endothelial cell-specific adhesion molecule	0007155 // cell adhesion // inferred from electronic annotation//0007156 // homophilic
NM_0259		0.0343			1.08	1.25	1.05	1.03	<i>Efh2</i>	EF hand domain containing 2	
NM_0265		0.0227			-1.13	1.06	1.05	-1.03	<i>LOC102642137</i> ///Rps13//Rps13-ps1//Rp	40S ribosomal protein S13//ribosomal protein S13//ribosomal protein S13, pseudog	0006412 // translation // not recorded//0033119 // negative regulation of RNA splicing ,
NM_0012		0.0435			1.05	1.35	1.05	1.06	<i>Sqstm1</i>	sequestosome 1	0001934 // positive regulation of protein phosphorylation // not recorded//0002376 // i
NM_0233		0.0489	0.048		-1.03	1.09	1.05	1.10	<i>Snap29</i>	synaptosomal-associated protein 29	0006810 // transport // inferred from electronic annotation//0006887 // exocytosis // n
NM_0115		0.0021			-1.09	1.10	1.05	1.18	<i>Surf4</i>	surfeit gene 4	0007030 // Golgi organization // not recorded//0010638 // positive regulation of organe
NM_0011		0.049			-1.08	1.12	1.05	1.01	<i>Naip2</i>	NLR family, apoptosis inhibitory protein 2	0002376 // immune system process // inferred from electronic annotation//0006915 //
NM_0011		0.0037			1.03	-1.12	1.05	1.01	<i>Cacul1</i>	CDK2 associated, cullin domain 1	0000082 // G1/S transition of mitotic cell cycle // not recorded//0006511 // ubiquitin-de

RefSeq	Tri	p 24h	p 48h	p 72h	FD Air	FD 24h	FD 48h	FD 72h	Gene Symbol	Gene Title	Gene Ontology Biological Process
NM_0135		0.014			-1.01	-1.28	1.05	-1.20	<i>Mbd1</i>	methyl-CpG binding domain protein 1	0000122 // negative regulation of transcription from RNA polymerase II promoter // not r
NM_009837			0.009		-1.09	-1.17	1.05	-1.14	<i>Cct4</i>	chaperonin containing Tcp1, subunit 4 (delta)	0006457 // protein folding // inferred from electronic annotation//0007339 // binding c
NM_0271		0.0316			1.05	1.24	1.05	1.09	<i>Nup37</i>	nucleoporin 37	0006810 // transport // inferred from electronic annotation//0007049 // cell cycle // inf
NM_145946	//XM		0.03		-1.06	-1.04	1.05	-1.04	<i>Fanci</i>	Fanconi anemia, complementation group I	0006281 // DNA repair // inferred from electronic annotation//0006974 // cellular resp
NM_0311		0.0214	0.041		-1.27	-1.56	1.05	-1.00	<i>Hspa8</i>	heat shock protein 8	0001916 // positive regulation of T cell mediated cytotoxicity // not recorded//0006351
NM_0011		0.0291		0.027	-1.02	1.08	1.05	1.14	<i>Igsf5</i>	immunoglobulin superfamily, member 5	0016337 // single organismal cell-cell adhesion // inferred from direct assay//0050767 //
NM_0115		0.0268	0.031		-1.28	1.04	1.05	-1.26	<i>Alyref</i> // <i>Alyref2</i>	Aly/REF export factor//Aly/REF export factor 2	0006397 // mRNA processing // inferred from electronic annotation//0006406 // mRNA
NM_0168		0.0162			1.15	-1.13	1.05	1.17	<i>Usp2</i>	ubiquitin specific peptidase 2	0000122 // negative regulation of transcription from RNA polymerase II promoter // not r
NM_0011		0.0125	0.041		-1.09	1.09	1.05	-1.08	<i>Col18a1</i>	collagen, type XVIII, alpha 1	0001525 // angiogenesis // inferred from direct assay//0001525 // angiogenesis // infer
NM_011817			0.033		-1.34	-1.04	1.05	-1.74	<i>Gadd45g</i>	growth arrest and DNA-damage-inducible 45 gamma	0000185 // activation of MAPKK activity // not recorded//0000186 // activation of MAI
NM_027256	//XM	0.0650	0.044		-1.06	1.02	1.05	1.09	<i>Ints4</i>	integrator complex subunit 4	0016180 // snRNA processing // not recorded
NM_0093		0.0424			-1.01	1.13	1.05	-1.05	<i>Tfam</i>	transcription factor A, mitochondrial	0006338 // chromatin remodeling // not recorded//0006351 // transcription, DNA-temp
NM_133435	//XM	0.0653	0.028		-1.01	1.11	1.05	1.26	<i>Nmnat1</i>	nicotinamide nucleotide adenyltransferase 1	0006457 // protein folding // non-traceable author statement//0006511 // ubiquitin-de
NM_175195	//XM	0.0651	0.047		1.07	1.08	1.05	-1.14	<i>Spl2b</i>	signal peptide peptidase like 2B	0006508 // proteolysis // inferred from electronic annotation//0006509 // membrane p
NM_1337		0.0259			1.08	1.19	1.05	1.03	<i>Dcp1a</i>	DCP1 decapping enzyme homolog A (S. cerevisiae)	0000184 // nuclear-transcribed mRNA catabolic process, nonsense-mediated decay // inf
NM_0307		0.0408			1.02	1.10	1.05	-1.02	<i>Uck2</i>	uridine-cytidine kinase 2	0006206 // pyrimidine nucleobase metabolic process // not recorded//0006222 // UMP
NM_0111		0.0136			-1.11	1.18	1.05	1.09	<i>Psmb5</i>	proteasome (prosome, macropain) subunit, beta type 5	0006508 // proteolysis // inferred from electronic annotation//0006979 // response to c
NM_022980		#####			-1.17	-1.06	1.05	-1.05	<i>Rcan3</i>	regulator of calcineurin 3	0019722 // calcium-mediated signaling // inferred from electronic annotation//005079C
NM_008389	//XM	0.0650	0.034		1.02	1.06	1.05	1.10	<i>Ipp</i>	IAP promoted placental gene	0016567 // protein ubiquitination // not recorded
NM_172739	//XM		0.026		1.17	1.12	1.05	1.24	<i>Arhgap35</i>	Rho GTPase activating protein 35	0000122 // negative regulation of transcription from RNA polymerase II promoter // not r
NM_0110		0.0362			-1.17	1.26	1.05	-1.13	<i>Pfn1</i>	profilin 1	0001843 // neural tube closure // inferred from genetic interaction//0006357 // regulat
NM_0011		0.0048			1.05	1.38	1.05	1.23	<i>Arpc4</i>	actin related protein 2/3 complex, subunit 4	0030041 // actin filament polymerization // inferred from electronic annotation//00343
NM_001252519	//	0.016	0.049		-1.10	-1.03	1.05	-1.05	<i>Zfp82</i>	zinc finger protein 82	0006351 // transcription, DNA-templated // inferred from electronic annotation//00063
NM_0080		0.0474	0.01		-1.06	1.10	1.05	1.09	<i>Fgf7</i>	fibroblast growth factor 7	0001541 // ovarian follicle development // not recorded//0002230 // positive regulator
NM_0111		0.0428			-1.02	1.22	1.05	1.31	<i>Psmc1</i>	proteasome (prosome, macropain) activator subunit 1 (PA28 alpha)	0002479 // antigen processing and presentation of exogenous peptide antigen via MHC c
NM_0263		0.0493			-1.06	1.11	1.05	-1.01	<i>Tceb2</i> // <i>Gm9238</i>	transcription elongation factor B (SIII), polypeptide 2//transcription elongation factor	0006351 // transcription, DNA-templated // inferred from electronic annotation//00063
NM_0012		0.0227			1.02	-1.37	1.06	1.04	<i>Cadps2</i>	Ca2+-dependent activator protein for secretion 2	0006810 // transport // inferred from electronic annotation//0006887 // exocytosis // ir
NM_001190258	//NM_02	0.039			1.07	1.09	1.06	-1.01	<i>Rps27</i> // <i>Rps27rt</i>	ribosomal protein S27//ribosomal protein S27, retrogene	0006412 // translation // inferred from electronic annotation
NM_0255		0.0024	0.005		-1.15	-1.01	1.06	-1.16	<i>Copsr</i>	coordinator of PRMT5, differentiation stimulator	0006351 // transcription, DNA-templated // inferred from electronic annotation//00063
NM_0235		0.032			-1.05	1.15	1.06	1.02	<i>Pecr</i>	peroxisomal trans-2-enoyl-CoA reductase	0006629 // lipid metabolic process // inferred from electronic annotation//0006631 // f
NM_0010		0.0177			1.03	-1.24	1.06	1.10	<i>Cadm1</i>	cell adhesion molecule 1	0001889 // liver development // not recorded//0002376 // immune system process // i
NM_001293644	//NM_02	0.026			-1.07	1.03	1.06	1.22	<i>Ccdc109b</i>	coiled-coil domain containing 109B	0006810 // transport // inferred from electronic annotation//0006811 // ion transport /
NM_010683		0.041	0.01		-1.01	-1.06	1.06	1.12	<i>Lamc1</i>	laminin, gamma 1	0006461 // protein complex assembly // not recorded//0007155 // cell adhesion // not r
NM_001034097	//NM_00	0.026			1.04	1.14	1.06	1.27	<i>Tnfrsf13</i> // <i>Tnfrsfm13</i>	tumor necrosis factor (ligand) superfamily, member 13//tumor necrosis factor (ligand	0000125 // angiogenesis // inferred from electronic annotation//0002376 // immune sy
NM_0010		0.0224			-1.07	-1.36	1.06	1.09	<i>Dusp16</i>	dual specificity phosphatase 16	0000188 // inactivation of MAPK activity // inferred from direct assay//0006470 // prote
NM_0012		0.0425			1.04	-1.20	1.06	1.08	<i>Slit2</i>	slit homolog 2 (Drosophila)	0001656 // metanephros development // inferred from mutant phenotype//0001657 //
NM_015814	//XM		0.01		-1.24	-1.26	1.06	-1.05	<i>Dkk3</i>	dickkopf homolog 3 (Xenopus laevis)	0007275 // multicellular organismal development // inferred from electronic annotation/
NM_0257		0.0088			1.01	-1.10	1.06	1.08	<i>Cy85a</i>	cytochrome b5 type A (microsomal)	0006631 // fatty acid metabolic process // inferred by curator//0006810 // transport //
NM_0157		0.0336			1.10	1.02	1.06	1.34	<i>Tmprss2</i>	transmembrane protease, serine 2	0006508 // proteolysis // inferred from direct assay//0006508 // proteolysis // not rec
NM_008579	//XM	0.0649	0.049		-1.03	-1.23	1.06	1.19	<i>Meig1</i>	meiosis expressed gene 1	0007283 // spermatogenesis // inferred from electronic annotation//0030154 // cell diff
NM_0012		0.0448	0.046		-1.06	1.05	1.06	1.03	<i>Kif3a</i>	kinesin family member 3A	0001701 // in utero embryonic development // inferred from genetic interaction//00018
NM_0011		0.0242			1.06	-1.09	1.06	1.21	<i>Shoc2</i>	soc-2 (suppressor of clear) homolog (C. elegans)	0046579 // positive regulation of Ras protein signal transduction // not recorded
NM_0254		0.0115			-1.16	1.19	1.06	-1.20	<i>Rps4l</i>	ribosomal protein S4-like	0006412 // translation // ---//0006412 // translation // inferred from electronic annotat
NM_0102		0.0339			1.11	2.51	1.06	1.09	<i>Fos</i>	FBJ osteosarcoma oncogene	0001661 // conditioned taste aversion // inferred from electronic annotation//0006355
NM_008231	//XM		0.042		1.13	1.06	1.06	1.01	<i>Hdgf</i>	hepatoma-derived growth factor	0000122 // negative regulation of transcription from RNA polymerase II promoter // not r
NM_1979		0.0018			1.18	-1.11	1.06	1.12	<i>Ces2g</i>	carboxylesterase 2G	0008152 // metabolic process // inferred from electronic annotation
NM_0252		0.0011			1.01	-1.09	1.06	1.11	<i>Atp6v0e</i>	ATPase, H+ transporting, lysosomal V0 subunit E	0006810 // transport // inferred from electronic annotation//0006811 // ion transport /
NM_001122683	//	0.001	0.047		-1.07	-1.03	1.06	1.14	<i>Bdh1</i>	3-hydroxybutyrate dehydrogenase, type 1	0008152 // metabolic process // inferred from electronic annotation//00055114 // oxidat
NM_0214		0.0068	0.018		-1.03	1.05	1.06	1.08	<i>Slc35b4</i>	solute carrier family 35, member B4	0006111 // regulation of gluconeogenesis // inferred from mutant phenotype//0006810
NM_0086		0.0202			-1.08	1.02	1.06	1.04	<i>Nedd1</i>	neural precursor cell expressed, developmentally down-regulated gene 1	0007019 // microtubule depolymerization // not recorded//0007049 // cell cycle // infer
NM_1723		0.0496			1.16	1.38	1.06	1.05	<i>Limd2</i>	LIM domain containing 2	
NM_0011		0.0297			1.08	-1.08	1.06	1.24	<i>Vps26a</i>	vacuolar protein sorting 26 homolog A (yeast)	0006810 // transport // inferred from electronic annotation//0006886 // intracellular pr
NM_0012		0.041			1.25	1.06	1.06	1.10	<i>Eps8l1</i>	EPS8-like 1	0007266 // Rho protein signal transduction // not recorded//0016601 // Rac protein sig
NM_008182	//XM	0.0651	0.042		1.10	1.14	1.06	1.34	<i>Gsta2</i> // <i>Gm3776</i> // <i>Gsta1</i>	glutathione S-transferase, alpha 2 (Yc2)//predicted gene 3776//glutathione S-transf	0006749 // glutathione metabolic process // inferred from sequence or structural similar
NM_0011		0.0114	0.013		-1.01	1.10	1.06	1.08	<i>Tlk2</i>	tousled-like kinase 2 (Arabidopsis)	0001672 // regulation of chromatin assembly or disassembly // not recorded//0006468
NM_0013		0.0147			1.04	-1.03	1.06	1.14	<i>Rnf10</i>	ring finger protein 10	0006351 // transcription, DNA-templated // inferred from electronic annotation//00063
NM_0011		0.038			1.07	-1.07	1.06	1.03	<i>Rnmt</i>	RNA (guanine-7) methyltransferase	0006370 // 7-methylguanosine mRNA capping // not recorded//0006397 // mRNA proc
NM_001290486	//	0.007			-1.13	-1.21	1.06	-1.06	<i>Lpar1</i>	lysophosphatidic acid receptor 1	0000187 // activation of MAPK activity // inferred from direct assay//0007165 // signal t
NM_0090		0.0011			1.10	1.40	1.06	1.08	<i>Rasa3</i>	RAS p21 protein activator 3	0007165 // signal transduction // inferred from electronic annotation//0034605 // cellu
NM_0011		0.0061			1.02	-1.30	1.06	-1.04	<i>Snrk</i>	SNF related kinase	0006468 // protein phosphorylation // not recorded//0016310 // phosphorylation // inf
NM_145705	//XM		0.02		1.16	1.15	1.06	-1.01	<i>Tinfr</i>	Terf1 (TRF1)-interacting nuclear factor 2	0010833 // telomere maintenance via telomere lengthening // not recorded//0010836 /
NM_011163	//XM		0.011		-1.02	1.06	1.06	1.02	<i>Eif2ak2</i>	eukaryotic translation initiation factor 2-alpha kinase 2	0000186 // activation of MAPK activity // not recorded//0001819 // positive regulatio
NM_0296		0.0113			1.02	1.15	1.06	-1.03	<i>Srxn1</i>	sulfiredoxin 1 homolog (S. cerevisiae)	0006979 // response to oxidative stress // inferred from direct assay//0006979 // respo
NM_001081183	//	0.038			-1.05	-1.00	1.06	1.05	<i>110037F02Rik</i>	RIKEN cDNA 110037F02 gene	0006397 // mRNA processing // inferred from electronic annotation//0008380 // RNA s

RefSeq	Tri.p	24h	p	48h	p	72h	FD Air	FD 24h	FD 48h	FD 72h	Gene Symbol	Gene Title	Gene Ontology Biological Process
NM_177150//XM_006531	0.032	-1.05	1.03	1.06	1.12	<b>Cenpt</b>	centromere protein T	0000278	// mitotic cell cycle // not recorded//0007049	// cell cycle // inferred from elec			
NM_001146100//NM_0101	0.014	1.05	1.10	1.06	-1.03	<b>Hk1//Gm10362//Rpl17//Rpl17-ps5//R</b>	hexokinase 1//predicted gene 10362//ribosomal protein L17//ribosomal protein L1	0001678	// cellular glucose homeostasis // not recorded//0002931	// response to ischer			
NM_0010	0.0256	1.02	-1.13	1.06	1.26	<b>C1s1</b>	complement component 1, s subcomponent 1	0002375	// immune system process // inferred from electronic annotation//0006508	//			
NM_144543//XM_0022		-1.02	1.02	1.06	1.02	<b>Thyn1</b>	thymocyte nuclear protein 1						
NM_0216	0.0051	1.11	1.01	1.06	1.10	<b>Agrn</b>	agrin	0001932	// regulation of protein phosphorylation // not recorded//0001934	// positive i			
NM_0010	0.0283	-1.01	1.13	1.06	1.08	<b>Mtmr7</b>	myotubularin related protein 7	0006470	// protein dephosphorylation // inferred from electronic annotation//0016311				
NM_001201413//	0.02	-1.09	-1.15	1.06	-1.10	<b>Apb2</b>	amyloid beta (A4) precursor protein-binding, family B, member 2	0001764	// neuron migration // inferred from genetic interaction//0006355	// regulatio			
NM_0102	0.0274	1.06	-1.04	1.06	1.02	<b>Gdap2</b>	ganglioside-induced differentiation-associated-protein 2	0032526	// response to retinoic acid // inferred from direct assay				
NM_0012	0.0478	-1.02	1.22	1.06	1.10	<b>Rgs19</b>	regulator of G-protein signaling 19	0009968	// negative regulation of signal transduction // inferred from electronic annotat				
NM_145600		0.023	-1.04	1.03	1.06	<b>Zfp330</b>	zinc finger protein 330						
NM_0012	0.0207	-1.03	-1.21	1.06	1.15	<b>Spin1</b>	spindlin 1	0007049	// cell cycle // inferred from electronic annotation//0007143	// female meiotic			
NM_0011	0.0146	1.03	-1.08	1.06	1.00	<b>Pdik1</b>	PDLIM1 interacting kinase 1 like	0006468	// protein phosphorylation // inferred from electronic annotation//0016310	//			
NM_0271	0.0041	1.07	1.41	1.06	1.06	<b>Dph1//Ovca2</b>	DPH1 homolog (S. cerevisiae)//candidate tumor suppressor in ovarian cancer 2	0008283	// cell proliferation // inferred from mutant phenotype//0017183	// peptidyl-d			
NM_0187	0.0196	1.00	1.18	1.06	1.28	<b>Eif3d</b>	eukaryotic translation initiation factor 3, subunit D	0001731	// formation of translation preinitiation complex // inferred from electronic ann				
NM_013691//XM_006501	0.022	-1.23	-1.13	1.06	1.05	<b>Thbs3</b>	thrombospondin 3	0003417	// growth plate cartilage development // inferred from genetic interaction//00				
NM_001305273//	0.015	-1.03	1.02	1.06	1.02	<b>Rngtt</b>	RNA guanylyltransferase and 5'-phosphatase	0006370	// 7-methylguanosine mRNA capping // not recorded//0006396	// RNA proces			
NM_0010	0.0135	1.11	-1.35	1.06	1.25	<b>Fam117b</b>	family with sequence similarity 117, member B						
NM_0263	0.0119	1.02	-1.06	1.06	-1.12	<b>Tprgl</b>	transformation related protein 63 regulated like						
NM_009252//XM_011244	0.03	-1.20	-1.02	1.06	1.25	<b>Serpina3n</b>	serine (or cysteine) peptidase inhibitor, clade A, member 3N	0006953	// acute-phase response // inferred from electronic annotation//0010466	// ne			
NM_00084	0.0037	-1.16	1.52	1.06	-1.04	<b>Irgb2</b>	integrin beta 2	0002523	// leukocyte migration involved in inflammatory response // not recorded//000				
NM_0012	0.0154	1.06	-1.09	1.06	1.03	<b>Trim2</b>	tripartite motif-containing 2	0016567	// protein ubiquitination // inferred from electronic annotation//0016567	// pr			
NM_0011	0.0358	-1.09	1.05	1.06	1.15	<b>Srp54a//Srp54b//Srp54c</b>	signal recognition particle 54A//signal recognition particle 54B//signal recognition p	0006614	// SRP-dependent cotranslational protein targeting to membrane // not recorde				
NM_175313//XM_006501	0.034	-1.06	-1.04	1.07	1.15	<b>Eogt</b>	EGF domain-specific O-linked N-acetylglucosamine (GlcNAc) transferase	0006493	// protein O-linked glycosylation // inferred from direct assay//0008152	// met			
NM_0094	0.0013	#####	-1.14	1.03	1.07	<b>Tuba3a//Tuba3b</b>	tubulin, alpha 3A//tubulin, alpha 3B	0007017	// microtubule-based process // inferred from electronic annotation//0008152				
NM_001146174//	0.047	0.021	-1.09	-1.05	1.07	<b>Rangap1</b>	RAN GTPase activating protein 1	0007165	// signal transduction // inferred from electronic annotation//0043547	// posit			
NM_0010	0.007	-1.07	-1.33	1.07	1.03	<b>Cstf3</b>	cleavage stimulation factor, 3' pre-RNA, subunit 3	0006379	// mRNA cleavage // not recorded//0006396	// RNA processing // inferred fror			
NM_0116	0.0239	-1.00	1.24	1.07	-1.21	<b>Vars</b>	valyl-tRNA synthetase	0006412	// translation // inferred from electronic annotation//0006418	// tRNA aminoa			
NM_0010	0.0058	-1.03	1.09	1.07	1.01	<b>Ckif</b>	chemokine-like factor	0006935	// chemotaxis // inferred from electronic annotation//0008283	// cell prolifera			
NM_001042593//NM_00	0.021	-1.06	-1.12	1.07	1.03	<b>Hbs1</b>	Hbs1-like (S. cerevisiae)	0006412	// translation // inferred from electronic annotation//0006414	// translational			
NM_001277273//	0.048	-1.04	1.09	1.07	-1.08	<b>Fancl</b>	Fanconi anemia, complementation group L	0002230	// positive regulation of defense response to virus by host // not recorded//00				
NM_016866//XM_0021	0.021	-1.03	-1.05	1.07	1.03	<b>Stk39</b>	serine/threonine kinase 39	0001933	// negative regulation of protein phosphorylation // inferred from direct assay//				
NM_0110	0.0011	1.26	-1.30	1.07	1.47	<b>Per2</b>	period circadian clock 2	0000122	// negative regulation of transcription from RNA polymerase II promoter // infer				
NM_0103	0.0018	-1.08	1.29	1.07	1.10	<b>Gsr</b>	glutathione reductase	0006749	// glutathione metabolic process // inferred by curator//0006749	// glutathion			
NM_001256516//	0.012	-1.04	-1.09	1.07	-1.01	<b>Zfp672</b>	zinc finger protein 672	0006351	// transcription, DNA-templated // inferred from electronic annotation//000063				
NM_0010	0.0099	1.05	-1.06	1.07	1.00	<b>Akirin2</b>	akirin 2	0000122	// negative regulation of transcription from RNA polymerase II promoter // not i				
NM_0095	0.0409	-1.02	1.13	1.07	1.02	<b>Vhl</b>	von Hippel-Lindau tumor suppressor	0000122	// negative regulation of transcription from RNA polymerase II promoter // not i				
NM_025338//XM_006531	0.023	1.12	1.13	1.07	-1.03	<b>Aurkaip1</b>	aurora kinase A interacting protein 1	0016310	// phosphorylation // inferred from electronic annotation//0016567	// protein			
NM_0157	0.047	1.10	-1.19	1.07	1.03	<b>Tpa</b>	tocopherol (alpha) transfer protein	0001890	// placenta development // inferred from mutant phenotype//0001892	// emb			
NM_0010	0.0036	1.03	1.34	1.07	-1.09	<b>Gmfg</b>	glia maturation factor, gamma	0034316	// negative regulation of Arp2/3 complex-mediated actin nucleation // inferred				
NM_0011	0.0018	0.002	-1.00	1.14	1.07	<b>Nt5c2</b>	5'-nucleotidase, cytosolic II	0006470	// protein dephosphorylation // --//0006470	// protein dephosphorylation // i			
NM_1339	0.0247	-1.09	1.14	1.07	-1.06	<b>Emilin1</b>	elastin microfibril interfacer 1	0007155	// cell adhesion // inferred from electronic annotation//0010811	// positive reg			
NM_026177	0.017	-1.04	1.01	1.07	1.04	<b>Gpalpp1</b>	GPALPP motifs containing 1						
NM_0273	#####	-1.00	1.21	1.07	1.05	<b>Gorasp2</b>	golgi reassembly stacking protein 2	0006996	// organelle organization // not recorded//0007030	// Golgi organization // no			
NM_1339	0.0149	1.07	-1.16	1.07	1.12	<b>Mlxip</b>	MLX interacting protein	0006351	// transcription, DNA-templated // inferred from electronic annotation//00063				
NM_0187	0.0384	1.03	1.22	1.07	-1.18	<b>Gipc1</b>	GIPC PDZ domain containing family, member 1	0006605	// protein targeting // inferred from mutant phenotype//0006605	// protein ta			
NM_001288578//NM_00	0.031	-1.04	-1.11	1.07	1.09	<b>Adh5</b>	alcohol dehydrogenase 5 (class III), chi polypeptide	0001523	// retinoid metabolic process // inferred from mutant phenotype//0003016	//			
NM_0011	0.0271	1.04	-1.21	1.07	1.13	<b>Gtf3c4</b>	general transcription factor IIIC, polypeptide 4	0006351	// transcription, DNA-templated // inferred from electronic annotation//00165				
NM_001032413//NM_00	0.047	1.14	1.08	1.07	-1.03	<b>Pear1</b>	platelet endothelial aggregation receptor 1	0043654	// recognition of apoptotic cell // inferred from direct assay//0043654	// recog			
NM_0307	0.0396	0.049	-1.10	1.11	1.07	-1.12	<b>Lactb</b>	lactamase, beta	0008152	// metabolic process // inferred from electronic annotation			
NM_0288	#####	-1.03	1.19	1.07	1.02	<b>Arpc5l</b>	actin related protein 2/3 complex, subunit 5-like	0030833	// regulation of actin filament polymerization // inferred from electronic annota				
NM_0010	0.0207	-1.05	1.07	1.07	1.19	<b>Furin</b>	furin (paired basic amino acid cleaving enzyme)	0006465	// signal peptide processing // not recorded//0006508	// proteolysis // inferre			
NM_0010	0.0015	0.002	-1.05	1.04	1.07	-1.04	<b>Ogfrl1</b>	opioid growth factor receptor-like 1					
NM_0010	0.0255	-1.06	1.17	1.07	1.21	<b>H3f3a-ps1//H3f3b//H3f3c</b>	H3 histone, family 3A//H3 histone, family 3A, pseudogene 1//H3 histone, family 3B//	0000183	// chromatin silencing at rDNA // traceable author statement//0001649	// oste			
NM_010162	0.041	-1.09	-1.13	1.07	1.11	<b>Ext1</b>	exostoses (multiple) 1	0001503	// ossification // not recorded//0006024	// glycosaminoglycan biosynthetic prc			
NM_0076	#####	-1.05	-1.47	1.07	-1.18	<b>Cdr2</b>	cerebellar degeneration-related 2						
NM_1813	0.0163	1.03	-1.03	1.07	1.02	<b>Anapc13</b>	anaphase promoting complex subunit 13	0007049	// cell cycle // inferred from electronic annotation//0007067	// mitotic nuclear			
NM_0213	0.0091	-1.07	1.09	1.07	-1.10	<b>Itgax</b>	integrin alpha X	0007155	// cell adhesion // inferred from electronic annotation//0007229	// integrin-mu			
NM_0012	0.0439	0.023	-1.01	1.15	1.07	-1.03	<b>Nfam1</b>	Nfat activating molecule with ITAM motif 1	0007165	// signal transduction // not recorded//0007165	// signal transduction // infer		
NM_0119	0.0407	1.13	-1.00	1.07	1.21	<b>Mapk3</b>	mitogen-activated protein kinase 3	0000165	// MAPK cascade // not recorded//0000189	// MAPK import into nucleus // no			
NM_1724	0.0147	1.10	-1.01	1.07	1.12	<b>Dnajc8</b>	Dnaj (Hsp40) homolog, subfamily C, member 8						
NM_025934//XM_006524	0.05	-1.03	1.00	1.07	1.22	<b>Riok2</b>	RIO kinase 2 (yeast)	0006468	// protein phosphorylation // inferred from electronic annotation//0016310	//			
NM_177326//XM_006524	0.01	-1.03	-1.05	1.07	1.07	<b>Pak2</b>	p21 protein (Cdc42/Rac)-activated kinase 2	0006468	// protein phosphorylation // not recorded//0006915	// apoptotic process // ir			
NM_0330	#####	1.05	1.19	1.07	-1.06	<b>Nudt19</b>	nudix (nucleoside diphosphate linked moiety X)-type motif 19	0008152	// metabolic process // inferred from electronic annotation				
NM_029896//XM_011244	0.034	-1.08	-1.11	1.07	1.05	<b>Wdr82</b>	WD repeat domain containing 82	0051568	// histone H3-K4 methylation // inferred from mutant phenotype//0051568	//			

RefSeq	Tri	p 24h	p 48h	p 72h	FD Air	FD 24h	FD 48h	FD 72h	Gene Symbol	Gene Title	Gene Ontology Biological Process
NM_0205	0.0303				-1.04	1.15	1.07	1.16	<i>Nelfcd</i>	negative elongation factor complex member C/D, Th1	0006351 // transcription, DNA-templated // inferred from electronic annotation//00063
NM_1774	0.0337				-1.05	1.06	1.08	1.09	<i>Pum3</i>	pumilio RNA-binding family member 3	0006417 // regulation of translation // not recorded
NM_0011	0.0385				1.16	1.33	1.08	1.10	<i>Pkn1</i>	protein kinase N1	0001782 // B cell homeostasis // inferred from mutant phenotype//0001783 // B cell ap
NM_0078	0.0077				1.14	-1.03	1.08	1.05	<i>Dsg2</i>	desmoglein 2	0002934 // desmosome organization // not recorded//0003165 // Purkinje myocyte dev
NM_0010	0.0486		0.034		-1.08	1.13	1.08	1.33	<i>Rrn3</i>	RRN3 RNA polymerase I transcription factor homolog (yeast)	0001701 // in utero embryonic development // inferred from mutant phenotype//0006:
NM_1448	0.0174				1.09	-1.05	1.08	1.07	<i>Taok1</i>	TAO kinase 1	0000165 // MAPK cascade // --//0000186 // activation of MAPKK activity // not recorde
NM_0115	0.0494				1.08	1.02	1.08	1.13	<i>Timp2</i>	tissue inhibitor of metalloproteinase 2	0007417 // central nervous system development // inferred from electronic annotation//
NM_1705	0.0451				-1.06	-1.26	1.08	1.01	<i>Nup1</i>	nucleoporin like 1	0006810 // transport // inferred from electronic annotation//0006913 // nucleocytopla:
NM_025334			0.044		-1.02	-1.02	1.08	1.17	<i>Txndc12</i>	thioredoxin domain containing 12 (endoplasmic reticulum)	0045454 // cell redox homeostasis // inferred from electronic annotation//0055114 // o
NM_0075	0.0327				1.02	1.11	1.08	1.03	<i>Atp6v1b2</i>	ATPase, H+ transporting, lysosomal V1 subunit B2	0006810 // transport // inferred from electronic annotation//0006811 // ion transport /
NM_0011	0.0223				-1.01	1.25	1.08	1.09	<i>Sirpa</i>	signal-regulatory protein alpha	0002244 // hematopoietic progenitor cell differentiation // inferred from mutant phenot
NM_0117	0.0042				1.03	1.46	1.08	1.13	<i>Zfp36</i>	zinc finger protein 36	0000122 // negative regulation of transcription from RNA polymerase II promoter // infer
NM_0268	0.0146		0.018		-1.02	-1.29	1.08	1.03	<i>Trmt1</i>	tRNA methyltransferase 1 like	0002940 // tRNA N2-guanine methylation // --//0007610 // behavior // inferred from e
NM_0012	0.0172				-1.01	1.18	1.08	1.23	<i>Tmem173</i>	transmembrane protein 173	0002218 // activation of innate immune response // inferred from mutant phenotype//000
NM_001044386	///NM_01	0.034			1.01	-1.15	1.08	1.20	<i>Zfx</i>	zinc finger protein X-linked	0001541 // ovarian follicle development // inferred from mutant phenotype//0006351 /
NM_0215	0.0131				-1.07	1.19	1.08	-1.01	<i>Rcl1</i>	RNA terminal phosphate cyclase-like 1	0000479 // endonucleolytic cleavage of tricistronic rRNA transcript (5S-U-rRNA, 5.8S rRNA
NM_1386	0.0331				-1.05	1.09	1.08	1.02	<i>Mvd</i>	mevalonate (diphospho) decarboxylase	0006629 // lipid metabolic process // inferred from electronic annotation//0006694 // s
NM_172015	///XM	0.033			-1.09	-1.05	1.08	1.02	<i>Iars</i>	isoleucine-tRNA synthetase	0001649 // osteoblast differentiation // not recorded//0006412 // translation // inferre
NM_0010	0.017				1.02	-1.09	1.08	1.05	<i>Osbp</i>	oxysterol binding protein	0006810 // transport // inferred from electronic annotation//0006869 // lipid transport
NM_0199	0.0242				-1.11	1.14	1.08	1.05	<i>Litaf</i> ///Gm9861	LPS-induced TN factor//predicted gene 9861	0001817 // regulation of cytokine production // inferred from mutant phenotype//0006
NM_028680			0.013		-1.10	-1.07	1.08	-1.14	<i>Ift57</i>	intraflagellar transport 57	0001843 // neural tube closure // inferred from mutant phenotype//0001947 // heart lc
NM_1750	0.0085				-1.01	1.10	1.08	1.20	<i>Commd2</i>	COMM domain containing 2	0006351 // transcription, DNA-templated // inferred from electronic annotation//00063
NM_0011	0.0262		0.023		-1.19	-1.02	1.08	-1.01	<i>Ccdc127</i>	coiled-coil domain containing 127	
NM_0084	0.0162				-1.05	1.14	1.08	-1.02	<i>Irgb1bp1</i>	integrin beta 1 binding protein 1	0001525 // angiogenesis // inferred from electronic annotation//0002043 // blood vess
NM_0013	0.0058				1.02	1.29	1.08	1.06	<i>Usp3</i>	ubiquitin specific peptidase 3	0000122 // negative regulation of transcription from RNA polymerase II promoter // infer
NM_025692	///XM	0.034			-1.07	1.01	1.08	-1.20	<i>Uba5</i>	ubiquitin-like modifier activating enzyme 5	0033146 // regulation of intracellular estrogen receptor signaling pathway // not recorde
NM_0098	0.0245				-1.04	-1.20	1.08	-1.07	<i>Cebpg</i>	CCAAT/enhancer binding protein (C/EBP), gamma	0001889 // liver development // inferred from sequence or structural similarity//000188
NM_001316372	///	0.028			-1.04	1.06	1.08	1.07	<i>Pcpt</i>	phosphatidylcholine transfer protein	0006810 // transport // inferred from electronic annotation//0006869 // lipid transport
NM_013717	///XM	0.035			-1.01	1.03	1.08	1.02	<i>B9d1</i>	B9 protein domain 1	0001701 // in utero embryonic development // inferred from mutant phenotype//00018
NM_019951			0.037		-1.09	1.03	1.08	1.21	<i>Sec11a</i>	SEC11 homolog A, signal peptidase complex subunit	0006465 // signal peptide processing // inferred from electronic annotation//0006508 //
NM_1462	0.0327				-1.04	1.12	1.08	1.05	<i>Apeh</i>	acylpeptide hydrolase	0006508 // proteolysis // not recorded//0050435 // beta-amyloid metabolic process // r
NM_001110310	///	0.015			-1.04	1.03	1.08	1.06	<i>Snx12</i>	sorting nexin 12	0006810 // transport // inferred from electronic annotation//0006897 // endocytosis //
NM_0116	0.0116	0.043			-1.19	1.11	1.08	1.17	<i>Tubb5</i>	tubulin, beta 5 class I	0006457 // protein folding // traceable author statement//0007017 // microtubule-base
NM_019791		0.012			-1.20	-1.04	1.08	1.12	<i>Maged1</i>	melanoma antigen, family D, 1	0006357 // regulation of transcription from RNA polymerase II promoter // inferred from
NM_001253757	///NM_00	0.034			1.00	1.00	1.08	1.33	<i>Anp32e</i>	acidic (leucine-rich) nuclear phosphoprotein 32 family, member E	0001658 // chromatin modification // inferred from electronic annotation//0043086 // r
NM_001164223	///NM_02	0.045			1.06	1.01	1.08	-1.02	<i>Rpa1</i>	replication protein A1	0000723 // telomere maintenance // not recorded//0000724 // double-strand break re
NM_001289621	///	0.015			-1.01	1.03	1.08	1.05	<i>Mynn</i>	myoneurin	0006351 // transcription, DNA-templated // inferred from electronic annotation//00063
NM_029735	///XM	0.003			-1.09	-1.01	1.08	1.03	<i>Eprs</i>	glutamyl-prolyl-tRNA synthetase	0006412 // translation // inferred from electronic annotation//0006417 // regulation of
NM_0206	0.0259				1.05	1.15	1.08	1.00	<i>Srd5a3</i>	steroid 5 alpha-reductase 3	0006486 // protein glycosylation // inferred from electronic annotation//0006488 // dol
NM_0137	#####	0.044			-1.13	1.39	1.08	1.16	<i>Msrb1</i>	methionine sulfoxide reductase B1	0002376 // immune system process // inferred from electronic annotation//0006979 //
NM_033526	///XM	0.02			-1.05	-1.07	1.08	1.05	<i>Ubqln4</i>	ubiquilin 4	0006914 // autophagy // inferred from electronic annotation//0032434 // regulation of
NM_0011	0.0299				1.09	1.29	1.08	1.00	<i>Sin3b</i>	transcriptional regulator, SIN3B (yeast)	0000122 // negative regulation of transcription from RNA polymerase II promoter // not r
NM_0117	0.0233				-1.06	1.12	1.08	1.04	<i>Trpv2</i>	transient receptor potential cation channel, subfamily V, member 2	0006810 // transport // inferred from electronic annotation//0006811 // ion transport /
NM_019743		0.024			-1.01	1.06	1.08	-1.03	<i>Rybp</i>	RING1 and YY1 binding protein	0000122 // negative regulation of transcription from RNA polymerase II promoter // infer
NM_0011	0.0292				1.01	1.16	1.08	-1.10	<i>Ifnar2</i>	interferon (alpha and beta) receptor 2	0006357 // regulation of transcription from RNA polymerase II promoter // inferred from
NM_001161775	///NM_01	0.04			-1.21	-1.21	1.08	1.17	<i>Myh11</i>	myosin, heavy polypeptide 11, smooth muscle	0006939 // smooth muscle contraction // inferred from direct assay//0006939 // smoot
NM_009068	///XM	0.033			-1.03	-1.01	1.08	-1.05	<i>Ripk1</i>	receptor (TNFRSF)-interacting serine-threonine kinase 1	0001934 // positive regulation of protein phosphorylation // not recorded//0006468 // i
NM_1454	0.0221				1.00	-1.08	1.08	1.05	<i>Nipal2</i>	NIPA-like domain containing 2	0015693 // magnesium ion transport // inferred from electronic annotation//1903830 //
NM_0188	0.0061				-1.03	1.05	1.08	1.06	<i>Uqc1</i>	ubiquinol-cytochrome c reductase complex assembly factor 1	0034551 // mitochondrial respiratory chain complex III assembly // not recorded//00070:
NM_00229	0.0096				-1.05	1.09	1.08	1.09	<i>Nif3l1</i>	Ngg1 interacting factor 3-like 1 (S. pombe)	0030182 // neuron differentiation // inferred from mutant phenotype//0045893 // posi
NM_0167	0.0287				-1.13	1.18	1.09	-1.02	<i>Atp5b</i>	ATP synthase, H+ transporting mitochondrial F1 complex, beta subunit	0001525 // angiogenesis // not recorded//0001649 // osteoblast differentiation // not r
NM_0012	0.0067				1.00	1.45	1.09	-1.14	<i>Ncf1</i>	neutrophil cytosolic factor 1	0001878 // response to yeast // inferred from mutant phenotype//0001909 // leukocyte
NM_012055	///XM	0.014			-1.19	-1.02	1.09	-1.03	<i>Asns</i>	asparagine synthetase	0001889 // liver development // inferred from electronic annotation//0006520 // cellul
NM_030109	///XM	0.038			1.00	1.03	1.09	1.21	<i>Sf3b2</i>	splicing factor 3b, subunit 2	0000398 // mRNA splicing, via spliceosome // not recorded
NM_0224	0.0138				1.08	1.36	1.09	1.06	<i>Ptges</i>	prostaglandin E synthase	0001516 // prostaglandin biosynthetic process // not recorded//0002526 // acute inflan
NM_133900	///XM_006504	0.023			-1.08	-1.01	1.09	1.09	<i>Psph</i>	phosphoserine phosphatase	0006470 // protein dephosphorylation // --//0006470 // protein dephosphorylation // i
NM_001305284	///	0.05			-1.18	-1.28	1.09	1.06	<i>Mpdz</i>	multiple PDZ domain protein	0007155 // cell adhesion // inferred from direct assay//0042552 // myelination // not r
NM_080850	///XM	0.007			-1.06	-1.00	1.09	-1.16	<i>Pask</i>	PAS domain containing serine/threonine kinase	0006468 // protein phosphorylation // not recorded//0016310 // phosphorylation // inf
NM_0076	0.0021				1.13	2.89	1.09	1.11	<i>Cd79a</i>	CD79A antigen (immunoglobulin-associated alpha)	0002250 // adaptive immune response // inferred from electronic annotation//0002376
NM_011653		0.008			-1.14	-1.00	1.09	-1.01	<i>Tuba1a</i>	tubulin, alpha 1A	0007017 // microtubule-based process // inferred from electronic annotation//0008152
NM_001110512	///NM_14	0.02			1.04	1.09	1.09	1.18	<i>Mettl8</i>	methyltransferase like 8	0007519 // skeletal muscle tissue development // inferred from direct assay//0016573 /
NM_0119	0.0232				1.07	-1.07	1.09	1.22	<i>Fto</i>	fat mass and obesity associated	0001659 // temperature homeostasis // inferred from mutant phenotype//0006281 // C
NM_0082	0.0037				1.02	1.54	1.09	-1.30	<i>Hlx</i>	H2.0-like homeobox	0001889 // liver development // inferred from mutant phenotype//0006351 // transcrip
NM_0265	0.0246				-1.03	1.18	1.09	1.10	<i>Emc4</i>	ER membrane protein complex subunit 4	0006915 // apoptotic process // inferred from electronic annotation

RefSeq	Tri	p 24h	p 48h	p 72h	FD Air	FD 24h	FD 48h	FD 72h	Gene Symbol	Gene Title	Gene Ontology Biological Process
NM_1338	0.0074				-1.07	1.11	1.09	-1.11	<i>Dpp3</i>	dipeptidylpeptidase 3	0006508 // proteolysis // not recorded
NM_001290826	///NM_001	0.012			-1.04	1.04	1.09	1.14	<i>Cpeb3</i>	cytoplasmic polyadenylation element binding protein 3	0000122 // negative regulation of transcription from RNA polymerase II promoter // not r
NM_0092	0.034	0.007			-1.08	1.05	1.09	-1.05	<i>Sos1</i>	son of sevenless homolog 1 (Drosophila)	0001782 // B cell homeostasis // inferred from genetic interaction///0001942 // hair folli
NM_0011	0.0452				-1.05	-1.15	1.09	1.04	<i>2-Sep</i>	septin 2	0000910 // cytokinesis // non-traceable author statement///0002036 // regulation of L-g
NM_001163687	///	0.025			-1.10	-1.01	1.09	-1.08	<i>Naaa</i>	N-acyl ethanolamine acid amidase	0006629 // lipid metabolic process // inferred from electronic annotation
NM_0013	#####				1.09	-1.01	1.09	1.02	<i>Actg1</i>	actin, gamma, cytoplasmic 1	0001895 // retina homeostasis // inferred from electronic annotation///0045214 // sarcc
NM_019836	///XM	0.013			1.05	1.04	1.09	-1.06	<i>Noa1</i>	nitric oxide associated 1	0006915 // apoptotic process // inferred from electronic annotation///0010941 // regula
NM_0087	0.0186				1.08	1.38	1.09	1.06	<i>Pafah1b3</i>	platelet-activating factor acetylhydrolase, isoform 1b, subunit 3	0006629 // lipid metabolic process // inferred from electronic annotation///0007283 // s
NM_1451	0.0379				1.02	1.21	1.09	1.16	<i>Eif3l</i>	eukaryotic translation initiation factor 3, subunit L	0001731 // formation of translation preinitiation complex // inferred from electronic ann
NM_001110211	///	0.011			-1.08	1.05	1.09	1.39	<i>Anxa6</i>	annexin A6	0006816 // calcium ion transport // inferred from mutant phenotype///0006937 // regul
NM_025516	///XM	0.035			-1.00	-1.04	1.09	1.24	<i>Ergic3</i>	ERGIC and golgi 3	0006810 // transport // inferred from electronic annotation///0006888 // ER to Golgi ves
NM_199199		0.019			-1.08	1.00	1.09	-1.02	<i>Tmem199</i>	transmembrane protein 199	
NM_001306205	///NM_02	0.009			1.11	1.14	1.09	-1.16	<i>Mvk</i>	mevalonate kinase	0006629 // lipid metabolic process // inferred from electronic annotation///0006694 // s
NM_0104	0.0164				-1.10	1.39	1.09	1.26	<i>Id2</i>	inhibitor of DNA binding 2	0000122 // negative regulation of transcription from RNA polymerase II promoter // infer
NM_001291197	///NM_00	0.049			-1.05	-1.02	1.09	1.13	<i>Tpd52l2</i>	tumor protein D52-like 2	
NM_0136	0.0338				1.02	1.20	1.09	-1.01	<i>Odc1</i> /// <i>Gm9115</i>	ornithine decarboxylase, structural 1///ornithine decarboxylase, structural 1 pseudoge	0001822 // kidney development // inferred from mutant phenotype///0006595 // polyar
NM_011794	///XM	0.012	0.015		-1.21	-1.20	1.09	1.16	<i>Bpnt1</i>	bisphosphate 3'-nucleotidase 1	0006135 // nucleobase-containing compound metabolic process // not recorded///0006
NM_0173	0.0181				-1.02	1.15	1.09	-1.15	<i>Ostf1</i>	osteoclast stimulating factor 1	
NM_0011	0.0458				1.01	-1.15	1.09	1.06	<i>Zfp275</i>	zinc finger protein 275	0006355 // regulation of transcription, DNA-templated // inferred from electronic annotz
NM_1308	#####				-1.01	1.18	1.09	1.04	<i>Anp32b</i>	acidic (leucine-rich) nuclear phosphoprotein 32 family, member B	0000082 // G1/S transition of mitotic cell cycle // not recorded///0001944 // vasculare
NM_0013	0.0384				-1.04	1.13	1.09	-1.17	<i>Mbd3</i>	methyl-CpG binding domain protein 3	0000122 // negative regulation of transcription from RNA polymerase II promoter // infer
NM_009148	///XM	0.012	0.046		-1.09	-1.06	1.09	1.01	<i>Exoc4</i>	exocyst complex component 4	0006612 // protein targeting to membrane // not recorded///0006810 // transport // inf
NM_0294	0.0226				-1.06	-1.44	1.09	-1.05	<i>Slc10a6</i>	solute carrier family 10 (sodium/bile acid cotransporter family), member 6	0006810 // transport // inferred from electronic annotation///0006811 // ion transport /
NM_0242	0.0037	0.031	0.035		-1.04	1.10	1.09	1.05	<i>Anapc4</i>	anaphase promoting complex subunit 4	0007049 // cell cycle // inferred from electronic annotation///0007067 // mitotic nuclear
NM_144884		0.026			-1.09	1.02	1.09	-1.08	<i>Tor1a</i>	torin family 1, member A (torin A)	0000338 // protein deneddylation // not recorded///0006979 // response to oxidative sti
NM_173865			0.002		1.01	1.07	1.09	1.33	<i>Slc41a1</i>	solute carrier family 41, member 1	0006810 // transport // inferred from electronic annotation///0006811 // ion transport /
NM_022011	///XM	0.03	0.011		-1.13	-1.15	1.09	1.10	<i>Gtf2h2</i>	general transcription factor II H, polypeptide 2	0002031 // G-protein coupled receptor internalization // not recorded///0006281 // DNz
NM_001136070	///	0.036			1.02	1.08	1.10	1.09	<i>Eif2d</i>	eukaryotic translation initiation factor 2D	0001731 // formation of translation preinitiation complex // not recorded///0002192 // DNz
NM_0138	0.0076				-1.09	-1.58	1.10	1.01	<i>Bag3</i>	BCL2-associated athanogene 3	0006915 // apoptotic process // inferred from electronic annotation///0007420 // brain r
NM_026521		0.032			-1.05	-1.02	1.10	-1.02	<i>Zfp706</i>	zinc finger protein 706	0006417 // regulation of translation // inferred from electronic annotation///0045892 //
NM_0011	0.0327				1.03	-1.14	1.10	1.07	<i>Zfp790</i>	zinc finger protein 790	0006355 // regulation of transcription, DNA-templated // inferred from electronic annotz
NM_009730	///XM_006498	0.021			1.15	1.04	1.10	-1.10	<i>Atrn</i>	atractin	0006954 // inflammatory response // inferred from electronic annotation///0006979 // r
NM_001291358	///NM_14	0.044			-1.04	-1.01	1.10	1.31	<i>Pgap2</i>	post-GPI attachment to proteins 2	0006506 // GPI anchor biosynthetic process // not recorded///0006974 // cellular respon
NM_172592	///XM_006511	0.046			-1.01	1.04	1.10	1.21	<i>Srek1</i>	splicing regulatory glutamine/lysine-rich protein 1	0006397 // mRNA processing // inferred from electronic annotation///0008380 // RNA sp
NM_001042491	///NM_00	0.017			1.10	1.09	1.10	-1.02	<i>Anapc5</i>	anaphase-promoting complex subunit 5	0007049 // cell cycle // inferred from electronic annotation///0007067 // mitotic nuclear
NM_133238		0.022			-1.23	-1.14	1.10	-1.05	<i>Cd209a</i>	CD209a antigen	0006897 // endocytosis // inferred from electronic annotation///0010468 // regulation o
NM_0013	0.0126				-1.05	1.18	1.10	1.04	<i>Ppp1r1b</i>	protein phosphatase 1, regulatory (inhibitor) subunit 1B	0001975 // response to amphetamine // inferred from genetic interaction///0006351 // r
NM_0010	0.0353				-1.04	1.11	1.10	1.02	<i>Nasp</i>	nuclear autoantigenic sperm protein (histone-binding)	0001824 // blastocyst development // inferred from mutant phenotype///0006260 // DN
NM_001170332	///	0.016			-1.04	1.01	1.10	-1.04	<i>Clec4a2</i> /// <i>Clec4b1</i>	C-type lectin domain family 4, member a2///C-type lectin domain family 4, member b1	0000250 // adaptive immune response // inferred from electronic annotation///0002376
NM_1461	0.0046				-1.04	1.22	1.10	1.09	<i>Tubb4b</i> /// <i>Tubb4b-ps1</i>	tubulin, beta 4B class IVB///tubulin, beta 4B class IVB, pseudogene 1	0007017 // microtubule-based process // non-traceable author statement///0008152 //
NM_0011	0.0419				-1.02	1.11	1.10	1.01	<i>Cebpz</i>	CCAAT/enhancer binding protein (C/EBP), zeta, opposite strand	
NM_0259	0.0483				1.09	-1.04	1.10	1.11	<i>Mettl6</i>	methyltransferase like 6	0032259 // methylation // inferred from electronic annotation
NM_0117	0.0455				-1.03	-1.19	1.10	-1.04	<i>Ercc5</i>	excision repair cross-complementing rodent repair deficiency, complementation group	0006281 // DNA repair // inferred from mutant phenotype///0006283 // transcription-cc
NM_001314013	///	0.03	0.027		1.02	1.06	1.10	1.15	<i>Atg5</i>	autophagy related 5	0000045 // autophagosome assembly // inferred from mutant phenotype///0000422 // r
NM_0076	0.0357				1.04	1.56	1.10	-1.14	<i>Cd48</i>	CD48 antigen	0007165 // signal transduction // inferred from direct assay///0042110 // T cell activatio
NM_0012	0.0198				-1.02	1.19	1.10	1.35	<i>Gapdh</i> /// <i>Gapdh-ps15</i> /// <i>Gm10313</i> /// <i>Gm12</i>	glyceraldehyde-3-phosphate dehydrogenase pseudogene///glyceraldehyde-3-phosph	0000226 // microtubule cytoskeleton organization // not recorded///0005975 // carbohy
NM_001161746	///NM_01	0.041			1.24	1.34	1.10	-1.12	<i>Tnfrsf12a</i>	tumor necrosis factor receptor superfamily, member 12a	0001525 // angiogenesis // inferred from electronic annotation///0006915 // apoptotic c
NM_001136067	///	0.04			1.01	1.06	1.10	1.18	<i>Ikbkg</i>	inhibitor of kappaB kinase gamma	0001782 // B cell homeostasis // inferred from mutant phenotype///0006351 // transcrip
NM_0013	0.0213				1.00	1.17	1.10	1.20	<i>Scfd1</i>	Sec1 family domain containing 1	0000902 // cell morphogenesis // inferred from sequence or structural similarity///0001E
NM_001294322	///	0.042			-1.07	-1.00	1.10	1.16	<i>Mpv17</i>	Mpv17 mitochondrial inner membrane protein	0000002 // mitochondrial genome maintenance // not recorded///0007605 // sensory pr
NM_0010	0.0082				1.10	1.37	1.10	1.08	<i>Grk6</i>	G protein-coupled receptor kinase 6	0002029 // desensitization of G-protein coupled receptor protein signaling pathway // nc
NM_009786		0.015			-1.37	-1.78	1.10	-1.35	<i>Cacybp</i>	calyculin binding protein	0007507 // heart development // inferred from electronic annotation///0007568 // agin
NM_1751	0.0346				1.05	-1.01	1.10	1.05	<i>Emc3</i>	ER membrane protein complex subunit 3	0034975 // protein folding in endoplasmic reticulum // not recorded
NM_0011	0.038				1.01	1.22	1.10	-1.22	<i>Crif2</i>	cytokine receptor-like factor 2	0002380 // immunoglobulin secretion involved in immune response // inferred from dire
NM_0105	#####				1.20	2.94	1.10	1.08	<i>Cyr61</i>	cysteine rich protein 61	0001558 // regulation of cell growth // inferred from electronic annotation///0001649 //
NM_001098271	///NM_02	0.015			-1.03	1.02	1.10	1.16	<i>Tmem176a</i>	transmembrane protein 176A	2001199 // negative regulation of dendritic cell differentiation // inferred from mutant pl
NM_0103	0.0289				1.02	1.43	1.10	1.27	<i>H2-DMb1</i> /// <i>H2-DMb2</i> /// <i>LOC102642102</i>	histocompatibility 2, class II, locus Mb1///histocompatibility 2, class II, locus Mb2///un	0002376 // immune system process // inferred from electronic annotation///0002504 //
NM_028131	///XM	0.014			-1.06	1.06	1.10	1.00	<i>Cenpn</i>	centromere protein N	0007059 // chromosome segregation // inferred from electronic annotation///0007067 //
NM_0306	0.0081				-1.12	1.27	1.10	1.27	<i>Gpx2</i>	glutathione peroxidase 2	0001659 // temperature homeostasis // inferred from genetic interaction///0002862 // n
NM_0114	0.0083				1.08	1.30	1.10	1.00	<i>Sptlc2</i>	serine palmitoyltransferase, long chain base subunit 2	0006629 // lipid metabolic process // inferred from electronic annotation///0006665 // s
NM_024475	///XM_006534	0.026			-1.00	1.00	1.10	1.20	<i>Ublcp1</i>	ubiquitin-like domain containing CTD phosphatase 1	0006470 // protein dephosphorylation // not recorded
NM_1449	0.0236	0.013			1.00	1.14	1.10	-1.00	<i>Smyd5</i>	SET and MYND domain containing 5	0032259 // methylation // inferred from electronic annotation
NM_0011	0.0055				1.03	-1.06	1.10	1.10	<i>Aplp2</i>	amyloid beta (A4) precursor-like protein 2	0001967 // suckling behavior // inferred from genetic interaction///0006878 // cellular c
NM_001048057	///	0.032			-1.07	-1.01	1.10	1.04	<i>Rpl38</i>	ribosomal protein L38	0001501 // skeletal system development // inferred from mutant phenotype///0001501 .

RefSeq	Tri	p 24h	p 48h	p 72h	FD Air	FD 24h	FD 48h	FD 72h	Gene Symbol	Gene Title	Gene Ontology Biological Process
NM_0252		0.0394	0.018		-1.08	1.03	1.10	-1.02	<b>Mecr</b>	mitochondrial trans-2-enoyl-CoA reductase	0006629 // lipid metabolic process // inferred from electronic annotation//0006631 // f.
NM_0011		0.0181		0.027	-1.03	1.13	1.10	1.15	<b>Slc35b3</b>	solute carrier family 35, member B3	0002230 // positive regulation of defense response to virus by host // not recorded//000
NM_008858	//XM	0.014			-1.14	-1.23	1.10	1.03	<b>Prkd1</b>	protein kinase D1	0001525 // angiogenesis // inferred from electronic annotation//0001938 // positive reg
NM_027357		0.038			-1.11	-1.01	1.10	1.08	<b>Psmc1</b>	proteasome (prosome, macropain) 26S subunit, non-ATPase, 1	0042176 // regulation of protein catabolic process // inferred from electronic annotation
NM_026030		0.023			-1.10	1.01	1.10	1.01	<b>Eif2s2</b>	eukaryotic translation initiation factor 2, subunit 2 (beta)	0001701 // in utero embryonic development // inferred from mutant phenotype//0002:
NM_012012	//XM	0.02			-1.12	1.04	1.10	-1.06	<b>Exo1</b>	exonuclease 1	0002376 // immune system process // inferred from electronic annotation//0002455 //
NM_0010		0.0043			1.30	1.00	1.10	1.27	<b>Atp2b2</b>	ATPase, Ca++ transporting, plasma membrane 2	0000902 // cell morphogenesis // inferred from mutant phenotype//0006810 // transp
NM_0012		0.0435			-1.02	1.05	1.11	1.01	<b>Pfkfb</b>	phosphofructokinase, platelet	0006002 // fructose 6-phosphate metabolic process // not recorded//0006096 // glycol
NM_009838		0.042			-1.07	-1.11	1.11	1.02	<b>Cct6a</b>	chaperonin containing Tcp1, subunit 6a (zeta)	0006457 // protein folding // inferred from electronic annotation//0007339 // binding c
NM_0120		0.0107			-1.03	1.13	1.11	1.18	<b>Cops6</b>	COP9 (constitutive photomorphogenic) homolog, subunit 6 (Arabidopsis thaliana)	0010388 // cullin deneddylation // not recorded
NM_001285452	//	0.014	0.026		-1.33	-1.38	1.11	1.09	<b>Tmem33</b>	transmembrane protein 33	0034613 // cellular protein localization // not recorded//0051292 // nuclear pore compl
NM_001303423	//NM_00	0.022			-1.01	-1.10	1.11	1.32	<b>Aldoc</b>	aldolase C, fructose-bisphosphate	0006096 // glycolytic process // inferred from electronic annotation//0006915 // apopt
NM_1810		0.0375			1.08	-1.00	1.11	-1.07	<b>Plekhh1</b>	pleckstrin homology domain containing, family H (with MyTH4 domain) member 1	
NM_0111		0.0086			1.17	2.12	1.11	1.14	<b>Pou2af1</b>	POU domain, class 2, associating factor 1	0006351 // transcription, DNA-templated // inferred from electronic annotation//00063
NM_0082		0.003			-1.14	1.36	1.11	1.09	<b>Hcls1</b>	hematopoietic cell specific Lyn substrate 1	0000122 // negative regulation of transcription from RNA polymerase II promoter // infer
NM_1537		0.0497			-1.00	1.18	1.11	1.03	<b>Pygb</b>	brain glycogen phosphorylase	0005975 // carbohydrate metabolic process // inferred from electronic annotation//000
NM_019814	//XM	0.032			-1.14	-1.03	1.11	1.04	<b>Higd1a</b>	HIG1 domain family, member 1A	0006810 // transport // inferred from electronic annotation//0042149 // cellular respon
NM_021518	//XM	0.011			-1.04	1.01	1.11	1.01	<b>Rab2a</b>	RAB2A, member RAS oncogene family	0006810 // transport // inferred from electronic annotation//0006886 // intracellular pr
NM_0091		0.0199			-1.12	1.11	1.11	1.11	<b>S100a10</b> // <b>LOC105242499</b>	S100 calcium binding protein A10 (calpactin)//protein S100-A10-like	0001765 // membrane raft assembly // not recorded//0006900 // membrane budding /
NM_0265		0.0445	0.031		1.01	1.06	1.11	-1.02	<b>N6amt2</b>	N-6 adenine-specific DNA methyltransferase 2 (putative)	0032259 // methylation // inferred from electronic annotation
NM_0011		0.0096			-1.05	-1.33	1.11	-1.01	<b>Erlin1</b>	ER lipid raft associated 1	0006629 // lipid metabolic process // inferred from electronic annotation//0008202 // s
NM_1340		0.0139	0.003		-1.10	1.13	1.11	-1.04	<b>Fbxo4</b>	F-box protein 4	0000209 // protein polyubiquitination // not recorded//0000723 // telomere maintain
NM_1339		0.0159			1.07	-1.14	1.11	1.07	<b>Plekha1</b>	pleckstrin homology domain containing, family A (phosphoinositide binding specific) r	0001553 // luteinization // inferred from genetic interaction//0007283 // spermatogene
NM_0284		0.0417			1.02	1.17	1.11	-1.05	<b>Prrc1</b>	proline-rich coiled-coil 1	
NM_0010		0.0068			1.09	1.54	1.11	1.17	<b>Capp</b>	capping protein (actin filament), gelsolin-like	0030031 // cell projection assembly // inferred from direct assay//0051016 // barbed-er
NM_021457		0.023			-1.01	1.06	1.11	1.16	<b>Fzd1</b>	frizzled homolog 1 (Drosophila)	0001934 // positive regulation of protein phosphorylation // inferred from mutant phenc
NM_026792		0.033			-1.07	-1.06	1.11	1.02	<b>Agnat5</b>	1-acylglycerol-3-phosphate O-acyltransferase 5 (lysophosphatidic acid acyltransferase,	0002244 // hematopoietic progenitor cell differentiation // inferred from genetic interact
NM_024433		0.021			-1.02	1.07	1.11	1.03	<b>Mtap</b>	methylthioadenosine phosphorylase	0006166 // purine ribonucleoside salvage // inferred from electronic annotation//00091
NM_0010		0.0461	0.039		1.06	-1.01	1.11	1.09	<b>Vprbp</b>	Vpr (HIV-1) binding protein	0000122 // negative regulation of transcription from RNA polymerase II promoter // not r
NM_0089		0.0107			-1.07	1.24	1.11	1.12	<b>Psmb6</b>	proteasome (prosome, macropain) subunit, beta type 6	0006508 // proteolysis // inferred from electronic annotation//0010499 // proteasomal
NM_021539		0.004			-1.07	1.01	1.11	1.05	<b>Wsb2</b>	WD repeat and SOCS box-containing 2	0016567 // protein ubiquitination // inferred from electronic annotation//0035556 // in
NM_0256		0.0401			1.05	1.24	1.11	1.04	<b>Pspc1</b>	paraspeckle protein 1	0000398 // mRNA splicing, via spliceosome // not recorded//0006351 // transcription, C
NM_0173		0.0071	0.011		1.55	1.11	1.11	1.74	<b>Tef</b>	thyrotroph embryonic factor	0006351 // transcription, DNA-templated // inferred from electronic annotation//00063
NM_0217		0.0187			-1.16	1.52	1.11	-1.09	<b>Ms4a4b</b>	membrane-spanning 4-domains, subfamily A, member 4B	
NM_010751	//XM	0.025			-1.06	1.03	1.11	-1.20	<b>Mxd1</b>	MAX dimerization protein 1	0000122 // negative regulation of transcription from RNA polymerase II promoter // not r
NM_001242349	//	0.005	0.005		-1.15	1.16	1.11	1.20	<b>Ano1</b>	anoctamin 1, calcium activated chloride channel	0006810 // transport // inferred from electronic annotation//0006811 // ion transport /
NM_0012		0.0017			-1.15	1.16	1.11	1.20	<b>Ano1</b>	anoctamin 1, calcium activated chloride channel	0006810 // transport // inferred from electronic annotation//0006811 // ion transport /
NM_1445		0.0111			1.05	1.19	1.11	1.23	<b>Bre</b>	brain and reproductive organ-expressed protein	0006281 // DNA repair // inferred from electronic annotation//0006302 // double-stran
NM_0264		0.0136			1.06	1.23	1.11	1.03	<b>Atp5g2</b> // <b>LOC102641133</b>	ATP synthase, H+ transporting, mitochondrial FO complex, subunit C2 (subunit 9)//AT	0006810 // transport // inferred from electronic annotation//0006811 // ion transport /
NM_0084		0.0483			-1.07	1.13	1.11	1.12	<b>Itn2a</b>	integral membrane protein 2A	
NM_001039718	//	0.023			-1.01	1.06	1.11	-1.14	<b>Cntf</b> // <b>Zfp91</b> // <b>Zfp91Cntf</b>	ciliary neurotrophic factor//zinc finger protein 91//Zfp91-Cntf readthrough transcrip	0007250 // activation of NF-kappaB-inducing kinase activity // not recorded//0007259 /
NM_026842	//NM	0.034			-1.11	-1.11	1.11	-1.08	<b>Ubqln1</b>	ubiquilin 1	0006914 // autophagy // inferred from electronic annotation//0016241 // regulation of
NM_0010		0.0209			-1.01	1.19	1.11	1.10	<b>Med15</b>	mediator complex subunit 15	0006351 // transcription, DNA-templated // inferred from electronic annotation//00063
NM_0012		0.0282	0.014	0.02	-1.13	1.00	1.11	1.03	<b>Farsb</b>	phenylalanyl-tRNA synthetase, beta subunit	0006412 // translation // inferred from electronic annotation//0006432 // phenylalanyl-
NM_0286		0.047			1.04	-1.11	1.11	1.12	<b>Mcee</b>	methylmalonyl CoA epimerase	0046491 // L-methylmalonyl-CoA metabolic process // not recorded
NM_0012		0.0489			1.03	-1.08	1.11	-1.15	<b>Fam105a</b>	family with sequence similarity 105, member A	
NM_0263		0.0229			1.02	1.19	1.11	1.02	<b>Poldip2</b>	polymerase (DNA-directed), delta interacting protein 2	0070584 // mitochondrion morphogenesis // inferred from mutant phenotype
NM_0196		0.0487			1.00	-1.04	1.11	1.14	<b>Socs5</b>	suppressor of cytokine signaling 5	0006469 // negative regulation of protein kinase activity // not recorded//0007173 // eq
NM_001271531	//NM_00	0.035			-1.01	1.03	1.11	1.15	<b>Insig2</b>	insulin induced gene 2	0006629 // lipid metabolic process // inferred from electronic annotation//0006641 //
NM_0256		0.0487			1.01	1.08	1.11	1.14	<b>Smc6</b>	structural maintenance of chromosomes 6	0000722 // telomere maintenance via recombination // not recorded//0000724 // doub
NM_1535		0.0107			-1.02	1.12	1.11	1.07	<b>Bcl2l13</b>	BCL2-like 13 (apoptosis facilitator)	0006915 // apoptotic process // inferred from reviewed computational analysis//00429:
NM_0011		0.0254			1.04	1.21	1.11	1.00	<b>H13</b>	histocompatibility 13	0006508 // proteolysis // inferred from electronic annotation//0033619 // membrane p
NM_0012		0.0139	0.01		-1.37	-2.16	1.11	-1.21	<b>Ahsa2</b>	AHA1, activator of heat shock protein ATPase 2	0006950 // response to stress // inferred from electronic annotation//0032781 // posit
NM_0011		0.0366	0.031		1.01	1.13	1.12	1.07	<b>Orc3</b>	origin recognition complex, subunit 3	0006260 // DNA replication // traceable author statement//0061351 // neural precursor
NM_1986		0.0301			1.09	1.27	1.12	1.01	<b>Ap2s1</b>	adaptor-related protein complex 2, sigma 1 subunit	0006810 // transport // inferred from electronic annotation//0006886 // intracellular pr
NM_001163332	//	0.043			-1.18	-1.49	1.12	1.07	<b>Cttnbp2nl</b>	CTTNBP2 N-terminal like	0006470 // protein dephosphorylation // inferred from direct assay//0006470 // protein
NM_1339		0.048			1.02	1.18	1.12	1.05	<b>Fig4</b>	FIG4 homolog (S. cerevisiae)	0007033 // vacuole organization // inferred from mutant phenotype//0007626 // locom
NM_1528		0.024	0.007		-1.08	1.11	1.12	-1.05	<b>Ttc27</b>	tetratricopeptide repeat domain 27	
NM_0267		0.0148			-1.03	1.23	1.12	-1.01	<b>Mphosph6</b>	M phase phosphoprotein 6	0000460 // maturation of 5.8S rRNA // not recorded//0006364 // rRNA processing // inf
NM_134010	//XM	0.036			-1.01	1.09	1.12	1.08	<b>Nup107</b>	nucleoporin 107	0000973 // posttranscriptional tethering of RNA polymerase II gene DNA at nuclear perip
NM_025578		0.01			-1.02	-1.02	1.12	1.00	<b>Mmps25</b>	mitochondrial ribosomal protein S25	0032543 // mitochondrial translation // inferred by curator
NM_0260		0.006			-1.03	1.24	1.12	1.00	<b>Cdt1</b>	chromatin licensing and DNA replication factor 1	0000076 // DNA replication checkpoint // inferred from direct assay//0000076 // DNA r
NM_1462		0.0278			1.10	-1.12	1.12	1.04	<b>Msantd2</b>	Myb/SANT-like DNA-binding domain containing 2	
NM_021511		0.025			-1.10	1.02	1.12	1.08	<b>Rrs1</b>	RRS1 ribosome biogenesis regulator homolog (S. cerevisiae)	0000055 // ribosomal large subunit export from nucleus // ---//0000447 // endonucleo

RefSeq	Tri	p 24h	p 48h	p 72h	FD Air	FD 24h	FD 48h	FD 72h	Gene Symbol	Gene Title	Gene Ontology Biological Process
NM_0083		0.0224			1.05	-1.07	1.12	1.12	<i>Sdc2</i>	syndecan 2	0007399 // nervous system development // inferred from electronic annotation//00164
NM_0261		0.0218	0.003	0.013	-1.11	1.02	1.12	1.05	<i>Ergic1</i>	endoplasmic reticulum-golgi intermediate compartment (ERGIC) 1	0006810 // transport // inferred from electronic annotation//0006888 // ER to Golgi ves
NM_001164406	///	0.014			-1.02	1.06	1.12	1.00	<i>Apbb3//Sra1</i>	amyloid beta (A4) precursor protein-binding, family B, member 3//steroid receptor RI	0006351 // transcription, DNA-templated // inferred from electronic annotation//00063
NM_0265		0.0462			1.04	1.33	1.12	-1.05	<i>Psmc8</i>	proteasome (prosome, macropain) 26S subunit, non-ATPase, 8	0006508 // proteolysis // inferred from electronic annotation//0031647 // regulation of
NM_007512	///XM	0.05			-1.09	1.01	1.12	1.09	<i>Atpf1</i>	ATPase inhibitory factor 1	0001937 // negative regulation of endothelial cell proliferation // not recorded//000678
NM_0223	#####				1.02	-1.56	1.12	-1.09	<i>Herpud1</i>	homocysteine-inducible, endoplasmic reticulum stress-inducible, ubiquitin-like domain	0006511 // ubiquitin-dependent protein catabolic process // inferred from direct assay//
NM_0254		0.0205	0.006		-1.08	1.12	1.12	-1.09	<i>Sec11c</i>	SEC11 homolog C, signal peptidase complex subunit	0006465 // signal peptide processing // inferred from electronic annotation//0006508 //
NM_001142357	///	#####			-1.01	-1.01	1.12	1.04	<i>Alg12</i>	asparagine-linked glycosylation 12 (alpha-1,6-mannosyltransferase)	0006486 // protein glycosylation // inferred from electronic annotation//0006487 // prc
NM_0103		0.0029	0.004		-1.07	1.15	1.12	1.13	<i>Got2</i>	glutamate-oxaloacetate transaminase 2, mitochondrial	0006103 // 2-oxoglutarate metabolic process // inferred from sequence or structural sim
NM_0256		0.024	0.037		-1.02	-1.10	1.12	1.05	<i>Agg1</i>	angiogenic factor with G patch and FHA domains 1	0001525 // angiogenesis // inferred from electronic annotation//0001938 // positive reg
NM_0118		0.0086			1.04	1.27	1.12	1.16	<i>Esy1</i>	extended synaptotagmin-like protein 1	0006810 // transport // inferred from electronic annotation//0006869 // lipid transport
NM_001164107	///NM_00		0.048		-1.07	1.16	1.12	1.11	<i>Ripk3</i>	receptor-interacting serine-threonine kinase 3	0001914 // regulation of T cell mediated cytotoxicity // inferred from genetic interaction/
NM_008597			0.011		-1.09	-1.10	1.12	1.06	<i>Mgp</i>	matrix Gla protein	0001503 // ossification // inferred from electronic annotation//0006461 // protein com
NM_0281		0.0066	0.004		1.01	1.15	1.12	1.17	<i>Scaf11</i>	SR-related CTD-associated factor 11	0000245 // spliceosomal complex assembly // not recorded//0000375 // RNA splicing, v
NM_008490	#####				-1.03	1.01	1.12	-1.03	<i>Lcat</i>	lecithin cholesterol acyltransferase	0006629 // lipid metabolic process // inferred from electronic annotation//0006644 // p
NM_0173		0.0193	0.005		-1.06	1.04	1.12	-1.04	<i>Ppp2cb</i>	protein phosphatase 2 (formerly 2A), catalytic subunit, beta isoform	0006470 // protein dephosphorylation // not recorded//0008637 // apoptotic mitochon
NM_009255	///XM	0.006			-1.16	-1.26	1.12	1.02	<i>Serpine2</i>	serine (or cysteine) peptidase inhibitor, clade E, member 2	0007275 // multicellular organismal development // inferred from electronic annotation//
NM_0076		0.0113			-1.02	1.23	1.12	-1.07	<i>Cd38</i>	CD38 antigen	0001666 // response to hypoxia // not recorded//0007204 // positive regulation of cyto
NM_031248		0.039			-1.02	1.06	1.12	1.09	<i>Lamtor2</i>	late endosomal/lysosomal adaptor, MAPK and MTOR activator 2	0000186 // activation of MAPKK activity // inferred from direct assay//0016049 // cell gr
NM_145531	///NM	0.03			1.01	1.04	1.12	1.15	<i>Spp11</i>	spastic paraplegia 11	0007409 // axonogenesis // not recorded//0008088 // axon cargo transport // inferred f
NM_0101		0.0053			-1.00	1.78	1.12	-1.03	<i>Egr2</i>	early growth response 2	0006351 // transcription, DNA-templated // inferred from electronic annotation//00063
NM_0011		0.0476	0.015		-1.01	1.09	1.12	-1.00	<i>Slc25a13</i>	solute carrier family 25 (mitochondrial carrier, adenine nucleotide translocator), mem	0006754 // ATP biosynthetic process // not recorded//0006810 // transport // inferred f
NM_001177629	///	0.012			-1.11	-1.17	1.12	1.08	<i>Grb10</i>	growth factor receptor bound protein 10	0007165 // signal transduction // traceable author statement//0008286 // insulin recep
NM_0266		0.0014			1.18	-1.14	1.12	-1.17	<i>Zmyx1</i>	zinc finger, MYM domain containing 1	
NM_024188		0.012			-1.13	-1.09	1.12	-1.03	<i>Oxct1</i>	3-oxoacid CoA transferase 1	0007420 // brain development // inferred from electronic annotation//0007507 // heart
NM_0283		0.0159	0.011		-1.06	1.13	1.12	1.00	<i>Dis3</i>	DIS3 mitotic control homolog (S. cerevisiae)	0006364 // rRNA processing // not recorded//0006402 // mRNA catabolic process // no
NM_001301269		0.02	0.015		-1.11	-1.05	1.12	1.15	<i>Inafm2</i>	InaF motif containing 2	
NM_0011		0.0323			1.03	1.12	1.12	1.11	<i>Nol11</i>	nucleolar protein 11	0006351 // transcription, DNA-templated // inferred from electronic annotation//00063
NM_0012		0.0033			1.13	1.01	1.12	1.27	<i>Slc7a7</i>	solute carrier family 7 (cationic amino acid transporter, y+ system), member 7	0000821 // regulation of arginine metabolic process // inferred from mutant phenotype/
NM_0013		0.0404			-1.11	1.20	1.12	1.15	<i>Il2rg</i>	interleukin 2 receptor, gamma chain	0010468 // regulation of gene expression // inferred from mutant phenotype//0010628
NM_001039084	///	0.021			1.02	1.02	1.12	1.01	<i>Mrp1</i>	mitochondrial ribosomal protein L1	0006412 // translation // not recorded
NM_0200		0.043			1.06	1.26	1.12	-1.19	<i>Taf10</i>	TAF10 RNA polymerase II, TATA box binding protein (TBP)-associated factor	0000082 // G1/S transition of mitotic cell cycle // inferred from mutant phenotype//000
NM_0074		0.005			-1.10	1.19	1.12	1.21	<i>Slc25a5</i>	solute carrier family 25 (mitochondrial carrier, adenine nucleotide translocator), mem	0006810 // transport // inferred from electronic annotation//0007059 // chromosome s
NM_0086		0.003	0.004		-1.15	1.09	1.12	-1.14	<i>Mthfd2</i>	methylentetrahydrofolate dehydrogenase (NAD+ dependent), methylentetrahydrofolo	0006730 // one-carbon metabolic process // not recorded//0008152 // metabolic proce
NM_0280		0.0293			-1.03	-1.10	1.12	-1.08	<i>Cnn3</i>	calponin 3, acidic	0030855 // epithelial cell differentiation // inferred from electronic annotation//003103
NM_009836		0.006	0.039		-1.11	-1.12	1.12	1.06	<i>Cct3</i>	chaperonin containing Tcp1, subunit 3 (gamma)	0006457 // protein folding // inferred from electronic annotation//0007339 // binding c
NM_001033201		0.027			-1.01	1.03	1.12	1.05	<i>Ncbp1</i>	nuclear cap binding protein subunit 1	0000184 // nuclear-transcribed mRNA catabolic process, nonsense-mediated decay // no
NM_010617	///XM	0.027			-1.04	-1.08	1.13	1.10	<i>Kif13a</i>	kinesin family member 13A	0000910 // cytokinesis // not recorded//0006810 // transport // inferred from electroni
NM_026555	///XM	0.025			-1.10	-1.03	1.13	-1.24	<i>Rcn3</i>	reticulocalbin 3, EF-hand calcium binding domain	
NM_1454		0.0323	0.008		1.03	1.12	1.13	1.04	<i>Ube4a</i>	ubiquitination factor E4A	0000209 // protein polyubiquitination // inferred from direct assay//0006511 // ubiquiti
NM_175451		0.023			-1.12	-1.01	1.13	1.15	<i>Ckap4</i>	cytoskeleton-associated protein 4	
NM_0011		0.0461			1.09	1.34	1.13	1.13	<i>Mef2c</i>	myocyte enhancer factor 2C	0000122 // negative regulation of transcription from RNA polymerase II promoter // infer
NM_019698	///NM	0.005	0.05		-1.15	1.01	1.13	1.07	<i>Aldh18a1</i>	aldehyde dehydrogenase 18 family, member A1	0006536 // glutamate metabolic process // not recorded//0006561 // proline biosynthe
NM_0228		0.0216			1.11	-1.01	1.13	1.09	<i>Svep1</i>	sushi, von Willebrand factor type A, EGF and pentraxin domain containing 1	0007155 // cell adhesion // inferred from electronic annotation
NM_0010		0.0281			1.03	-1.11	1.13	1.14	<i>Cbx5</i>	chromobox 5	0045892 // negative regulation of transcription, DNA-templated // inferred from direct a
NM_173180	///XM	0.025			-1.00	-1.00	1.13	1.04	<i>Pmpca</i>	peptidase (mitochondrial processing) alpha	0006508 // proteolysis // not recorded//0006627 // protein processing involved in prote
NM_145552	///XM	0.03			-1.06	-1.01	1.13	1.03	<i>Gnl2</i>	guanine nucleotide binding protein-like 2 (nucleolar)	0042254 // ribosome biogenesis // not recorded
NM_0011		0.0313			1.06	-1.18	1.13	1.05	<i>Gppb1</i>	GC-rich promoter binding protein 1	0006351 // transcription, DNA-templated // inferred from electronic annotation//00063
NM_0531		0.0137	#####		-1.03	1.13	1.13	-1.01	<i>Mrp13</i>	mitochondrial ribosomal protein L3	0006412 // translation // not recorded
NM_0011		0.0079			1.04	1.23	1.13	1.16	<i>Pcx</i>	pyruvate carboxylase	0006090 // pyruvate metabolic process // not recorded//0006094 // gluconeogenesis //
NM_0112		0.0173			-1.07	1.23	1.13	-1.14	<i>Ranbp1</i>	RAN binding protein 1	0007051 // spindle organization // inferred from direct assay//0010976 // positive regul
NM_0254		0.0165			1.05	1.27	1.13	1.29	<i>Alg5</i>	asparagine-linked glycosylation 5 (dolichyl-phosphate beta-glucosyltransferase)	0006486 // protein glycosylation // inferred from electronic annotation//0006487 // prc
NM_146067	///XM_00652	0.045			-1.04	1.08	1.13	1.09	<i>Cpped1</i>	calcineurin-like phosphoesterase domain containing 1	0006470 // protein dephosphorylation // inferred from electronic annotation//0008152
NM_0105		0.0312	0.022		1.20	1.11	1.13	1.12	<i>Jup</i>	junction plakoglobin	0002159 // desmosome assembly // inferred from mutant phenotype//0002159 // desm
NM_001301364	///	0.029	0.049		-1.05	1.04	1.13	1.20	<i>Hdlbp</i>	high density lipoprotein (HDL) binding protein	0006629 // lipid metabolic process // inferred from electronic annotation//0006810 // t
NM_198103		0.042			1.03	-1.04	1.13	1.15	<i>Exoc8</i>	exocyst complex component 8	0001927 // exocyst assembly // not recorded//0006810 // transport // inferred from el
NM_0011		0.0091			1.14	-1.01	1.13	1.23	<i>Rnf145</i>	ring finger protein 145	0000209 // protein polyubiquitination // ---//0042787 // protein ubiquitination involv
NM_031843	///XR_	0.037			-1.06	-1.03	1.13	1.07	<i>Dpp7</i>	dipeptidylpeptidase 7	0006508 // proteolysis // not recorded
NM_026438		0.029			-1.15	1.03	1.13	-1.11	<i>Ppa1</i>	pyrophosphatase (inorganic) 1	0006796 // phosphate-containing compound metabolic process // inferred by curator
NM_0095		0.0176			-1.06	1.19	1.13	1.00	<i>Vcp</i>	valosin containing protein	0006281 // DNA repair // inferred from electronic annotation//0006302 // double-stran
NM_0010		0.0079	0.02	0.001	-1.12	1.05	1.13	1.22	<i>Klhl42</i>	kelch-like 42	0000209 // protein polyubiquitination // not recorded//0007049 // cell cycle // inferred
NM_023232		0.019			-1.03	1.06	1.13	1.13	<i>Diablo</i>	diablo homolog (Drosophila)	0006915 // apoptotic process // inferred from electronic annotation//0006919 // activa
NM_0265		0.0465			1.07	1.00	1.13	1.22	<i>Mrp124</i>	mitochondrial ribosomal protein L24	0006412 // translation // inferred from electronic annotation
NM_0010		0.001	0.022		-1.15	1.23	1.13	-1.02	<i>Rnf149</i>	ring finger protein 149	0016567 // protein ubiquitination // inferred from electronic annotation//0031647 // re



RefSeq	Tri	p 24h	p 48h	p 72h	FD Air	FD 24h	FD 48h	FD 72h	Gene Symbol	Gene Title	Gene Ontology Biological Process
NM_145972	//XM	0.006			-1.02	-1.07	1.13	1.04	<b>Nepr</b>	nucleolus and neural progenitor protein	0045665 // negative regulation of neuron differentiation // inferred from direct assay//K
NM_0083	0.0089				-1.04	1.15	1.13	1.12	<b>ldh3g</b>	isocitrate dehydrogenase 3 (NAD+), gamma	0006099 // tricarboxylic acid cycle // not recorded//0006102 // isocitrate metabolic pro
NM_008661	//NM	0.04			-1.06	-1.06	1.13	1.14	<b>Myo5b</b>	myosin VB	0006810 // transport // inferred from electronic annotation//0008152 // metabolic pro
NM_0011	0.0397	0.009			-1.58	-1.08	1.13	-1.14	<b>Pde4b</b>	phosphodiesterase 4B, cAMP specific	0001780 // neutrophil homeostasis // inferred from mutant phenotype//0006198 // cAI
NM_0134	0.0045				-1.01	1.72	1.13	1.11	<b>Cd2</b>	CD2 antigen	0007155 // cell adhesion // inferred from electronic annotation//0016337 // single orga
NM_0109	0.0179				1.07	-1.17	1.13	1.15	<b>Nfe2l2</b>	nuclear factor, erythroid derived 2, like 2	0006351 // transcription, DNA-templated // inferred from electronic annotation//00063
NM_001077411	//	0.035			-1.04	1.01	1.13	1.13	<b>Gba</b>	glucosidase, beta, acid	0005975 // carbohydrate metabolic process // inferred from electronic annotation//000
NM_0012	0.0157				-1.04	1.26	1.13	1.42	<b>Gapdh</b> // <b>Gapdh-ps15</b> // <b>Gm10313</b> // <b>Gm12</b>	glyceraldehyde-3-phosphate dehydrogenase//glyceraldehyde-3-phosphate dehydrog	0000226 // microtubule cytoskeleton organization // not recorded//0005975 // carbohy
NM_025860	//XM	0.012			-1.00	1.04	1.14	1.13	<b>Ddx18</b>	DEAD (Asp-Glu-Ala-Asp) box polypeptide 18	0010501 // RNA secondary structure unwinding // not recorded
NM_0260	0.0274	0.023			-1.09	1.12	1.14	1.17	<b>Eef1g</b>	eukaryotic translation elongation factor 1 gamma	0006412 // translation // inferred from electronic annotation//0006414 // translational
NM_0012	0.0471				-1.01	1.15	1.14	1.02	<b>Prnp</b>	prion protein	0001933 // negative regulation of protein phosphorylation // inferred from mutant phen
NM_0270	0.0213				-1.16	1.07	1.14	1.12	<b>Rfc3</b>	replication factor C (activator 1) 3	0006260 // DNA replication // not recorded//0006261 // DNA-dependent DNA replicat
NM_019491	0.022				-1.03	1.05	1.14	-1.06	<b>Rala</b>	v-ral simian leukemia viral oncogene homolog A (ras related)	0000910 // cytokinesis // not recorded//0001843 // neural tube closure // inferred from
NM_0011	0.0235				1.01	-1.03	1.14	-1.06	<b>Ino80</b> // <b>Rpl35a</b> // <b>Rpl35a-ps2</b> // <b>Rpl35a-ps</b>	INO80 homolog //ribosomal protein L35A//ribosomal protein L35A, pseudogene 2//	0000070 // mitotic sister chromatid segregation // not recorded//0000724 // double-str
NM_0076	0.0013	0.011			-1.04	1.08	1.14	1.15	<b>Casp7</b>	caspace 7	0006508 // proteolysis // not recorded//0006508 // proteolysis // inferred from reviewe
NM_0254	0.0241	0.036			-1.10	1.12	1.14	-1.05	<b>Mrps22</b>	mitochondrial ribosomal protein S22	
NM_0104	0.0337				-1.01	1.17	1.14	1.07	<b>Hexb</b>	hexosaminidase B	0001501 // skeletal system development // inferred from genetic interaction//0005975 ,
NM_0167	0.0187				1.09	1.25	1.14	1.07	<b>Smad3</b>	SMAD family member 3	0001122 // negative regulation of transcription from RNA polymerase II promoter // infer
NM_0010	0.0209				-1.03	1.15	1.14	1.04	<b>Eif4e2</b>	eukaryotic translation initiation factor 4E member 2	0001701 // in utero embryonic development // inferred from mutant phenotype//0006
NM_0104	0.0074	0.015			-1.10	1.09	1.14	-1.02	<b>Icam1</b>	intercellular adhesion molecule 1	0001541 // ovarian follicle development // inferred from electronic annotation//000166
NM_019639	0.042				1.07	-1.02	1.14	1.01	<b>Ubc</b>	ubiquitin C	0007623 // circadian rhythm // traceable author statement//0010992 // ubiquitin home
NM_001010937	//	0.041			-1.09	-1.01	1.14	-1.28	<b>Gjb6</b>	gap junction protein, beta 6	0006915 // apoptotic process // inferred from electronic annotation//0007154 // cell co
NM_0012	0.0477				1.07	1.25	1.14	1.12	<b>Hgf</b>	hepatocyte growth factor	0000187 // activation of MAPK activity // inferred from direct assay//0000902 // cell mc
NM_025460	0.013	0.048			-1.14	1.01	1.14	1.14	<b>Tmem126a</b>	transmembrane protein 126A	0021554 // optic nerve development // not recorded
NM_021336	//XR_391365	0.001			-1.03	1.03	1.14	1.23	<b>Snrpa1</b>	small nuclear ribonucleoprotein polypeptide A'	0000398 // mRNA splicing, via spliceosome // ---//0006397 // mRNA processing // infer
NM_018884	//XM	0.002			-1.08	-1.12	1.14	1.09	<b>Pdzrn3</b>	PDZ domain containing RING finger 3	0007528 // neuromuscular junction development // inferred from mutant phenotype//K
NM_172490	//XM	0.006			-1.02	1.06	1.14	1.22	<b>Secseps</b>	Sep (O-phosphoserine) tRNA:Sec (selenocysteine) tRNA synthase	0001514 // selenocysteine incorporation // inferred from direct assay//0006412 // trans
NM_008079	//XM	0.021	0.04		1.03	1.02	1.14	1.14	<b>Galc</b>	galactosylceramidase	0005975 // carbohydrate metabolic process // inferred from electronic annotation//000
NM_010914	//XM	0.036			-1.03	1.03	1.14	1.22	<b>Nfyb</b>	nuclear transcription factor-Y beta	0006351 // transcription, DNA-templated // inferred from electronic annotation//00063
NM_0095	0.0293				1.19	-1.07	1.14	1.29	<b>Wee1</b>	WEE 1 homolog 1 (S. pombe)	0000226 // microtubule cytoskeleton organization // inferred from mutant phenotype//
NM_0112	0.0318				-1.02	1.13	1.14	1.16	<b>Rfc1</b>	replication factor C (activator 1) 1	0001122 // negative regulation of transcription from RNA polymerase II promoter // not i
NM_0011	0.0283	0.018			-1.02	1.16	1.14	-1.02	<b>Nek6</b>	NIMA (never in mitosis gene a)-related expressed kinase 6	0006468 // protein phosphorylation // not recorded//0006915 // apoptotic process // ir
NM_008971	//XM_006506	0.022			-1.04	1.01	1.14	1.22	<b>Gm4887</b> // <b>Twf1</b>	predicted gene 4887//twinfilin, actin-binding protein, homolog 1 (Drosophila)	0018108 // peptidyl-tyrosine phosphorylation // inferred from direct assay//0030837 //
NM_0011	0.0054				-1.07	1.22	1.14	-1.07	<b>Raly</b>	hnRNP-associated with lethal yellow	0006397 // mRNA processing // inferred from electronic annotation//0008380 // RNA sp
NM_001304574	//	0.017			1.02	1.11	1.14	1.20	<b>Arf2</b>	ADP-ribosylation factor 2	0006810 // transport // inferred from electronic annotation//0007264 // small GTPase r
NM_001291146	//	0.008			-1.08	-1.10	1.14	1.09	<b>Derl2</b>	Der1-like domain family, member 2	0001967 // suckling behavior // inferred from mutant phenotype//0006986 // response
NM_172393	//XM	0.036			-1.06	-1.03	1.14	1.11	<b>Aim1</b>	absent in melanoma 1	
NM_025331	0.008				-1.03	-1.04	1.14	-1.24	<b>Gng11</b>	guanine nucleotide binding protein (G protein), gamma 11	0007165 // signal transduction // inferred from electronic annotation//0007186 // G-pr
NM_0010	0.0281				1.12	-1.01	1.14	1.09	<b>Sdcbp</b>	syndecan binding protein	0007265 // Ras protein signal transduction // inferred from physical interaction//00072
NM_133895	//XM	0.02			-1.05	-1.04	1.14	1.08	<b>Slc15a4</b>	solute carrier family 15, member 4	0006810 // transport // inferred from electronic annotation//0006857 // oligopeptide tr
NM_172146	0.042				-1.01	-1.04	1.14	1.14	<b>Ppat</b>	phosphoribosyl pyrophosphate amidotransferase	0000082 // G1/S transition of mitotic cell cycle // inferred from electronic annotation//0
NM_009191	//XM	0.023			-1.02	-1.02	1.14	-1.03	<b>Clpb</b>	ClpB caseinolytic peptidase B	0008152 // metabolic process // inferred from electronic annotation//0034605 // cellul
NM_0010	0.0209				1.02	1.24	1.15	1.17	<b>Casp8</b>	caspace 8	0001525 // angiogenesis // inferred from mutant phenotype//0001841 // neural tube fc
NM_001008238	//	0.042			-1.10	1.07	1.15	-1.04	<b>Brip2</b>	BCL2/adenovirus E1B interacting protein 2	0001824 // blastocyst development // inferred from mutant phenotype//0006915 // ap
NM_0010	0.0024				-1.04	1.26	1.15	-1.03	<b>Nme2</b>	NME/NM23 nucleoside diphosphate kinase 2	0002742 // negative regulation of myeloid leukocyte differentiation // not recorded//00
NM_026850	0.041				-1.04	-1.02	1.15	1.04	<b>Pdcl3</b>	phosducin-like 3	0001525 // angiogenesis // inferred from electronic annotation//0001938 // positive reg
NM_0295	0.0328				1.05	-1.02	1.15	1.16	<b>Tax1bp3</b>	Tax1 (human T cell leukemia virus type I) binding protein 3	0007266 // Rho protein signal transduction // not recorded//0008285 // negative regula
NM_198831	//NR_	0.015			1.04	1.12	1.15	-1.03	<b>Mrp148</b> // <b>LOC102643207</b> // <b>Mrp148-ps</b>	mitochondrial ribosomal protein L48//uncharacterized LOC102643207//mitochondrial ribosomal protein L48 pseudogene	
NM_0011	0.011				1.10	1.37	1.15	1.23	<b>Trp53</b>	transformation related protein 53	0000060 // protein import into nucleus, translocation // inferred from direct assay//000
NM_0076	0.0033	0.043			-1.04	-1.10	1.15	1.15	<b>Scarb2</b>	scavenger receptor class B, member 2	0006622 // protein targeting to lysosome // inferred from mutant phenotype//0006622
NM_001033257	//	0.048			1.01	-1.18	1.15	-1.04	<b>Phactr2</b>	phosphatase and actin regulator 2	0043086 // negative regulation of catalytic activity // inferred from electronic annotation
NM_007735	//XM	0.019			1.02	1.09	1.15	1.01	<b>Col4a4</b>	collagen, type IV, alpha 4	0032836 // glomerular basement membrane development // inferred from mutant phen
NM_001285852	//NM_00	0.041			1.02	1.06	1.15	1.16	<b>Gsip1</b>	SH3-domain GRB2-like (endophilin) interacting protein 1	0002021 // response to dietary excess // inferred from sequence or structural similarity//
NM_025319	//XM	0.023	0.009		-1.21	-1.03	1.15	1.08	<b>O61009B22Rik</b>	RIKEN cDNA O61009B22 gene	0006351 // transcription, DNA-templated // inferred from electronic annotation//00063
NM_134101	//NR_	0.014			-1.04	1.10	1.15	1.20	<b>Psm2</b>	proteasome (prosome, macropain) 26S subunit, non-ATPase, 2	0042176 // regulation of protein catabolic process // inferred from electronic annotation
NM_0010	0.0407				1.05	1.23	1.15	1.34	<b>Slc39a7</b>	solute carrier family 39 (zinc transporter), member 7	0006810 // transport // inferred from electronic annotation//0006811 // ion transport /
NM_019673	//XM	0.029			-1.04	-1.08	1.15	1.06	<b>Actl6a</b>	actin-like 6A	0003407 // neural retina development // inferred from electronic annotation//0006281
NM_019656	0.006				-1.00	-1.05	1.15	1.02	<b>Tspan6</b>	tetraspanin 6	0007165 // signal transduction // ---//0007165 // signal transduction // inferred from el
NM_144835	0.007				-1.05	1.12	1.15	-1.04	<b>Heatr1</b>	HEAT repeat containing 1	0000462 // maturation of SSU-rRNA from tricistronic rRNA transcript (SSU-rRNA, 5.8S rR
NM_001291134	//NM_00	0.009			1.04	1.12	1.15	1.23	<b>Rprd1b</b>	regulation of nuclear pre-mRNA domain containing 1B	0006351 // transcription, DNA-templated // inferred from electronic annotation//00063
NM_0259	0.0015				-1.07	1.22	1.15	1.04	<b>Rpl11</b>	ribosomal protein L11	0000027 // ribosomal large subunit assembly // ---//0006364 // rRNA processing // not i
NM_1453	0.0189	0.035			-1.05	1.18	1.15	1.00	<b>Nsun2</b>	NOL1/NOP2/Sun domain family member 2	0007049 // cell cycle // inferred from electronic annotation//0007067 // mitotic nuclear
NM_0076	0.0226	0.021			-1.18	1.03	1.15	1.08	<b>Cct5</b>	chaperonin containing Tcp1, subunit 5 (epsilon)	0006457 // protein folding // inferred from electronic annotation//0007339 // binding c
NM_025387	//XM	0.006			-1.07	1.07	1.15	1.20	<b>Gm4246</b> // <b>Tmem14c</b>	predicted gene 4246//transmembrane protein 14C	0006783 // heme biosynthetic process // inferred from electronic annotation//0006839

RefSeq	Tri	p 24h	p 48h	p 72h	FD Air	FD 24h	FD 48h	FD 72h	Gene Symbol	Gene Title	Gene Ontology Biological Process
NM_0011		0.002			-1.00	1.25	1.15	1.18	<i>Rnh1</i>	ribonuclease/angiogenin inhibitor 1	0043086 // negative regulation of catalytic activity // not recorded//0045765 // regulati
NM_0011		0.0097	0.018		-1.12	1.18	1.15	1.18	<i>Kars</i>	lysyl-tRNA synthetase	0006412 // translation // inferred from electronic annotation//0006418 // tRNA aminoa
NM_0808		0.0368			-1.03	1.16	1.15	-1.02	<i>Mydgf</i>	myeloid derived growth factor	0001525 // angiogenesis // inferred from electronic annotation//0001934 // positive reg
NM_001313906	///NM_00	0.029			-1.11	1.02	1.15	1.36	<i>Prmt5</i>	protein arginine N-methyltransferase 5	0000122 // negative regulation of transcription from RNA polymerase II promoter // infer
NM_0089		0.0264	0.009		-1.08	-1.01	1.15	1.06	<i>Prmt1</i>	DNA primase, p49 subunit	0006260 // DNA replication // inferred from electronic annotation//0006269 // DNA rep
NM_0258		0.0341			-1.04	1.08	1.15	1.11	<i>Tax1bp1</i>	Tax1 (human T cell leukemia virus type I) binding protein 1	0006915 // apoptotic process // inferred from electronic annotation//0032088 // negati
NM_021457		0.002			-1.01	1.05	1.16	1.16	<i>Fzd1</i>	frizzled homolog 1 (Drosophila)	0001934 // positive regulation of protein phosphorylation // inferred from mutant phen
NM_145630		0.031			-1.05	1.01	1.16	1.07	<i>Pdk3</i>	pyruvate dehydrogenase kinase, isoenzyme 3	0005975 // carbohydrate metabolic process // inferred from electronic annotation//000
NM_0258	#####				-1.18	-2.54	1.16	-1.08	<i>Chordc1</i>	cysteine and histidine-rich domain (CHORD)-containing, zinc-binding protein 1	0010824 // regulation of centrosome duplication // inferred from mutant phenotype//00
NM_026234			0.038		1.16	1.02	1.16	-1.06	<i>Pigm</i>	phosphatidylinositol glycan anchor biosynthesis, class M	0006506 // GPI anchor biosynthetic process // not recorded//0097502 // mannosylate
NM_0110		0.0083			-1.02	-1.57	1.16	-1.17	<i>Pigo</i>	phosphatidylinositol glycan anchor biosynthesis, class A	0006506 // GPI anchor biosynthetic process // inferred from mutant phenotype//00090
NM_025820		0.01			1.02	1.12	1.16	1.08	<i>Crnk1</i>	Crn, crooked neck-like 1 (Drosophila)	0000245 // spliceosomal complex assembly // not recorded//0000398 // mRNA splicing,
NM_001136086	///	0.024			-1.08	-1.07	1.16	1.10	<i>Dpysl3</i>	dihydropyrimidinase-like 3	0007399 // nervous system development // inferred from direct assay//0008152 // met:
NM_0254		0.0086			-1.08	1.04	1.16	1.13	<i>Mrps14</i>	mitochondrial ribosomal protein S14	0006412 // translation // not recorded
NM_001277309	///	0.036			-1.06	-1.00	1.16	1.08	<i>Mea1</i>	male enhanced antigen 1	0007275 // multicellular organismal development // inferred from electronic annotation/
NM_172410	///XXM	0.031			1.02	1.13	1.16	1.20	<i>Nup93</i>	nucleoporin 93	0002230 // positive regulation of defense response to virus by host // not recorded//000
NM_0107		0.0281			-1.01	1.10	1.16	1.03	<i>Lmnb1</i>	lamin B1	0031662 // positive regulation of cyclin-dependent protein serine/threonine kinase activ
NM_0010		0.0055			1.01	1.19	1.16	1.22	<i>Capz2</i>	capping protein (actin filament) muscle Z-line, beta	0000902 // cell morphogenesis // not recorded//0007010 // cytoskeleton organization /
NM_026141	///XXM	0.024	0.016		-1.11	1.02	1.16	1.20	<i>Ppil4</i>	peptidylprolyl isomerase (cyclophilin)-like 4	0000413 // protein peptidyl-prolyl isomerization // not recorded//0006457 // protein fo
NM_0260		0.0262	0.027		-1.10	1.06	1.16	-1.06	<i>Cmtm6</i>	CKLF-like MARVEL transmembrane domain containing 6	0006935 // chemotaxis // inferred from electronic annotation
NM_183106	///XXM	0.014			-1.02	1.06	1.16	1.07	<i>Ttc17</i>	tetratricopeptide repeat domain 17	0030030 // cell projection organization // inferred from electronic annotation//0030041
NM_001164677	///	0.004			1.04	1.02	1.16	1.04	<i>Pdcd6ip</i>	programmed cell death 6 interacting protein	0000920 // cell separation after cytokinesis // not recorded//0006810 // transport // inf
NM_0081		0.0163			1.04	-1.11	1.16	1.48	<i>Gstm2</i>	glutathione S-transferase, mu 2	0006749 // glutathione metabolic process // not recorded//0008152 // metabolic proce
NM_0012		0.0023	0.041		1.01	1.21	1.16	1.08	<i>Gabpb1</i>	GA repeat binding protein, beta 1	0006351 // transcription, DNA-templated // inferred from electronic annotation//00063
NM_001277266	///	0.05			-1.05	1.09	1.16	1.15	<i>Adam17</i>	a disintegrin and metalloproteinase domain 17	0001666 // response to hypoxia // not recorded//0001934 // positive regulation of prot
NM_008948		0.003			-1.09	1.05	1.16	1.17	<i>Psmc3</i>	proteasome (prosome, macropain) 26S subunit, ATPase 3	0001824 // blastocyst development // inferred from mutant phenotype//0030163 // prc
NM_0119	#####				-1.01	1.32	1.16	1.04	<i>Tlr2</i>	toll-like receptor 2	0001774 // microglial cell activation // not recorded//0002224 // toll-like receptor signa
NM_0013		0.0082	0.045		-1.05	1.14	1.16	1.06	<i>Rps27l</i>	ribosomal protein S27-like	0000028 // ribosomal small subunit assembly // ---//0006281 // DNA repair // not recor
NM_001038612	///	0.003			-1.02	1.03	1.16	1.05	<i>Olfm1</i>	olfactomedin 1	0003190 // atrioventricular valve formation // inferred from sequence or structural simil
NM_0206		0.013	0.037		-1.08	1.06	1.16	1.18	<i>Smarca1</i>	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamih	0006337 // nucleosome disassembly // not recorded//0006338 // chromatin remodeling
NM_025828		0.012			-1.08	-1.02	1.16	1.09	<i>Lman2</i>	lectin, mannose-binding 2	0006810 // transport // inferred from electronic annotation//0006890 // retrograde ves
NM_025679		0.034			1.04	1.04	1.16	1.04	<i>Sike1</i>	suppressor of IKBKE 1	
NM_013492	///XXM	0.005	0.003		-1.10	1.02	1.17	1.33	<i>Clu</i>	clusterin	0000902 // cell morphogenesis // not recorded//0001774 // microglial cell activation //
NM_008303		0.031			-1.47	-1.56	1.17	-1.23	<i>Hspe1</i>	heat shock protein 1 (chaperonin 10)	0001649 // osteoblast differentiation // not recorded//0006457 // protein folding // inf
NM_0206		0.0028			1.03	1.28	1.17	1.07	<i>Taf1b</i>	TATA box binding protein (Tbp)-associated factor, RNA polymerase I, B	0001189 // RNA polymerase I transcriptional preinitiation complex assembly at the prom
NM_0081		0.043			1.26	1.47	1.17	1.23	<i>H1f0</i>	H1 histone family, member 0	0006334 // nucleosome assembly // inferred from electronic annotation
NM_0119		0.0091			1.13	1.46	1.17	1.00	<i>Nubp1</i>	nucleotide binding protein 1	0006879 // cellular iron ion homeostasis // not recorded//0010826 // negative regulati
NM_001316716	///	0.023			-1.02	-1.15	1.17	1.20	<i>Ddo</i>	D-aspartate oxidase	0006531 // aspartate metabolic process // inferred from mutant phenotype//0006533 //
NM_133653	///XXM_00651	0.037			1.03	1.11	1.17	1.31	<i>Mat1a</i>	methionine adenosyltransferase I, alpha	0006556 // S-adenosylmethionine biosynthetic process // not recorded//0006730 // ont
NM_008434	///XXM	0.026			-1.01	1.05	1.17	1.03	<i>Kcna1</i>	potassium voltage-gated channel, subfamily Q, member 1	0002230 // positive regulation of defense response to virus by host // not recorded//000
NM_0011		0.0266			1.07	1.37	1.17	1.21	<i>Lgals3</i>	lectin, galactose binding, soluble 3	0001501 // skeletal system development // inferred from genetic interaction//0002376 ,
NM_031256	///XXM	0.025			-1.01	1.00	1.17	-1.08	<i>Plekha3</i>	pleckstrin homology domain-containing, family A (phosphoinositide binding specific) member 3	
NM_001313906	///	0.003			-1.11	1.02	1.17	1.36	<i>Prmt5</i>	protein arginine N-methyltransferase 5	0000122 // negative regulation of transcription from RNA polymerase II promoter // infer
NM_0261		0.0298			-1.04	1.05	1.17	1.04	<i>Med4</i>	mediator complex subunit 4	0006351 // transcription, DNA-templated // inferred from electronic annotation//00063
NM_016752	///XXM	0.015			-1.21	1.04	1.17	1.13	<i>Slc35b1</i>	solute carrier family 35, member B1	0006810 // transport // inferred from electronic annotation//0008643 // carbohydrate t
NM_0218		0.0019			1.06	1.38	1.17	1.11	<i>Fads3</i>	fatty acid desaturase 3	0006629 // lipid metabolic process // inferred from electronic annotation//0006631 // f.
NM_0223	#####				-1.08	1.28	1.17	1.06	<i>Ctsz</i>	cathepsin Z	0006508 // proteolysis // inferred from electronic annotation//0051603 // proteolysis in
NM_1535	#####	0.011	0.013		-1.17	1.15	1.17	-1.10	<i>Pilra</i>	paired immunoglobulin-like type 2 receptor alpha	0007165 // signal transduction // not recorded//0007169 // transmembrane receptor pi
NM_008569	///XXM	0.035			1.05	1.07	1.17	1.11	<i>Anapc1</i>	anaphase promoting complex subunit 1	0007049 // cell cycle // inferred from electronic annotation//0007067 // mitotic nuclear
NM_011192	///XXM	0.025			1.04	1.14	1.17	1.12	<i>Psme3</i>	proteasome (prosome, macropain) activator subunit 3 (PA28 gamma, Ki)	0002479 // antigen processing and presentation of exogenous peptide antigen via MHC c
NM_0013		0.011			1.02	1.78	1.17	-1.01	<i>Il6</i>	interleukin 6	0001781 // neutrophil apoptotic process // inferred from direct assay//0001781 // neut
NM_0275		0.0108			1.06	1.30	1.17	1.05	<i>P2ry12</i>	purinergic receptor P2Y, G-protein coupled 12	0001973 // adenosine receptor signaling pathway // not recorded//0006930 // substrat
NM_0010		0.0316			1.11	1.76	1.17	-1.08	<i>Fam65b</i>	family with sequence similarity 65, member B	0007605 // sensory perception of sound // not recorded
NM_0103		0.0371			-1.01	1.16	1.17	1.03	<i>Emb</i>	embigin	0007155 // cell adhesion // not recorded//0035879 // plasma membrane lactate transp
NM_011937	///NR_028061	0.031			-1.06	1.11	1.17	1.15	<i>Gm8615</i> ///Gnpd1	glucosamine-6-phosphate deaminase 1 pseudogene//glucosamine-6-phosphate deam	0005975 // carbohydrate metabolic process // inferred from electronic annotation//000
NM_010887		0.034			1.01	1.01	1.17	1.04	<i>Ndufs4</i>	NADH dehydrogenase (ubiquinone) Fe-S protein 4	0001932 // regulation of protein phosphorylation // not recorded//0006810 // transpor
NM_0083		0.0382			-1.03	1.72	1.17	1.02	<i>Il1b</i>	interleukin 1 beta	0000122 // negative regulation of transcription from RNA polymerase II promoter // not r
NM_001039718	///	0.01			1.03	1.12	1.18	-1.01	<i>Cntf</i> ///Zfp91//Zfp91Cntf	ciliary neurotrophic factor//zinc finger protein 91//Zfp91-Cntf readthrough transcrip	0007250 // activation of NF-kappaB-inducing kinase activity // not recorded//0007259 /
NM_001291448	///	0.038			1.01	1.08	1.18	-1.00	<i>Foxred1</i>	FAD-dependent oxidoreductase domain containing 1	0006810 // transport // inferred from electronic annotation//0032981 // mitochondrial
NM_026423	///XXM_00653	0.013			1.18	1.20	1.18	-1.23	<i>Mri1</i>	methylthioribose-1-phosphate isomerase homolog (S. cerevisiae)	0008652 // cellular amino acid biosynthetic process // inferred from electronic annotatio
NM_0258		0.0205	0.004		-1.12	1.10	1.18	1.14	<i>Psm12</i>	proteasome (prosome, macropain) 26S subunit, non-ATPase, 12	0043161 // proteasome-mediated ubiquitin-dependent protein catabolic process // not r
NM_001252332	///	0.033			1.05	1.02	1.18	1.16	<i>8-Sep</i>	septin 8	
NM_027994		0.045			-1.07	1.02	1.18	1.26	<i>Cand1</i>	cullin associated and neddylation disassociated 1	0010265 // SCF complex assembly // not recorded//0016567 // protein ubiquitination //
NM_0119		0.0484			-1.03	1.17	1.18	-1.01	<i>Psm1</i>	proteasome (prosome, macropain) subunit, alpha type 1	0002376 // immune system process // inferred from electronic annotation//0002862 //

RefSeq	Tri	p 24h	p 48h	p 72h	FD Air	FD 24h	FD 48h	FD 72h	Gene Symbol	Gene Title	Gene Ontology Biological Process
NM_144902	///XM	0.012			-1.01	1.04	1.18	1.02	<i>Slc35a3</i>	solute carrier family 35 (UDP-N-acetylglucosamine (UDP-GlcNAc) transporter), membe	0006810 // transport // inferred from electronic annotation///0008643 // carbohydrate
NM_0012	0.032				1.11	-1.28	1.18	1.06	<i>Nnat</i>	neuronatin	0007275 // multicellular organismal development // inferred from electronic annotation/
NM_001253700	///	0.034	0.04		-1.03	1.06	1.18	1.25	<i>Elp5</i>	elongator acetyltransferase complex subunit 5	0006351 // transcription, DNA-templated // inferred from electronic annotation///00063
NM_0012	0.0193	0.023	0.025		-1.10	1.10	1.18	1.09	<i>Txndc5</i>	thioredoxin domain containing 5	0006457 // protein folding // not recorded///0008152 // metabolic process // inferred fr
NM_0012	0.0066				1.01	1.24	1.18	1.14	<i>Casp3</i>	caspase 3	0001666 // response to hypoxia // inferred from electronic annotation///0001782 // B ce
NM_026913	///XM	0.008			-1.06	1.06	1.18	1.11	<i>Mitd1</i>	MIT, microtubule interacting and transport, domain containing 1	0000281 // mitotic cytokinesis // not recorded///0000920 // cell separation after cyto
NM_133933	///	0.013			-1.17	-1.06	1.18	-1.12	<i>Rpn1</i>	ribophorin I	0006486 // protein glycosylation // inferred from electronic annotation///0018279 // prc
NM_1531	0.0429				1.23	1.63	1.18	1.04	<i>Gimap6</i>	GTPase, IMAP family member 6	
NM_183225	///XM	0.011			1.01	1.06	1.18	1.10	<i>Usp24</i>	ubiquitin specific peptidase 24	0006508 // proteolysis // inferred from electronic annotation///0006511 // ubiquitin-dep
NM_001008497	///NM_00	0.028			-1.04	1.05	1.18	1.16	<i>P2ry14</i>	purinergic receptor P2Y, G-protein coupled, 14	0006955 // immune response // not recorded///0007165 // signal transduction // inferre
NM_0012	0.0033				-1.04	1.45	1.18	1.12	<i>Cd84</i>	CD84 antigen	0007155 // cell adhesion // inferred from electronic annotation
NM_0169	0.0264				1.04	1.23	1.18	1.08	<i>Sec61a1</i>	Sec61 alpha 1 subunit (S. cerevisiae)	0006614 // SRP-dependent cotranslational protein targeting to membrane // not recorde
NM_0010	0.0278				1.00	1.10	1.18	1.15	<i>Pdxdc1</i>	pyridoxal-dependent decarboxylase domain containing 1	0019752 // carboxylic acid metabolic process // inferred from electronic annotation
NM_001290368	///	0.029			1.00	-1.03	1.18	1.12	<i>Nmt2</i>	N-myristoyltransferase 2	0006499 // N-terminal protein myristoylation // traceable author statement///0018008 //
NM_001164197	///	0.01			-1.08	-1.03	1.18	1.03	<i>Mmp19</i>	matrix metalloproteinase 19	0001525 // angiogenesis // inferred from electronic annotation///0001541 // ovarian foll
NM_1339	0.0389				-1.03	1.13	1.18	1.00	<i>Lsm8</i>	LSM8 homolog, U6 small nuclear RNA associated (S. cerevisiae)	0000398 // mRNA splicing, via spliceosome // not recorded///0006397 // mRNA processi
NM_0079	0.0412				-1.01	1.21	1.18	1.00	<i>Fbl</i> ///LOC102643269	fibrillarin///rRNA 2'-O-methyltransferase fibrillarin	0000494 // box C/D snoRNA 3'-end processing // not recorded///0001649 // osteoblast c
NM_0135	0.0155	0.04			-1.07	1.12	1.18	1.21	<i>Emg1</i>	EMG1 nucleolar protein homolog (S. cerevisiae)	0001824 // blastocyst development // inferred from mutant phenotype///0006364 // rRi
NM_0010	0.0051				1.04	1.53	1.18	1.20	<i>Gm10052</i> ///Gm5643///Gm5803///Hnrnpa	heterogeneous nuclear ribonucleoprotein A1 pseudogene///predicted gene 5803///he	0000380 // alternative mRNA splicing, via spliceosome // inferred from direct assay///00
NM_0260	0.0485	0.042			-1.01	1.13	1.18	1.15	<i>Med31</i>	mediator complex subunit 31	0006351 // transcription, DNA-templated // inferred from electronic annotation///00063
NM_001314041	///	0.002	0.049		-1.08	1.03	1.18	1.21	<i>Itga5</i>	integrin alpha 5 (fibronectin receptor alpha)	0007044 // cell-substrate junction assembly // inferred from direct assay///0007155 // ce
NM_013625	///NR	0.046			-1.02	1.08	1.18	1.11	<i>Pafah1b1</i>	platelet-activating factor acetylhydrolase, isoform 1b, subunit 1	0000132 // establishment of mitotic spindle orientation // not recorded///0000226 // pi
NM_0113	0.0093				-1.04	1.26	1.18	1.09	<i>Gm7285</i> ///Rps7	predicted gene 7285///ribosomal protein S7	0001843 // neural tube closure // inferred from mutant phenotype///0006364 // rRNA p
NM_0012	0.0423	0.007	0.002		-1.01	1.22	1.18	1.18	<i>Clip4</i>	CAP-GLY domain containing linker protein family, member 4	
NM_1722	0.0014	0.026			-1.05	1.18	1.18	1.07	<i>Eif2b5</i>	eukaryotic translation initiation factor 2B, subunit 5 epsilon	0001541 // ovarian follicle development // not recorded///0006412 // translation // infe
NM_001204165	///	0.043			1.00	-1.05	1.18	1.28	<i>Rapgef4</i>	Rap guanine nucleotide exchange factor (GEF) 4	0001932 // regulation of protein phosphorylation // inferred from electronic annotation/
NM_0098	#####				1.04	2.32	1.18	-1.02	<i>Ch25h</i>	cholesterol 25-hydroxylase	0006629 // lipid metabolic process // inferred from electronic annotation///0006633 // f.
NM_0011	0.0031				1.36	-1.13	1.18	1.61	<i>Pfkfb3</i>	6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase 3	0006000 // fructose metabolic process // inferred from electronic annotation///0006003
NM_0079	0.0332				1.00	1.16	1.19	1.09	<i>Aimp1</i>	aminoacyl tRNA synthetase complex-interacting multifunctional protein 1	0001525 // angiogenesis // inferred from electronic annotation///0001937 // negative re
NM_0011	0.0043				1.01	1.11	1.19	1.26	<i>Rnf14</i>	ring finger protein 14	0000209 // protein polyubiquitination // not recorded///0006351 // transcription, DNA-t
NM_0013	0.0088				-1.05	1.57	1.19	1.14	<i>Arhgdib</i>	Rho, GDP dissociation inhibitor (GDI) beta	0008152 // metabolic process // inferred from electronic annotation///0043547 // positi
NM_008775	///XM	0.019			-1.06	1.00	1.19	1.08	<i>Pafah1b2</i>	platelet-activating factor acetylhydrolase, isoform 1b, subunit 2	0006629 // lipid metabolic process // inferred from electronic annotation///0006928 // n
NM_018856	///NM_20767	0.039			1.23	1.10	1.19	1.11	<i>Ccnl2</i>	cyclin L2	0000079 // regulation of cyclin-dependent protein serine/threonine kinase activity // inf
NM_007743	0.039				-1.26	-1.12	1.19	1.01	<i>Col1a2</i>	collagen, type I, alpha 2	0001501 // skeletal system development // not recorded///0001568 // blood vessel deve
NM_011809		0.042			1.17	1.13	1.19	1.07	<i>Ets2</i>	E26 avian leukemia oncogene 2, 3' domain	0000122 // negative regulation of transcription from RNA polymerase II promoter // not i
NM_001159908	///	0.018			1.05	-1.05	1.19	1.09	<i>Zfand2a</i>	zinc finger, ANK1-type domain 2A	0032436 // positive regulation of proteasomal ubiquitin-dependent protein catabolic pr
NM_0084	0.0016				1.26	1.90	1.19	1.03	<i>Junb</i>	jun B proto-oncogene	0000122 // negative regulation of transcription from RNA polymerase II promoter // not i
NM_008065	///XM	0.018	0.018		-1.02	1.03	1.19	1.14	<i>Gabpa</i>	GA repeat binding protein, alpha	0000122 // negative regulation of transcription from RNA polymerase II promoter // infer
NM_0194	0.0402				1.03	1.23	1.19	1.19	<i>Myo10</i>	myosin X	0006810 // transport // inferred from electronic annotation///0007165 // signal transdu
NM_153774	///XM	0.005	0.039		-1.15	-1.03	1.19	1.14	<i>Ipo9</i>	importin 9	0006606 // protein import into nucleus // inferred from direct assay///0006610 // riboso
NM_0011	0.0011				-1.23	-2.44	1.19	-1.16	<i>Dnaja1</i>	Dnaj (Hsp40) homolog, subfamily A, member 1	0006457 // protein folding // inferred from electronic annotation///0007283 // spermatc
NM_0109	0.0257	0.041			-1.02	1.20	1.19	1.01	<i>Mrpl40</i>	mitochondrial ribosomal protein L40	
NM_0075	0.0311				-1.01	1.22	1.19	-1.04	<i>Atp1b3</i>	ATPase, Na <sup>+</sup> /K <sup>+</sup> transporting, beta 3 polypeptide	0006810 // transport // inferred from electronic annotation///0006811 // ion transport /
NM_0119	0.0135				1.03	1.18	1.19	1.10	<i>Cops3</i>	COP9 (constitutive photomorphogenic) homolog, subunit 3 (Arabidopsis thaliana)	0001701 // in utero embryonic development // inferred from mutant phenotype///0006:
NM_1455	0.0196				-1.04	1.20	1.19	1.08	<i>Dars</i>	aspartyl-tRNA synthetase	0006412 // translation // inferred from electronic annotation///0006418 // tRNA aminoa
NM_0012	#####	0.041	0.002		-1.19	1.13	1.19	1.09	<i>Asnsd1</i>	asparagine synthetase domain containing 1	0006529 // asparagine biosynthetic process // not recorded///0006541 // glutamine det
NM_0012	0.0022				1.00	1.24	1.19	-1.05	<i>Psmg1</i>	proteasome (prosome, macropain) subunit, alpha type 7	0006508 // proteolysis // inferred from electronic annotation///0006511 // ubiquitin-det
NM_172924	///XM	0.02			1.06	1.09	1.19	-1.05	<i>Peak1</i>	pseudopodium-enriched atypical kinase 1	0006468 // protein phosphorylation // not recorded///0016310 // phosphorylation // inf
NM_0010	0.05				1.04	1.31	1.19	1.09	<i>Adar</i>	adenosine deaminase, RNA-specific	0001649 // osteoblast differentiation // inferred from mutant phenotype///0001701 // ir
NM_009763	///XM	0.009	0.003		-1.22	1.02	1.19	1.08	<i>Bst1</i>	bone marrow stromal cell antigen 1	0008152 // metabolic process // not recorded///0030890 // positive regulation of B ce
NM_001080932	///	0.004			-1.05	-1.09	1.19	1.11	<i>Foxk2</i>	forkhead box K2	0006351 // transcription, DNA-templated // inferred from electronic annotation///00063
NM_0010	#####	0.004			-1.06	1.11	1.19	1.34	<i>Banf1</i>	barrier to autointegration factor 1	0015074 // DNA integration // inferred from direct assay///0075713 // establishment of i
NM_145512	0.02				1.02	1.06	1.19	1.04	<i>Sft2d2</i>	SFT2 domain containing 2	0006810 // transport // inferred from electronic annotation///0015031 // protein transp
NM_007898	0.017				1.04	1.07	1.19	1.09	<i>Ebp</i>	phenylalkylamine Ca2+ antagonist (emopamil) binding protein	0006629 // lipid metabolic process // inferred from electronic annotation///0006694 // s
NM_0013	0.0189				-1.20	1.29	1.19	1.05	<i>Alox5ap</i>	arachidonate 5-lipoxygenase activating protein	0002540 // leukotriene production involved in inflammatory response // inferred from m
NM_019833	///XM	0.031			1.04	1.05	1.20	1.13	<i>Fam69b</i>	family with sequence similarity 69, member B	
NM_026667	0.044				-1.04	-1.01	1.20	1.06	<i>Fam114a1</i>	family with sequence similarity 114, member A1	
NM_0012	0.0036				1.04	1.19	1.20	1.19	<i>Dnajc5</i>	Dnaj (Hsp40) homolog, subfamily C, member 5	0043524 // negative regulation of neuron apoptotic process // inferred from genetic inte
NM_0205	0.0433				-1.13	1.05	1.20	1.02	<i>Atp5j2</i>	ATP synthase, H+ transporting, mitochondrial FO complex, subunit F2	0006754 // ATP biosynthetic process // inferred from electronic annotation///0006810 //
NM_134138	///XM	0.026			1.07	1.18	1.20	1.14	<i>Psmg2</i>	proteasome (prosome, macropain) assembly chaperone 2	0007094 // mitotic spindle assembly checkpoint // inferred from direct assay///0043066
NM_001311790	///	0.032	0.036		-1.12	1.09	1.20	1.14	<i>Ctsc</i>	cathepsin C	0001913 // T cell mediated cytotoxicity // inferred from genetic interaction///0006508 //
NM_010485	///XM	0.033	0.015		-1.07	-1.02	1.20	1.15	<i>Elavl1</i>	ELAV (embryonic lethal, abnormal vision)-like 1 (Hu antigen R)	0006417 // regulation of translation // not recorded///0045727 // positive regulation of
NM_008255	///XM	0.024			1.05	1.18	1.20	1.07	<i>Hmgcr</i>	3-hydroxy-3-methylglutaryl-Coenzyme A reductase	0006629 // lipid metabolic process // inferred from electronic annotation///0006694 // s
NM_0114	0.0163	0.011			-1.00	1.09	1.20	1.20	<i>LOC100862468</i> ///Nhp211	NHP2-like protein 1///NHP2 non-histone chromosome protein 2-like 1 (S. cerevisiae)	0006397 // mRNA processing // inferred from electronic annotation///0007338 // single

RefSeq	Tri	p 24h	p 48h	p 72h	FD Air	FD 24h	FD 48h	FD 72h	Gene Symbol	Gene Title	Gene Ontology Biological Process
NM_0116	0.0274				1.04	1.23	1.20	1.04	<i>Ugcg</i>	UDP-glucose ceramide glucosyltransferase	0006629 // lipid metabolic process // inferred from electronic annotation///0006665 // s
NM_0306	0.0134				1.04	1.29	1.20	-1.07	<i>Serp1</i>	stress-associated endoplasmic reticulum protein 1	0001501 // skeletal system development // inferred from mutant phenotype///0006006
NM_001080974	///	0.045			-1.02	1.07	1.20	1.21	<i>Sri</i>	sorcin	0006508 // proteolysis // not recorded///0006816 // calcium ion transport // inferred fr
NM_0011	0.0225				1.02	1.24	1.20	1.01	<i>Hmbs</i>	hydroxymethylbilane synthase	0001666 // response to hypoxia // inferred from electronic annotation///0006779 // por
NM_001289770	///	0.043	0.006		-1.04	1.01	1.20	1.09	<i>Exoc1</i>	exocyst complex component 1	0006810 // transport // inferred from electronic annotation///0006887 // exocytosis // n
NM_025664		0.018			1.00	1.15	1.20	-1.02	<i>Snx9</i>	sorting nexin 9	0000281 // mitotic cytokinesis // not recorded///0006810 // transport // inferred from el
NM_1451	0.0133	0.018	0.018		-1.07	1.22	1.20	1.22	<i>Lpcat3</i>	lysophosphatidylcholine acyltransferase 3	0006629 // lipid metabolic process // inferred from electronic annotation///0006644 // p
NM_0010	0.0352				1.00	1.16	1.20	1.05	<i>Trappc1</i>	trafficking protein particle complex 1	0006810 // transport // inferred from electronic annotation///0006888 // ER to Golgi ves
NM_001111043	///	0.011			-1.42	-1.57	1.20	1.02	<i>Serpinh1</i>	serine (or cysteine) peptidase inhibitor, clade H, member 1	0003433 // chondrocyte development involved in endochondral bone morphogenesis //
NM_019953	///XM	0.049			1.02	1.09	1.20	1.03	<i>Cnpy2</i>	canopy 2 homolog (zebrafish)	0010629 // negative regulation of gene expression // inferred from mutant phenotype//
NM_011149		0.038			-1.02	1.05	1.20	1.05	<i>Ppib</i>	peptidylprolyl isomerase B	0000413 // protein peptidyl-prolyl isomerization // not recorded///0006457 // protein fo
NM_0167	0.0022	0.04			-1.08	1.10	1.20	1.14	<i>Hsd17b10</i>	hydroxysteroid (17-beta) dehydrogenase 10	0007569 // cell aging // inferred from electronic annotation///0008033 // tRNA processir
NM_0268	0.0066				1.03	1.25	1.20	1.23	<i>Chmp2a</i>	charged multivesicular body protein 2A	0000920 // cell separation after cytokinesis // not recorded///0006810 // transport // inf
NM_001037997	///	0.019			1.02	1.02	1.20	-1.01	<i>Fer</i>	fer (fms/fps related) protein kinase	0000226 // microtubule cytoskeleton organization // not recorded///0000278 // mitotic
NM_0255	#####				-1.09	1.09	1.20	1.21	<i>Cyb5b</i>	cytochrome b5 type B	0006810 // transport // inferred from electronic annotation///0043085 // positive regula
NM_001166480	///	0.042			-1.00	1.12	1.20	1.14	<i>Ssr4</i>	signal sequence receptor, delta	
NM_0083	0.0077	0.017			-1.08	1.38	1.20	1.00	<i>Itga7</i>	integrin alpha 7	0007155 // cell adhesion // inferred from mutant phenotype///0007155 // cell adhesion
NM_176979	///XM	0.008			-1.08	1.03	1.21	1.06	<i>Topbp1</i>	topoisomerase (DNA) II binding protein 1	0006281 // DNA repair // inferred from electronic annotation///0006974 // cellular resp
NM_1391	0.038				-1.01	1.85	1.21	1.44	<i>Plac8</i>	placenta-specific 8	0008284 // positive regulation of cell proliferation // inferred from direct assay///000940
NM_001290725	///	0.044			1.03	1.04	1.21	1.18	<i>Ppp1r8</i>	protein phosphatase 1, regulatory (inhibitor) subunit 8	0006351 // transcription, DNA-templated // inferred from electronic annotation///00063
NM_010481		0.045			-1.00	1.07	1.21	-1.06	<i>Hspa9</i>	heat shock protein 9	0006457 // protein folding // inferred from electronic annotation///0006611 // protein e
NM_001136059	///	0.021			-1.67	-1.64	1.21	-1.57	<i>Cyp1a1</i>	cytochrome P450, family 1, subfamily a, polypeptide 1	0001666 // response to hypoxia // inferred from electronic annotation///0001889 // livei
NM_0116	0.0104				-1.11	1.65	1.21	-1.15	<i>Tyropb</i>	TYRO protein tyrosine kinase binding protein	0002281 // macrophage activation involved in immune response // inferred from mutant
NM_1340	0.0261	0.002			-1.10	1.11	1.21	-1.11	<i>Kdelr3</i>	KDEL (Lys-Asp-Glu-Leu) endoplasmic reticulum protein retention receptor 3	0006621 // protein retention in ER lumen // inferred from electronic annotation///00068
NM_0012	0.0351	0.002			-1.08	1.05	1.21	1.04	<i>Pus7</i>	pseudouridylate synthase 7 homolog (S. cerevisiae)	0001522 // pseudouridine synthesis // inferred from electronic annotation///0001522 //
NM_0011	0.0083				-1.05	1.29	1.21	1.28	<i>Fxyd5</i>	FXD domain-containing ion transport regulator 5	0006810 // transport // inferred from electronic annotation///0006811 // ion transport /
NM_008083		0.024			-1.26	1.02	1.21	-1.12	<i>Gap43</i>	growth associated protein 43	0007275 // multicellular organismal development // inferred from electronic annotation//
NM_0205	0.0195	0.007	0.022		-1.44	1.37	1.21	1.04	<i>Retnla</i>	resistin like alpha	
NM_023065		0.003			-1.03	1.16	1.21	1.01	<i>Ifi30</i>	interferon gamma inducible protein 30	0002376 // immune system process // inferred from electronic annotation///0019886 //
NM_0254	0.0424	0.028			-1.01	1.17	1.21	1.08	<i>Llph</i>	LLP homolog, long-term synaptic facilitation (Aplysia)	
NM_00117	0.0062	0.047			1.00	1.15	1.21	1.43	<i>Coro1c</i>	coronin, actin binding protein 1C	0000147 // actin cortical patch assembly // traceable author statement///0001755 // nei
NM_0104	0.0375				1.02	1.23	1.21	1.03	<i>Hsd17b7</i>	hydroxysteroid (17-beta) dehydrogenase 7	0006629 // lipid metabolic process // inferred from electronic annotation///0006694 // s
NM_011284		0.034			1.06	1.10	1.21	1.17	<i>Rpa2</i>	replication protein A2	0000723 // telomere maintenance // not recorded///0000724 // double-strand break re
NM_0253	0.0468				1.03	1.34	1.21	1.03	<i>Aaed1</i>	AhpC/TSA antioxidant enzyme domain containing 1	
NM_016737		0.038			-1.54	-1.95	1.21	1.28	<i>Stip1</i>	stress-induced phosphoprotein 1	
NM_001146222	///	0.029			-1.05	1.05	1.21	1.11	<i>Dpy30</i>	dpy-30 homolog (C. elegans)	0006348 // chromatin silencing at telomere // not recorded///0006351 // transcription, t
NM_010158	///XM	0.033			-1.05	1.13	1.21	1.14	<i>Khdrbs3</i>	KH domain containing, RNA binding, signal transduction associated 3	0006351 // transcription, DNA-templated // inferred from electronic annotation///00063
NM_026330	///XM	0.005			-1.04	1.14	1.21	1.08	<i>Nsmce1</i>	non-SMC element 1 homolog (S. cerevisiae)	0000724 // double-strand break repair via homologous recombination // not recorded///
NM_0266	0.0136				-1.05	1.19	1.21	1.28	<i>Fam96a</i>	family with sequence similarity 96, member A	0007059 // chromosome segregation // not recorded///0016226 // iron-sulfur cluster as
NM_023397	///NR	0.01			1.06	1.08	1.21	1.18	<i>Mdp1</i>	magnesium-dependent phosphatase 1	0006470 // protein dephosphorylation // inferred from electronic annotation///0016311
NM_001113358	///	0.016			-1.12	-1.02	1.21	1.13	<i>Dad1</i>	defender against cell death 1	0001824 // blastocyst development // inferred from mutant phenotype///0006486 // prc
NM_0254	0.0209				1.02	1.28	1.21	-1.10	<i>Mrps28</i>	mitochondrial ribosomal protein S28	
NM_009007	///XM	0.039			1.01	1.14	1.21	1.02	<i>Rac1</i>	RAS-related C3 botulinum substrate 1	0001934 // positive regulation of protein phosphorylation // not recorded///0002093 // i
NM_022018	///XM	0.042			1.06	1.03	1.21	1.18	<i>Fam129a</i>	family with sequence similarity 129, member A	0001933 // negative regulation of protein phosphorylation // inferred from mutant phen
NM_0252	0.0146				-1.03	1.21	1.21	1.29	<i>Tbrg1</i>	transforming growth factor beta regulated gene 1	0006260 // DNA replication // not recorded///0006260 // DNA replication // inferred fr
NM_0012	0.0419				1.02	1.24	1.22	1.28	<i>Ramp2</i> ///Vps25	receptor (calcitonin) activity modifying protein 2///vacuolar protein sorting 25 (yeast)	0001525 // angiogenesis // not recorded///0001570 // vasculogenesis // not recorded///
NM_0104	#####				1.12	1.87	1.22	-1.19	<i>Ier2</i>	immediate early response 2	000182 // neuron differentiation // not recorded///0048870 // cell motility // not recor
NM_0084	0.0308				-1.19	1.08	1.22	1.11	<i>Lgals1</i>	lectin, galactose binding, soluble 1	0002317 // plasma cell differentiation // inferred from direct assay///0006915 // apopto
NM_1814	0.0403				1.14	-1.27	1.22	1.10	<i>Gm15583</i> ///Zbed4	predicted gene 15583///zinc finger, BED type containing 4	
NM_001172062	///	0.011			-1.04	1.03	1.22	1.09	<i>Lman1</i>	lectin, mannose-binding, 1	0006810 // transport // inferred from electronic annotation///0006888 // ER to Golgi ves
NM_001166368	///	0.017			-1.21	1.05	1.22	1.27	<i>Fkbp2</i>	FK506 binding protein 2	0000413 // protein peptidyl-prolyl isomerization // not recorded///0006457 // protein fo
NM_145851	///XM	0.00650	0.013		-1.12	1.19	1.22	1.05	<i>Cables2</i>	CDK5 and Abl enzyme substrate 2	0007049 // cell cycle // inferred from electronic annotation///0051301 // cell division // i
NM_008704		0.034			-1.05	1.10	1.22	1.02	<i>Nme1</i>	NME/NM23 nucleoside diphosphate kinase 1	0002762 // negative regulation of myeloid leukocyte differentiation // not recorded///00
NM_027959		0.004			-1.30	-1.12	1.22	1.09	<i>Pdia6</i>	protein disulfide isomerase associated 6	0006457 // protein folding // not recorded///0008152 // metabolic process // inferred fr
NM_054044	///XM	0.036			-1.03	-1.01	1.22	-1.00	<i>Adgra2</i>	adhesion G protein-coupled receptor A2	0001525 // angiogenesis // inferred from mutant phenotype///0002040 // sprouting ang
NM_0010	0.045				1.18	1.66	1.22	1.41	<i>Elov1</i>	elongation of very long chain fatty acids (FEN1/Elo2, SUR4/Elo3, yeast)-like 1	0006629 // lipid metabolic process // inferred from electronic annotation///0006631 // f
NM_0113	0.0245		0.014		-1.05	1.42	1.22	1.35	<i>Ccl11</i>	chemokine (C-C motif) ligand 11	0001938 // positive regulation of endothelial cell proliferation // not recorded///0002544
NR_002840	///NR	0.028543	0.043		1.56	1.70	1.22	-1.04	<i>Gas5</i> ///Snord47	growth arrest specific 5///small nucleolar RNA, C/D box 47	
NM_001134692	///	0.045			-1.01	1.06	1.22	1.22	<i>LOC102632739</i> ///Ost4	dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 4-like///oligosaccharyltransferase 4 homolog (S. cerevisiae)	0006520 // cellular amino acid metabolic process // inferred from electronic annotation//
NM_0081	0.0473	0.034			1.03	1.25	1.22	1.05	<i>GluD1</i>	glutamate dehydrogenase 1	0006461 // protein complex assembly // inferred from mutant phenotype///0030859 // t
NM_0011	0.0394		0.007		1.01	1.09	1.22	1.22	<i>Dlg5</i>	discs, large homolog 5 (Drosophila)	0002690 // positive regulation of leukocyte chemotaxis // not recorded///0006508 // prc
NM_0101	0.0051	#####			-1.11	1.18	1.22	1.02	<i>F7</i>	coagulation factor VII	0006810 // transport // inferred from electronic annotation///0006886 // intracellular pr
NM_018829	///XM	0.048			1.04	1.08	1.22	1.15	<i>Ap3m1</i>	adaptor-related protein complex 3, mu 1 subunit	0006508 // proteolysis // inferred from electronic annotation///0010243 // response to c
NM_0119	0.0053	0.037			-1.09	1.15	1.22	1.13	<i>Psmb2</i>	proteasome (prosome, macropain) subunit, beta type 2	

RefSeq	Tri p	24h	p	48h	p	72h	FD Air	FD 24h	FD 48h	FD 72h	Gene Symbol	Gene Title	Gene Ontology Biological Process
NM_010941			0.009				-1.01	1.10	1.22	1.05	<i>Nsdhl</i>	NAD(P) dependent steroid dehydrogenase-like	0001942 // hair follicle development // inferred from mutant phenotype//0006629 // lig
NM_022324			0.003				-1.43	-1.20	1.22	-1.27	<i>Sdf2l1</i>	stromal cell-derived factor 2-like 1	0000032 // cell wall mannoprotein biosynthetic process // not recorded//0007275 // mi
NM_0010	0.0253						1.47	1.09	1.22	1.18	<i>Pcdha11//Pcdha10//Pcdha12</i>	protocadherin alpha 11//protocadherin alpha 10//protocadherin alpha 11//protocadherin alpha 12	0007155 // cell adhesion // inferred from electronic annotation//0007155 // cell adhesi
NM_026532//NR		0.04					-1.04	1.02	1.22	1.29	<i>Nutf2//Nutf2-ps1//Nutf2-ps2</i>	nuclear transport factor 2//nuclear transport factor 2, pseudogene 1//nuclear transport factor 2	0000060 // protein import into nucleus, translocation // not recorded//0006606 // prot
NM_0259	0.041						1.11	-1.15	1.23	1.01	<i>Dnajb4</i>	Dnaj (Hsp40) homolog, subfamily B, member 4	0006457 // protein folding // inferred from electronic annotation
NM_007426				0.005			1.20	1.20	1.23	-1.14	<i>Angpt2</i>	angiopoietin 2	0001525 // angiogenesis // inferred from genetic interaction//0001666 // response to h
NM_0012	0.0194						-1.13	1.25	1.23	1.15	<i>Cd302</i>	CD302 antigen	0006909 // phagocytosis // not recorded
NM_0079	#####						1.17	4.07	1.23	1.25	<i>Egr1</i>	early growth response 1	0000122 // negative regulation of transcription from RNA polymerase II promoter // infer
NM_011234		0.045					-1.07	1.11	1.23	1.09	<i>Rad51</i>	RAD51 homolog	0000724 // double-strand break repair via homologous recombination // inferred from d
NM_0275	0.0083	#####	0.006				-1.13	1.07	1.23	1.17	<i>Pvr</i>	poliovirus receptor	0002860 // positive regulation of natural killer cell mediated cytotoxicity directed against
NM_0262	0.0135	0.008					-1.00	1.17	1.23	1.08	<i>Tmed9</i>	transmembrane emp24 protein transport domain containing 9	0006810 // transport // inferred from electronic annotation//0007030 // Golgi organiza
NM_0095	0.0315			0.02			-1.10	1.17	1.23	1.07	<i>Xrcc5</i>	X-ray repair complementing defective repair in Chinese hamster cells 5	0000237 // leptotene // inferred from mutant phenotype//0000723 // telomere mainte
NM_001113554//		0.004					-1.13	-1.00	1.23	1.12	<i>Nudcd1</i>	NudC domain containing 1	
NM_0103	0.0352	0.021					-1.06	1.18	1.23	1.10	<i>Gusb</i>	glucuronidase, beta	0005975 // carbohydrate metabolic process // inferred from direct assay//0006027 // gl
NM_0119	0.0322						-1.01	1.13	1.23	1.11	<i>Psm5</i>	proteasome (prosome, macropain) subunit, alpha type 5	0006508 // proteolysis // inferred from electronic annotation//0006511 // ubiquitin-deg
NM_0010	0.0302	0.01					1.01	1.18	1.23	1.16	<i>Slc7a2</i>	solute carrier family 7 (cationic amino acid transporter, y+ system), member 2	0002537 // nitric oxide production involved in inflammatory response // inferred from m
NM_175158		0.003					1.02	1.10	1.23	-1.00	<i>Utp20</i>	UTP20, small subunit (SSU) processome component, homolog (yeast)	0006364 // rRNA processing // not recorded
NM_0011	0.0144	0.041					-1.05	1.35	1.23	1.13	<i>Max</i>	Max protein	0006351 // transcription, DNA-templated // inferred from electronic annotation//00063
NM_028295//XR		0.042					-1.01	-1.01	1.23	-1.03	<i>Pdia5</i>	protein disulfide isomerase associated 5	0006457 // protein folding // not recorded//0008152 // metabolic process // inferred fr
NM_001290541//NM_00101029895//			0.038				-1.28	-1.32	1.23	1.03	<i>Acer2</i>	alkaline ceramidase 2	0001953 // negative regulation of cell-matrix adhesion // not recorded//0006629 // hpic
NM_001029895//		0.007					1.05	1.11	1.23	1.16	<i>Ate1</i>	arginyltransferase 1	0016598 // protein arginylation // inferred from direct assay
NM_0075	0.0024						1.04	1.76	1.23	1.16	<i>Btg2</i>	B cell translocation gene 2, anti-proliferative	0000122 // negative regulation of transcription from RNA polymerase II promoter // not i
NM_0114	0.0351						1.09	-1.10	1.23	1.18	<i>Smarca2</i>	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily B	0006325 // chromatin organization // traceable author statement//0006334 // nucleosc
NM_0012	0.0451						1.03	1.14	1.23	1.10	<i>B3gnt9</i>	UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 9	0006486 // protein glycosylation // inferred from electronic annotation
NM_001190804//		0.019					-1.25	-1.06	1.23	-1.03	<i>Dnajb11</i>	Dnaj (Hsp40) homolog, subfamily B, member 11	0006457 // protein folding // inferred from electronic annotation//0016556 // mRNA m
NM_0010	0.0331						-1.11	1.18	1.23	1.14	<i>Cd44</i>	CD44 antigen	0001558 // regulation of cell growth // not recorded//0001658 // branching involved in
NM_007523//XR		0.028					1.04	1.10	1.23	1.10	<i>Bak1</i>	BCL2-antagonist/killer 1	0001776 // leukocyte homeostasis // inferred from genetic interaction//0001782 // B c
NM_0196	0.0122	0.049	0.035				-1.14	1.28	1.23	1.20	<i>Hsd17b12</i>	hydroxysteroid (17-beta) dehydrogenase 12	0006629 // lipid metabolic process // inferred from electronic annotation//0006633 // f
NM_133859//XR		0.01	0.006				-1.11	1.01	1.23	1.23	<i>Olfml3//LOC269472</i>	olfactomedin-like 3//uncharacterized LOC269472	0007275 // multicellular organismal development // inferred from electronic annotation
NM_0011	0.0223	0.043					-1.08	1.06	1.24	1.03	<i>Galnt1</i>	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylglucosaminyltransferase 1	0006486 // protein glycosylation // inferred from electronic annotation//0006493 // prc
NM_0215	0.0126						1.01	1.17	1.24	1.18	<i>Rdh11</i>	retinol dehydrogenase 11	0006281 // DNA repair // inferred from electronic annotation//0006281 // DNA repair,
NM_0091	#####						1.06	1.39	1.24	1.28	<i>St3gal4</i>	ST3 beta-galactoside alpha-2,3-sialyltransferase 4	0001574 // ganglioside biosynthetic process // not recorded//0006486 // protein glycos
NM_009274//XM		0.037					1.01	1.06	1.24	1.30	<i>Srpk2</i>	serine/arginine-rich protein specific kinase 2	0000245 // spliceosomal complex assembly // inferred from direct assay//0000245 // sp
NM_001113246//		0.007					-1.09	1.05	1.24	1.14	<i>Chn1</i>	chimerin 1	0007165 // signal transduction // inferred from electronic annotation//0007399 // nerv
NM_145494//XM		0.043					1.00	1.22	1.24	1.11	<i>Me2</i>	malic enzyme 2, NAD(+)-dependent, mitochondrial	0006108 // malate metabolic process // inferred from electronic annotation//0008152 //
NM_0110	0.0108						1.00	-1.08	1.24	1.13	<i>Pea15a</i>	phosphoprotein enriched in astrocytes 15A	0000077 // DNA damage checkpoint // inferred from electronic annotation//0006810 //
NM_001001493//XM_001		0.01					1.02	1.03	1.24	1.23	<i>Gm2573//Wdr83os</i>	predicted gene 2573//WD repeat domain 83 opposite strand	
NM_0011	0.0025	0.025					-1.01	1.19	1.24	1.16	<i>Acp1//LOC102642088</i>	acid phosphatase 1, soluble//low molecular weight phosphotyrosine protein phosphatase 1	0006470 // protein dephosphorylation // inferred from electronic annotation//0035335
NM_001033420//		0.006					-1.07	-1.02	1.24	1.03	<i>Dock1</i>	dedicator of cytokinesis 1	0006457 // hematopoietic progenitor cell differentiation // inferred from genetic interact
NM_001039351//		0.001					1.03	1.07	1.24	1.30	<i>Nolc1</i>	nucleolar and coiled-body phosphoprotein 1	0007000 // nucleolus organization // inferred from direct assay
NM_178111//XM_006500		0.031					-1.04	-1.03	1.24	1.21	<i>Trp53inp2</i>	transformation related protein 53 inducible nuclear protein 2	0000045 // autophagosome assembly // not recorded//0001649 // osteoblast differenti
NM_0215	0.0227						1.01	1.22	1.24	1.15	<i>Smu1</i>	smu-1 suppressor of mec-8 and unc-52 homolog (C. elegans)	
NM_019710//XM		0.032					-1.09	1.03	1.24	1.22	<i>Smc1a</i>	structural maintenance of chromosomes 1A	0006281 // DNA repair // inferred from electronic annotation//0006974 // cellular resp
NM_181470//XM		0.039					1.02	1.13	1.24	1.21	<i>Ltv1</i>	LTV1 homolog (S. cerevisiae)	
NM_0010	0.0249	0.014					-1.03	1.18	1.24	1.12	<i>Ids</i>	iduronate 2-sulfatase	0008152 // metabolic process // inferred from electronic annotation
NM_0119	0.005						-1.02	1.52	1.24	1.25	<i>Abcd2</i>	ATP-binding cassette, sub-family D (ALD), member 2	0000038 // very long-chain fatty acid metabolic process // not recorded//0006635 // fat
NM_0012	0.0079	0.004					-1.12	1.22	1.24	1.16	<i>Fn1</i>	fibronectin 1	0001525 // angiogenesis // inferred from electronic annotation//0001775 // cell activati
NM_008448		0.048					1.09	1.11	1.25	1.19	<i>Kif5b</i>	kinesin family member 5B	0006839 // mitochondrial transport // traceable author statement//0007017 // microtu
NM_0093	0.0328	0.031					-1.09	1.14	1.25	1.18	<i>Tgfb2</i>	transforming growth factor, beta receptor II	0001569 // patterning of blood vessels // inferred from mutant phenotype//0001570 //
NM_0289	0.002						1.06	1.46	1.25	1.35	<i>Polr3c</i>	polymerase (RNA) III (DNA directed) polypeptide C	0002376 // immune system process // inferred from electronic annotation//0006351 //
NM_007591		0.018	0.022				-1.13	-1.11	1.25	1.22	<i>Calr</i>	calreticulin	0000122 // negative regulation of transcription from RNA polymerase II promoter // not i
NM_029701//XM		0.029	0.043				-1.16	1.01	1.25	1.14	<i>Spcs3</i>	signal peptidase complex subunit 3 homolog (S. cerevisiae)	0006465 // signal peptide processing // inferred from electronic annotation
NM_001039089//		0.017					-1.02	1.02	1.25	1.12	<i>Sel1l</i>	sel-1 suppressor of lin-12-like (C. elegans)	0007219 // Notch signaling pathway // inferred from electronic annotation//0030970 //
NM_1460	0.0059	0.015					-1.05	1.14	1.25	-1.05	<i>Clptm1l</i>	CLPTM1-like	0006915 // apoptotic process // inferred from electronic annotation
NM_001297606//		0.027					1.04	1.21	1.25	1.32	<i>Rad23a</i>	RAD23a homolog (S. cerevisiae)	0006281 // DNA repair // inferred from electronic annotation//0006289 // nucleotide-e
NM_0158	0.0018						-1.09	1.08	1.25	1.19	<i>Copb2</i>	coatomer protein complex, subunit beta 2 (beta prime)	0006810 // transport // inferred from electronic annotation//0006886 // intracellular pr
NM_0012	0.0084						1.03	1.42	1.25	1.09	<i>Esd</i>	esterase D/formylglutathione hydrolase	0046294 // formaldehyde catabolic process // inferred from electronic annotation
NM_0010	0.0142						1.03	1.43	1.25	-1.05	<i>Parl</i>	presenilin associated, rhomboid-like	0006508 // proteolysis // inferred from genetic interaction//0006508 // proteolysis // in
NM_00127970//		0.01					-1.15	-1.22	1.25	1.12	<i>Itag6</i>	integrin alpha 6	0007155 // cell adhesion // inferred from electronic annotation//0007160 // cell-matrix
NM_0013	0.0321						1.05	1.19	1.25	1.06	<i>Psm3</i>	proteasome (prosome, macropain) subunit, alpha type 3	0006508 // proteolysis // inferred from electronic annotation//0006511 // ubiquitin-deg
NM_010104		0.016					-1.27	-1.17	1.25	-1.14	<i>Edn1</i>	endothelin 1	0000122 // negative regulation of transcription from RNA polymerase II promoter // not i
NM_001313758//		0.032					1.00	1.12	1.25	1.14	<i>Prps2</i>	phosphoribosyl pyrophosphate synthetase 2	0006015 // 5-phosphoribose 1-diphosphate biosynthetic process // not recorded//0006
NM_001161419//		0.016					-1.06	1.16	1.25	1.15	<i>Atp5g1</i>	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit C1 (subunit 9)	0006810 // transport // inferred from electronic annotation//0006811 // ion transport /
NM_001290421//		0.015					1.06	1.14	1.25	1.31	<i>Flna</i>	filamin, alpha	0001837 // epithelial to mesenchymal transition // inferred from genetic interaction//OC

RefSeq	Tri.p	24h	p	48h	p	72h	FD Air	FD 24h	FD 48h	FD 72h	Gene Symbol	Gene Title	Gene Ontology Biological Process
NM_153806			0.037	0.02	-1.00	1.04	1.26	1.25			<b>Dnttp2</b>	deoxynucleotidyltransferase, terminal, interacting protein 2	0006351 // transcription, DNA-templated // inferred from electronic annotation//00063
NM_001035854	///		0.037		1.00	1.22	1.26	1.05			<b>Ap2b1</b>	adaptor-related protein complex 2, beta 1 subunit	0003279 // cardiac septum development // inferred from mutant phenotype//0003281
NM_0011	#####		0.003		-1.08	1.38	1.26	1.10			<b>Mal</b>	myelin and lymphocyte protein, T cell differentiation protein	0042552 // myelination // not recorded//13902043 // positive regulation of extrinsic apo
NM_001199177	///		0.012		-1.05	1.11	1.26	1.04			<b>Opa1</b>	optic atrophy 1	0000002 // mitochondrial genome maintenance // not recorded//0001843 // neural tut
NM_025936	///XM		0.031		-1.12	1.05	1.26	1.31			<b>Rars</b>	arginyl-tRNA synthetase	0006412 // translation // inferred from electronic annotation//0006418 // tRNA aminoa
NM_0531	0.0225				-1.05	1.16	1.26	1.45			<b>Echs1</b>	enoyl Coenzyme A hydratase, short chain, 1, mitochondrial	0006629 // lipid metabolic process // inferred from electronic annotation//0006631 // f.
NM_021446	///XM		0.025		1.04	1.13	1.26	1.27			<b>O610007P14RIK</b>	RIKEN cDNA O610007P14 gene	0006629 // lipid metabolic process // inferred from electronic annotation//0006694 // s
NM_0078	0.0156		0.012		-1.12	1.13	1.26	-1.02			<b>Ddost</b>	dolichyl-di-phosphooligosaccharide-protein glycotransferase	0006486 // protein glycosylation // inferred from sequence or structural similarity//0006
NM_0214	0.0122				1.14	1.57	1.26	1.17			<b>Stk4</b>	serine/threonine kinase 4	0000165 // MAPK cascade // --//0000186 // activation of MAPKK activity // not recorde
NM_007802	///XM		0.046		-1.09	1.08	1.26	1.04			<b>Ctsk</b>	cathepsin K	0001957 // intramembranous ossification // inferred from electronic annotation//00060
NM_0012	0.047				-1.06	1.24	1.26	-1.05			<b>Scarb1</b>	scavenger receptor class B, member 1	0001935 // endothelial cell proliferation // inferred from mutant phenotype//0006702 //
NM_001081635	///		0.046		-1.02	-1.07	1.26	-1.05			<b>Ccnd3</b>	cyclin D3	0001934 // positive regulation of protein phosphorylation // not recorded//0007049 // i
NM_0010	0.0032				1.03	1.48	1.26	1.21			<b>Gm10052///Gm5803///Hnrnpa1///Gm564</b>	heterogeneous nuclear ribonucleoprotein A1 pseudogene//predicted gene 5803//he	0000380 // alternative mRNA splicing, via spliceosome // inferred from direct assay//000
NM_0115	0.0105		0.02		1.08	1.30	1.26	1.15			<b>Sdc1</b>	syndecan 1	0001657 // ureteric bud development // inferred from electronic annotation//0006954 //
NM_026554			0.013		-1.03	-1.01	1.26	1.16			<b>Ncbp2</b>	nuclear cap binding protein subunit 2	0000184 // nuclear-transcribed mRNA catabolic process, nonsense-mediated decay // no
NM_024180	///XM		0.032		-1.05	1.01	1.26	1.19			<b>Ormdl2</b>	ORM1-like 2 (S. cerevisiae)	0006672 // ceramide metabolic process // not recorded//0090155 // negative regulatio
NM_0012	0.0237				-1.05	1.15	1.26	1.16			<b>Immt</b>	inner membrane protein, mitochondrial	0042407 // cristae formation // not recorded//0051560 // mitochondrial calcium ion ho
NM_029578			0.036		-1.02	1.15	1.26	1.11			<b>Tgds</b>	TDP-glucose 4,6-dehydratase	0009225 // nucleotide-sugar metabolic process // inferred from electronic annotation
NM_019824			0.012		-1.19	1.09	1.26	1.17			<b>Arpc3</b>	actin related protein 2/3 complex, subunit 3	0030833 // regulation of actin filament polymerization // inferred from electronic annota
NM_133225			0.024		1.06	1.21	1.27	1.03			<b>Acbd3</b>	acyl-Coenzyme A binding domain containing 3	0006629 // lipid metabolic process // inferred from electronic annotation//0006694 // s
NM_009840			0.013		-1.18	-1.10	1.27	1.31			<b>Cct8</b>	chaperonin containing Tcp1, subunit 8 (theta)	0006457 // protein folding // inferred from electronic annotation//0007339 // binding c
NM_001177556	///		0.003		-1.05	1.03	1.27	1.14			<b>Gng12</b>	guanin nucleotide binding protein (G protein), gamma 12	0007165 // signal transduction // inferred from electronic annotation//0007186 // G-pr
NM_010477	///XM		0.02		-1.41	-1.53	1.27	1.02			<b>Hspd1</b>	heat shock protein 1 (chaperonin)	0001666 // response to hypoxia // inferred from electronic annotation//0002236 // dete
NM_172685			0.005	0.024	-1.08	1.15	1.27	1.31			<b>Slc25a24</b>	solute carrier family 25 (mitochondrial carrier, phosphate carrier), member 24	0006810 // transport // inferred from electronic annotation//0006839 // mitochondria
NM_144514	///XM		#####		-1.07	1.06	1.27	1.16			<b>Commd1</b>	COMM domain containing 1	0006351 // transcription, DNA-templated // inferred from electronic annotation//00063
NM_1332	0.0105				1.01	-1.21	1.27	1.16			<b>Mtmr4</b>	myotubularin related protein 4	0006470 // protein dephosphorylation // inferred from electronic annotation//0007179
NM_001310746	///		0.04		-1.05	1.10	1.27	1.01			<b>Ubl5</b>	ubiquitin-like 5	0000398 // mRNA splicing, via spliceosome // not recorded//0006464 // cellular protei
NM_0085	0.0136		0.008		1.02	1.19	1.27	1.16			<b>Mcm3</b>	minichromosome maintenance deficient 3 (S. cerevisiae)	0006260 // DNA replication // inferred from electronic annotation//0006270 // DNA rep
NM_025388			0.006		1.02	1.16	1.27	1.13			<b>Ufc1</b>	ubiquitin-fold modifier conjugating enzyme 1	0034976 // response to endoplasmic reticulum stress // not recorded//0071569 // prote
NM_1460	0.0293		0.02	0.022	-1.06	1.12	1.27	1.07			<b>Cbwd1</b>	COBW domain containing 1	0006810 // transport // inferred from electronic annotation//0007565 // female pregna
NM_008096			0.008		-1.39	1.01	1.28	-1.02			<b>Gc</b>	group specific component	
NM_1338	0.0396		0.045		-1.06	1.23	1.28	1.12			<b>Lrrc59</b>	leucine rich repeat containing 59	
NM_001159384	///		0.032		1.04	1.06	1.28	1.15			<b>Mlx</b>	MAX-like protein X	0000122 // negative regulation of transcription from RNA polymerase II promoter // not i
NM_0078	0.0388		#####	0.015	-1.22	1.10	1.28	1.08			<b>Cyp7b1</b>	cytochrome P450, family 7, subfamily b, polypeptide 1	0006629 // lipid metabolic process // inferred from electronic annotation//0006699 // b
NM_008981	///XM		0.034		1.01	1.14	1.28	1.20			<b>Ptprg</b>	protein tyrosine phosphatase, receptor type, G	0006470 // protein dephosphorylation // inferred from electronic annotation//0010633
NM_0119	0.0043				1.06	1.35	1.28	1.32			<b>Xrn2</b>	5'-3' exoribonuclease 2	0000738 // DNA catabolic process, exonucleolytic // not recorded//0006139 // nucleob:
NM_0012	0.0229				1.04	-1.66	1.28	1.30			<b>Klf10</b>	Kruppel-like factor 10	0006351 // transcription, DNA-templated // inferred from electronic annotation//00063
NM_010790	///XM		0.017		-1.07	1.16	1.28	1.07			<b>Melk</b>	maternal embryonic leucine zipper kinase	0006468 // protein phosphorylation // inferred from electronic annotation//0006915 //
NM_0291	0.0181		0.003	0.048	-1.02	1.13	1.28	1.28			<b>Sf3a3</b>	splicing factor 3a, subunit 3	0000398 // mRNA splicing, via spliceosome // not recorded//0006397 // mRNA processi
NM_026609			0.011		1.00	1.21	1.28	1.14			<b>Leprot1</b>	leptin receptor overlapping transcript-like 1	
NM_025360	#####				-1.13	-1.01	1.29	1.13			<b>Tmed3</b>	transmembrane emp24 domain containing 3	0006810 // transport // inferred from electronic annotation//0015031 // protein transp
NM_0236	0.0112				1.09	1.39	1.29	-1.12			<b>Isyna1</b>	myo-inositol 1-phosphate synthase A1	0006021 // inositol biosynthetic process // inferred from electronic annotation//000662
NM_001205286	///		0.045		-1.03	-1.08	1.29	1.09			<b>Tmem39a</b>	transmembrane protein 39a	0002230 // positive regulation of defense response to virus by host // not recorded//000
NM_0094	0.013		0.028		1.01	1.24	1.29	1.16			<b>Gm10145///Gm10705///Ube213</b>	predicted gene 10145//predicted gene 10705//ubiquitin-conjugating enzyme E2L 3	0000209 // protein polyubiquitination // not recorded//0006351 // transcription, DNA-t
NM_0011	0.029		0.039		-1.05	1.18	1.29	1.33			<b>Uhrf1</b>	ubiquitin-like, containing PHD and RING finger domains, 1	0000122 // negative regulation of transcription from RNA polymerase II promoter // infer
NM_0108	0.0392				1.17	1.44	1.29	1.45			<b>Ncl</b>	nucleolin	0001525 // angiogenesis // not recorded//0006897 // endocytosis // not recorded//000
NM_0280	0.0483		0.015		-1.06	1.08	1.29	1.35			<b>Cyb5r1</b>	cytochrome b5 reductase 1	0006629 // lipid metabolic process // inferred from electronic annotation//0006694 // s
NM_010295	///XM		0.044	0.042	-1.05	1.17	1.29	1.18			<b>Gclc</b>	glutamate-cysteine ligase, catalytic subunit	0006534 // cysteine metabolic process // not recorded//0006536 // glutamate metaboli
NM_008720			0.04		-1.22	-1.03	1.29	1.36			<b>Npc1</b>	Niemann-Pick type C1	0006486 // protein glycosylation // inferred from direct assay//0006486 // protein glyco
NM_0010	0.0097				-1.06	-1.73	1.29	1.38			<b>Tsc22d3</b>	TSC22 domain family, member 3	0000122 // negative regulation of transcription from RNA polymerase II promoter // infer
NM_1724	0.0393				1.01	-1.29	1.30	1.19			<b>Slc38a5</b>	solute carrier family 38, member 5	0003333 // amino acid transmembrane transport // not recorded//0015804 // neutral a
NM_001304758	///		0.021		-1.04	1.18	1.30	1.18			<b>Coq7</b>	demethyl-Q 7	0000122 // negative regulation of transcription from RNA polymerase II promoter // not i
NM_0093	0.0125		0.018		-1.12	1.72	1.30	1.02			<b>Tfpi2</b>	tissue factor pathway inhibitor 2	0007596 // blood coagulation // inferred from electronic annotation//0007599 // hemo
NM_1528	0.0143				1.17	1.66	1.30	1.20			<b>Plk2</b>	polo-like kinase 2	0000082 // G1/S transition of mitotic cell cycle // not recorded//0000278 // mitotic cell
NM_0261	0.046		0.006		-1.11	1.14	1.30	1.08			<b>Gtf3c6</b>	general transcription factor IIC, polypeptide 6, alpha	0006351 // transcription, DNA-templated // not recorded//0006383 // transcription fro
NM_175096			0.016		-1.10	-1.59	1.31	-1.07			<b>Stbd1</b>	starch binding domain 1	0005975 // carbohydrate metabolic process // inferred from electronic annotation//0000
NM_0010	0.0119		0.013		-1.04	1.16	1.31	1.48			<b>Ralgapa1</b>	Ral GTPase activating protein, alpha subunit 1	0006355 // regulation of transcription, DNA-templated // inferred from direct assay//00
NM_0215	0.0251				-1.01	1.22	1.31	1.35			<b>LOC102642514///Nsa2</b>	ribosome biogenesis protein NSA2 homolog//NSA2 ribosome biogenesis homolog (S.	0006364 // rRNA processing // inferred from electronic annotation//0042254 // riboson
NM_0010	0.0034		0.016		1.00	1.19	1.31	1.20			<b>Gnptab</b>	N-acetylglucosamine-1-phosphate transferase, alpha and beta subunits	0007040 // lysosome organization // not recorded//0009306 // protein secretion // infe
NM_019642	///XM		0.029		-1.17	1.02	1.31	1.26			<b>Rpn2</b>	ribophorin II	0006486 // protein glycosylation // inferred from electronic annotation//0006487 // prc
NM_0117	0.0048		#####		-1.01	1.16	1.31	1.40			<b>Wdr1</b>	WD repeat domain 1	0007605 // sensory perception of sound // not recorded//0030036 // actin cytoskeleton
NM_010480			0.022		-1.39	-1.59	1.31	1.05			<b>Hsp90aa1</b>	heat shock protein 90, alpha (cytosolic), class A member 1	0001764 // neuron migration // not recorded//0006457 // protein folding // inferred frc
NM_0010	0.0046				-1.10	-1.55	1.31	1.28			<b>Tmem2</b>	transmembrane protein 2	0007275 // multicellular organismal development // inferred from electronic annotation
NM_001164190	///		0.043		1.08	1.05	1.32	1.46			<b>Mtm1</b>	X-linked myotubular myopathy gene 1	0006470 // protein dephosphorylation // not recorded//0006629 // lipid metabolic proc

RefSeq	Tri	p 24h	p 48h	p 72h	FD Air	FD 24h	FD 48h	FD 72h	Gene Symbol	Gene Title	Gene Ontology Biological Process
NM_0242		0.0069	0.002		-1.18	1.17	1.32	1.19	<b>Sec13</b>	SEC13 homolog, nuclear pore and COPII coat complex component	0006810 // transport // inferred from electronic annotation//0006888 // ER to Golgi ves
NM_0174		0.0062		0.028	-1.09	1.27	1.32	1.18	<b>Copp2</b>	coatamer protein complex, subunit gamma 2	0006810 // transport // inferred from electronic annotation//0006886 // intracellular pr
NM_011057	//XM_006520		0.005		1.42	1.40	1.32	1.19	<b>Pdgfb</b>	platelet derived growth factor, B polypeptide	0001568 // blood vessel development // inferred from expression pattern//0001666 // r
NM_028303	//XM	0.022			-1.04	1.08	1.32	1.09	<b>Pdzd11</b>	PDZ domain containing 11	0006887 // exocytosis // not recorded//0007269 // neurotransmitter secretion // not r
NM_0010		0.0432	0.015		-1.02	1.35	1.32	1.32	<b>Kdm7a</b>	lysine (K)-specific demethylase 7A	0006351 // transcription, DNA-templated // inferred from electronic annotation//00063
NM_023579	//XM	0.031			1.04	1.11	1.32	1.33	<b>Ipo5</b>	importin 5	0000059 // protein import into nucleus, docking // not recorded//0000060 // protein im
NM_0104		0.0396			1.27	3.72	1.32	1.07	<b>Nr4a1</b>	nuclear receptor subfamily 4, group A, member 1	0001938 // positive regulation of endothelial cell proliferation // not recorded//000204
NM_0011		0.0229			-1.10	1.48	1.32	-1.20	<b>Hist1h2aa</b> // <b>Hist1h2ap</b>	histone cluster 1, H2aoc//histone cluster 1, H2ap	0006325 // chromatin organization // not recorded//0006342 // chromatin silencing // i
NM_0089		0.0466			1.03	1.21	1.33	1.21	<b>Psma2</b>	proteasome (prosome, macropain) subunit, alpha type 2	0006508 // proteolysis // inferred from electronic annotation//0006511 // ubiquitin-deg
NM_0237		0.0237			1.16	1.64	1.33	1.65	<b>Etv5</b>	ets variant 5	0006355 // regulation of transcription, DNA-templated // inferred from electronic annot
NM_145953	//XM	0.021			-1.16	-1.24	1.33	-1.05	<b>Cth</b>	cystathionase (cystathionine gamma-lyase)	0006749 // glutathione metabolic process // not recorded//0008285 // negative regulat
NM_0012		0.0071	0.04		-1.13	1.32	1.33	1.18	<b>Psat1</b>	phosphoserine aminotransferase 1	0006564 // L-serine biosynthetic process // inferred from electronic annotation//00081
NM_1451		0.0188	0.03		-1.02	1.16	1.33	1.18	<b>Mgl2</b>	macrophage galactose N-acetyl-galactosamine specific lectin 2	
NM_0135		0.0224	0.018		-1.89	-4.51	1.33	-1.17	<b>Hsph1</b>	heat shock 105kDa/110kDa protein 1	0006986 // response to unfolded protein // traceable author statement//0043524 // ne
NM_001164787	//	0.015			-1.01	1.01	1.34	1.24	<b>Sprr2a1</b> // <b>Sprr2a2</b> // <b>Sprr2a3</b>	small proline-rich protein 2A1//small proline-rich protein 2A2//small proline-rich pr	0008360 // regulation of cell shape // traceable author statement//0008544 // epidermi
NM_0011		0.0134	0.044	0.048	-1.09	1.33	1.34	1.50	<b>Kit</b>	kit oncogene	0000187 // activation of MAPK activity // not recorded//0001541 // ovarian follicle deve
NM_010860	//XM	0.021			-1.07	1.02	1.34	1.31	<b>Myf6</b> // <b>Gm10080</b>	myosin, light polypeptide 6, alkali, smooth muscle and non-muscle//predicted gene 1	0006936 // muscle contraction // traceable author statement//0007519 // skeletal musc
NM_025310		0.028	0.011		1.01	1.17	1.34	1.20	<b>Ftsj3</b>	FtsJ homolog 3 (E. coli)	0000453 // enzyme-directed rRNA 2'-O-methylation // inferred from electronic annotati
NM_001301211	//	0.045			1.03	1.11	1.34	1.14	<b>Ap1g1</b>	adaptor protein complex AP-1, gamma 1 subunit	0000226 // microtubule cytoskeleton organization // not recorded//0006810 // transpo
NM_001025192	//	0.039			1.07	1.17	1.35	1.27	<b>Cxadr</b>	coxsackie virus and adenovirus receptor	0007005 // mitochondrion organization // inferred from mutant phenotype//0007155 //
NR_030708	//XM_	0.009			1.08	1.16	1.35	1.31	<b>6820431F20Rik</b> // <b>Gm21811</b>	cadherin 11 pseudogene//predicted gene, 21811	0007156 // homophilic cell adhesion via plasma membrane adhesion molecules // inferre
NM_025968	//XM	0.029			1.03	1.03	1.35	1.36	<b>Ptgr1</b>	prostaglandin reductase 1	0006693 // prostaglandin metabolic process // inferred from electronic annotation//000
NM_0092		0.0043			-1.01	2.18	1.35	-1.13	<b>Sprr1a</b>	small proline-rich protein 1A	0018149 // peptide cross-linking // not recorded//0030216 // keratinocyte differentiat
NM_020259	//XM	0.008	0.036		1.05	1.07	1.35	1.42	<b>Hhip</b>	Hedgehog-interacting protein	0005975 // carbohydrate metabolic process // inferred from electronic annotation//000
NM_0012		0.0262	0.021		1.05	1.27	1.36	1.20	<b>Ddx46</b>	DEAD (Asp-Glu-Ala-Asp) box polypeptide 46	0000398 // mRNA splicing, via spliceosome // not recorded//0006397 // mRNA processi
NM_0079		0.0087	0.033		-1.07	1.20	1.36	1.19	<b>Erh</b>	enhancer of rudimentary homolog (Drosophila)	0001649 // osteoblast differentiation // inferred from direct assay//0006221 // pyrimidi
NM_001145799	//	0.035			-1.19	-1.15	1.36	1.06	<b>Ctla2a</b> // <b>Ctla2b</b>	cytotoxic T lymphocyte-associated protein 2 alpha//cytotoxic T lymphocyte-associate	0010951 // negative regulation of endopeptidase activity // traceable author statement//
NM_00119	#####		0.033		-1.05	1.20	1.36	1.21	<b>Psma4</b>	proteasome (prosome, macropain) subunit, alpha type 4	0006936 // proteolysis // inferred from electronic annotation//0006511 // ubiquitin-deg
NM_0085		0.0374	0.025		1.03	1.26	1.36	1.22	<b>Met</b>	met proto-oncogene	0000122 // negative regulation of transcription from RNA polymerase II promoter // not r
NM_0089		0.0364			-1.11	1.11	1.36	1.42	<b>Psmc1</b>	protease (prosome, macropain) 26S subunit, ATPase 1	0030163 // protein catabolic process // inferred from electronic annotation//0030433 //
NM_030889	//XM	0.016			1.02	1.10	1.37	1.25	<b>Sorcs2</b>	sortilin-related VPS10 domain containing receptor 2	0006810 // transport // inferred from electronic annotation
NM_001033375	//	0.041			1.03	1.07	1.37	1.20	<b>A230046K03Rik</b>	RIKEN cDNA A230046K03 gene	0006810 // transport // inferred from electronic annotation//0007032 // endosome org
NM_001313711	//	0.018			1.09	1.22	1.37	1.11	<b>Prdx4</b>	peroxiredoxin 4	0007283 // spermatogenesis // inferred from mutant phenotype//0008584 // male gon
NM_010830		0.034	#####		-1.17	-1.05	1.37	1.13	<b>Msh6</b>	mutS homolog 6 (E. coli)	0000710 // meiotic mismatch repair // not recorded//0006281 // DNA repair // not rec
NM_0011	#####				-1.04	1.03	1.37	1.29	<b>Kif20a</b>	kinesin family member 20A	0000281 // mitotic cytokinesis // not recorded//0000910 // cytokinesis // not recorded/
NM_0255		0.0445	0.036		-1.14	1.02	1.37	1.26	<b>Ostc</b>	oligosaccharyltransferase complex subunit	
NM_0011		0.0346			1.05	1.00	1.37	1.57	<b>Cldn18</b>	claudin 18	0016338 // calcium-independent cell-cell adhesion via plasma membrane cell-adhesion n
NM_0011		0.0177	0.034		-1.06	1.10	1.37	1.20	<b>Glo1</b>	glyoxalase 1	0005975 // carbohydrate metabolic process // not recorded//0006357 // regulation of t
NM_033075	//XR_	0.05			-1.12	-1.11	1.38	1.50	<b>D17H6S56E-5</b>	DNA segment, Chr 17, human D6S56E 5	0019058 // viral life cycle // inferred from electronic annotation
NM_172118	//XM	0.019			-1.14	-1.03	1.38	1.39	<b>Myf9</b>	myosin, light polypeptide 9, regulatory	0070527 // platelet aggregation // not recorded
NM_1832		0.0327		0.043	-1.12	1.24	1.38	1.26	<b>Wfdc21</b>	WAP four-disulfide core domain 21	0010466 // negative regulation of peptidase activity // inferred from electronic annotati
NM_009443	//NM	0.011			1.04	1.21	1.38	1.23	<b>Tgln1</b> // <b>Tgln2</b>	trans-golgi network protein//trans-golgi network protein 2	0006895 // Golgi to endosome transport // not recorded
NM_0011		0.0021			1.10	1.40	1.38	1.36	<b>Dynlt1-ps1</b> // <b>Dynlt1a</b> // <b>Dynlt1b</b> // <b>Dynlt1c</b>	dynein light chain Tctex-type 1, pseudogene 1//dynein light chain Tctex-type 1A//d	0000132 // establishment of mitotic spindle orientation // inferred from mutant phenoty
NM_013463		0.015			1.10	1.13	1.38	1.22	<b>Gla</b>	galactosidase, alpha	0005975 // carbohydrate metabolic process // inferred from electronic annotation//000
NM_007392	//XM	0.049			-1.25	-1.13	1.38	1.12	<b>Acta2</b>	actin, alpha 2, smooth muscle, aorta	0006936 // muscle contraction // not recorded//0008217 // regulation of blood pressur
NM_0111		0.0274	0.005		-1.03	1.25	1.39	1.00	<b>Papola</b>	poly (A) polymerase alpha	0000398 // mRNA splicing, via spliceosome // ---//0006369 // termination of RNA poly
NM_007856	//XM	0.033			1.08	1.24	1.39	-1.04	<b>Dhcr7</b>	7-dehydrocholesterol reductase	0001568 // blood vessel development // inferred from mutant phenotype//0006629 // l
NM_001109971	//	0.022			-1.08	1.11	1.39	-1.04	<b>Sec61g</b>	protein transport protein Sec61 subunit gamma//protein transport protein Sec61 sub	0006605 // protein targeting // inferred from electronic annotation//0006810 // transp
NM_0011		0.0272	0.039		1.09	1.44	1.40	1.47	<b>Magi3</b>	membrane associated guanylate kinase, WW and PDZ domain containing 3	0007165 // signal transduction // inferred from electronic annotation//0016310 // phos
NM_0101		0.023	0.042		1.07	1.57	1.40	1.26	<b>S1pr3</b>	sphingosine-1-phosphate receptor 3	0001816 // cytokine production // inferred from mutant phenotype//0003376 // sphing
NM_001286062	//	0.029			1.08	1.29	1.41	1.09	<b>Angpt1</b>	angiopoietin 1	0001525 // angiogenesis // inferred from direct assay//0001525 // angiogenesis // infer
NM_173006	//XM	0.023			-1.02	1.13	1.41	1.31	<b>Pon3</b>	paraoxonase 3	0006470 // protein dephosphorylation // inferred from electronic annotation//0009636
NM_008924		0.002			-1.04	1.21	1.41	1.37	<b>Prkar2a</b>	protein kinase, cAMP dependent regulatory, type II alpha	0001932 // regulation of protein phosphorylation // inferred from electronic annotation/
NM_019699		0.014			1.04	1.18	1.41	1.06	<b>Fads2</b>	fatty acid desaturase 2	0006629 // lipid metabolic process // inferred from electronic annotation//0006631 // f
NM_1725		0.0055			1.29	1.14	1.41	1.41	<b>A730008H23Rik</b> // <b>Hjurp</b>	RIKEN cDNA A730008H23 gene//Holliday junction recognition protein//RIKEN cDNA	0007049 // cell cycle // inferred from electronic annotation//0007059 // chromosome s
NM_0011		0.0081			1.06	1.59	1.41	1.11	<b>Gm10693</b> // <b>Gm14548</b> // <b>Lilra6</b> // <b>Pira1</b> // <b>F</b>	predicted pseudogene 10693//predicted gene 14548//leukocyte immunoglobulin-lik	0001782 // B cell homeostasis // inferred from mutant phenotype//0002250 // adaptiv
NM_009610		0.009	0.037		-1.50	-1.14	1.42	1.19	<b>Actg2</b>	actin, gamma 2, smooth muscle, enteric	0010628 // positive regulation of gene expression // inferred from sequence or structural
NM_001277101	//	0.033			1.07	1.18	1.42	1.25	<b>Cops5</b>	COP9 (constitutive photomorphogenic) homolog, subunit 5 (Arabidopsis thaliana)	0000338 // protein deneddylation // not recorded//0006355 // regulation of transcripti
NM_011631		0.04			-1.29	-1.22	1.42	1.34	<b>Hsp90b1</b>	heat shock protein 90, beta (Grp94), member 1	0001666 // response to hypoxia // not recorded//0006457 // protein folding // inferre
		0.0042			1.67	4.36	1.42	1.10	<b>Ighd</b>	immunoglobulin heavy constant delta	0016064 // immunoglobulin mediated immune response // inferred from mutant phenot
NM_0084		0.0041	0.011		-1.14	1.67	1.43	1.37	<b>Lcn2</b>	lipocalin 2	0002376 // immune system process // inferred from electronic annotation//0006810 //
NM_0119	#####		0.007		1.02	1.64	1.45	1.38	<b>LOC102643033</b> // <b>Zfp146</b>	zinc finger protein OZF//zinc finger protein 146	0006355 // regulation of transcription, DNA-templated // not recorded
NM_0013		0.0032	0.008		-1.10	1.27	1.45	1.28	<b>Mcm5</b>	minichromosome maintenance deficient 5, cell division cycle 46 (S. cerevisiae)	0006260 // DNA replication // inferred from electronic annotation//0006270 // DNA rep
NM_019802	//XM	0.008	0.035	-1.06	1.09	1.45	1.39	<b>Gcxc</b>	gamma-glutamyl carboxylase	0017187 // peptidyl-glutamic acid carboxylation // not recorded	

RefSeq	Tri	p 24h	p 48h	p 72h	FD Air	FD 24h	FD 48h	FD 72h	Gene Symbol	Gene Title	Gene Ontology Biological Process
NM_0297		0.003	0.005		-1.07	2.00	1.45	-1.04	<i>Lrg1</i>	leucine-rich alpha-2-glycoprotein 1	0001938 // positive regulation of endothelial cell proliferation // inferred from mutant phenotype
NM_0010	#####				1.00	1.37	1.45	1.24	<i>Ddhd1</i>	DDHD domain containing 1	0006629 // lipid metabolic process // inferred from electronic annotation//0016042 // lipid
NM_1725		0.0073			1.30	1.14	1.46	1.45	<i>6430706D22Rik//A730008H23Rik//Hjurp</i>	RIKEN cDNA 6430706D22 gene//RIKEN cDNA A730008H23 gene//Holliday junction	0007049 // cell cycle // inferred from electronic annotation//0007059 // chromosome segregation
NM_0012		0.0025	0.015		1.01	1.87	1.46	1.24	<i>Cd68</i>	CD68 antigen	0071310 // cellular response to organic substance // inferred from direct assay
NM_001025431	///				1.05	1.24	1.46	1.32	<i>Btbd3</i>	BTB (POZ) domain containing 3	0007399 // nervous system development // inferred from electronic annotation//00219
NM_0254		0.0138	0.002		-1.12	1.11	1.47	1.18	<i>Ssr2</i>	signal sequence receptor, beta	
NM_010111	///XM				1.09	1.03	1.47	1.13	<i>Efnb2</i>	ephrin B2	0001525 // angiogenesis // inferred from electronic annotation//0001945 // lymph vessel
NM_008969	///XM				1.04	1.40	1.47	1.19	<i>Ptgs1</i>	prostaglandin-endoperoxide synthase 1	0001516 // prostaglandin biosynthetic process // inferred from mutant phenotype//000
NM_0011		0.0011	0.048		1.09	1.55	1.48	1.03	<i>Acot7</i>	acyl-CoA thioesterase 7	0009062 // fatty acid catabolic process // inferred from direct assay//0015937 // coenzyme
NM_0531	#####				-1.12	1.32	1.49	1.34	<i>Glrx</i>	glutaredoxin	0006810 // transport // inferred from electronic annotation//0032024 // positive regulation
NM_0013		0.0307	0.016		1.05	1.24	1.51	1.17	<i>Mcm6</i>	minichromosome maintenance deficient 6 (MISS homolog, S. pombe) (S. cerevisiae)	0006260 // DNA replication // inferred from electronic annotation//0006268 // DNA un
NM_026931					-1.10	-1.32	1.52	1.15	<i>1810011010Rik</i>	RIKEN cDNA 1810011010 gene	0002264 // endothelial cell activation involved in immune response // not recorded//00
NM_0134		0.0142	0.043		-1.21	1.49	1.52	1.06	<i>Ankrd1</i>	ankyrin repeat domain 1 (cardiac muscle)	0000122 // negative regulation of transcription from RNA polymerase II promoter // not r
NM_0012		0.009	0.03		-1.07	1.65	1.52	1.02	<i>Lilr4b//Lilrb4a</i>	leukocyte immunoglobulin-like receptor, subfamily B, member 4B//leukocyte immun	0002250 // adaptive immune response // inferred from electronic annotation//0002376
NM_008302					-1.30	-1.30	1.53	1.51	<i>Hsp90ab1</i>	heat shock protein 90 alpha (cytosolic), class B member 1	0001890 // placenta development // inferred from mutant phenotype//0006457 // prot
NM_0011	#####				-1.26	1.33	1.53	1.09	<i>Clec4n</i>	C-type lectin domain family 4, member n	0002250 // adaptive immune response // inferred from electronic annotation//0002376
NM_0011		0.0074			-1.10	1.45	1.53	1.02	<i>Itih4</i>	inter alpha-trypsin inhibitor, heavy chain 4	0006953 // acute-phase response // inferred from electronic annotation//0010466 // ne
NM_0111		0.0435			1.65	1.25	1.53	1.93	<i>Plod1</i>	procollagen-lysine, 2-oxoglutarate 5-dioxygenase 1	0001666 // response to hypoxia // inferred from electronic annotation//0008544 // epic
NM_009226					-1.07	1.15	1.53	1.17	<i>Snrpd1</i>	small nuclear ribonucleoprotein D1	0000245 // spliceosomal complex assembly // not recorded//0000387 // spliceosomal s
NM_0093		0.0018	0.009		-1.01	1.39	1.54	1.17	<i>Tgfb1</i>	transforming growth factor, beta induced	0001525 // angiogenesis // inferred from electronic annotation//0002062 // chondrocyt
NM_0098		0.0058			-1.07	1.88	1.54	1.27	<i>Chil3//Chil4</i>	chitinase-like 3//chitinase-like 4	0000272 // polysaccharide catabolic process // inferred from electronic annotation//00
NM_0011		0.0152	0.024		-1.05	1.46	1.55	1.36	<i>Il33</i>	interleukin 33	0002686 // negative regulation of leukocyte migration // inferred from genetic interacti
NM_001313977	///				1.03	1.31	1.56	1.16	<i>Prkch</i>	protein kinase C, eta	0006468 // protein phosphorylation // not recorded//0010744 // positive regulation of i
NM_0116		0.0087	0.006		-1.65	1.30	1.57	1.11	<i>Tnc</i>	tenascin C	0001649 // osteoblast differentiation // not recorded//0007155 // cell adhesion // infer
NM_026835					-1.09	1.14	1.58	1.15	<i>Ms4a6d</i>	membrane-spanning 4-domains, subfamily A, member 6D	
NM_001159564	///				1.14	1.35	1.58	1.44	<i>Itgb6</i>	integrin beta 6	0006954 // inflammatory response // inferred from mutant phenotype//0007155 // cell
NM_0074		0.0087	0.015		-1.25	1.36	1.58	1.11	<i>Arg1</i>	arginase, liver	0000050 // urea cycle // not recorded//0001889 // liver development // inferred from e
NM_009363					-1.08	-1.01	1.59	1.12	<i>Tff2</i>	trefoil factor 2 (spasmodic protein 1)	0008284 // positive regulation of cell proliferation // inferred from genetic interaction//i
NM_0195		0.0397			1.29	1.84	1.60	1.11	<i>Cxcl14</i>	chemokine (C-X-C motif) ligand 14	0006955 // immune response // inferred from electronic annotation//0045662 // negati
NM_0011		0.0054			-1.03	1.47	1.61	1.48	<i>Eif4a-ps4//Eif4a1</i>	eukaryotic translation initiation factor 4A, pseudogene 4//eukaryotic translation initi	0006412 // translation // inferred from electronic annotation//0006413 // translational
NM_011526					-1.16	1.02	1.61	1.41	<i>Tagln</i>	transgelin	0007010 // cytoskeleton organization // inferred from mutant phenotype//0030855 // e
NM_001168525	///				1.01	-1.01	1.67	1.48	<i>Sgms1</i>	sphingomyelin synthase 1	0006629 // lipid metabolic process // inferred from electronic annotation//0006665 // s
NM_0011		0.0131			1.60	1.39	1.68	1.61	<i>Wdfy1</i>	WD repeat and FYVE domain containing 1	0034141 // positive regulation of toll-like receptor 3 signaling pathway // inferred from nr
NM_008230	///XM				-1.05	1.31	1.68	1.22	<i>Hdc</i>	histidine decarboxylase	0001692 // histamine metabolic process // not recorded//0001694 // histamine biosynt
NM_0010		0.013	#####		-1.04	1.79	1.70	1.04	<i>Timp1</i>	tissue inhibitor of metalloproteinase 1	0001775 // cell activation // not recorded//0007568 // aging // inferred from electronic
NM_0012		0.0219			1.32	1.82	1.71	1.44	<i>Pira1//Pira2//Pira6//Gm10693//Gm14</i>	paired-Ig-like receptor A1//paired-Ig-like receptor A2//paired-Ig-like receptor A6//p	0001782 // B cell homeostasis // inferred from mutant phenotype//0002250 // adaptive
NM_0010		0.0145	0.005		1.07	1.47	1.71	1.28	<i>Lrp2</i>	low density lipoprotein receptor-related protein 2	0003281 // ventricular septum development // inferred from mutant phenotype//00067
NM_0012		0.0061	0.011		1.04	1.59	1.76	1.46	<i>Fdps</i>	farnesyl diphosphate synthetase	0006629 // lipid metabolic process // inferred from electronic annotation//0006694 // s
NM_001166173	///			0.031	1.00	1.20	1.77	1.64	<i>Dmkn</i>	dermokine	0030154 // cell differentiation // inferred from electronic annotation//1903575 // corni
NM_001289462	///				1.10	1.37	1.81	1.64	<i>Mme</i>	membrane metallo endopeptidase	0001822 // kidney development // inferred from sequence or structural similarity//0001
NM_1451	#####				-1.16	2.24	1.81	1.48	<i>Chil4//Chil3</i>	chitinase-like 4//chitinase-like 3	0005975 // carbohydrate metabolic process // inferred from electronic annotation//000
NM_001166672	///				1.18	2.04	1.83	1.34	<i>Gm10693//Gm14548//Lilra6//Pira1//F</i>	predicted pseudogene 10693//predicted gene 14548//leukocyte immunoglobulin-lik	0001782 // B cell homeostasis // inferred from mutant phenotype//0002250 // adaptive
NM_0118		0.0038	0.002	0.047	-1.06	2.42	1.84	1.35	<i>Slc26a4</i>	solute carrier family 26, member 4	0006810 // transport // inferred from electronic annotation//0006821 // chloride transp
NM_1776	#####				1.92	1.41	1.96	2.12	<i>Cep104</i>	centrosomal protein 104	
NM_0012		0.0059			1.41	2.23	2.03	1.62	<i>Pira1//Pira2//Pira6//Gm10693//Gm14</i>	paired-Ig-like receptor A1//paired-Ig-like receptor A2//paired-Ig-like receptor A6//p	0001782 // B cell homeostasis // inferred from mutant phenotype//0002250 // adaptive
NM_028757	///XM				1.09	1.45	2.23	1.77	<i>Nebl</i>	nebullette	0071691 // cardiac muscle thin filament assembly // inferred from sequence or structura
NM_017474	///XM				-1.13	1.13	3.08	1.26	<i>Clca1//Clca3a1</i>	chloride channel accessory 1//chloride channel accessory 3A1	0006508 // proteolysis // inferred from electronic annotation//0006810 // transport // i
XM_011238903	///				2.54	2.61	3.75	3.71	<i>Gm37416//Gm39743//Gm40611//Gm4</i>	predicted gene, 37416//predicted gene, 39743//predicted gene, 40611//predicted	0006278 // RNA-dependent DNA replication // inferred from electronic annotation//000



**Table S5. NFKB1-dependent basal lung genes.**

Selected genes varied  $\geq 1.5$ -fold between Nfkb1-WT and Nfkb1-KO mice (positive-higher in KO, negative-lower in KO). Moderated t-test ( $p < 0.05$ ). Order by fold difference (FD) between WT and KO mice exposed to air.

RefSeq	Transcript ID	p	FD	Air	Gene Symbol	Gene Title	Gene Ontology
NM_152839		0.006	-20.028		<i>Jchain</i>	immunoglobulin joining chain	0001895 // retina homeostasis // inferred from electronic annotation//0002250 // adaptive i
		0.034	-8.807		<i>Igkv15-103</i>	immunoglobulin kappa chain variable 15-103	0006898 // receptor-mediated endocytosis // ---//0006910 // phagocytosis, recognition // ---
NM_023835//XM_011		0.044	-6.990		<i>Trim12a</i>	tripartite motif-containing 12A	0008270 // zinc ion binding // inferred from electronic annotation//0046872 // metal ion bin
NM_139142		0.009	-5.330		<i>Slc6a20a</i>	solute carrier family 6 (neurotransmitter transporter), member 21	0003333 // amino acid transmembrane transport // not recorded//0006810 // transport // i
NM_018866		0.015	-4.263		<i>Cxcl13</i>	chemokine (C-X-C motif) ligand 13	0002518 // lymphocyte chemotaxis across high endothelial venule // inferred from mutant pt
NM_001281969//NM_		0.000	-3.620		<i>Glrh</i>	glycine receptor, beta subunit	0001964 // startle response // not recorded//0001964 // startle response // inferred from se
NM_001131054//NM_		0.000	-3.506		<i>Pttg1</i>	pituitary tumor-transforming gene 1	0001558 // regulation of cell growth // not recorded//0006281 // DNA repair // inferred fror
NM_053128		0.011	-3.332		<i>Pcdhb3</i>	protocadherin beta 3	0007155 // cell adhesion // inferred from electronic annotation//0007156 // homophilic cell
NM_001146049//NM_		0.048	-3.218		<i>Htatip2</i>	HIV-1 tat interactive protein 2, homolog (human)	0001525 // angiogenesis // inferred from electronic annotation//0006915 // apoptotic proce
NM_009234		0.010	-3.214		<i>Sox11</i>	SRY (sex determining region Y)-box 11	0000122 // negative regulation of transcription from RNA polymerase II promoter // inferred
NM_001310602//XM_		0.041	-3.163		<i>Trim5</i>	tripartite motif-containing 5	0002221 // pattern recognition receptor signaling pathway // ---//0016567 // protein ubiquit
NM_001164612//NM_		0.001	-3.009		<i>Atp13a4</i>	ATPase type 13A4	0006812 // cation transport // inferred from electronic annotation//0006874 // cellular calci
NM_153405//NM_171		0.000	-2.895		<i>Rbm45</i>	RNA binding motif protein 45	0007275 // multicellular organismal development // inferred from electronic annotation//00
NM_021050//XM_006		0.009	-2.823		<i>Cftr</i>	cystic fibrosis transmembrane conductance regulator	0003254 // regulation of membrane depolarization // inferred from mutant phenotype//000
NM_009052		0.001	-2.817		<i>Bex1</i>	brain expressed gene 1	0002052 // positive regulation of neuroblast proliferation // not recorded//0007275 // multi
NM_011704//XM_006		0.003	-2.732		<i>Vnn1</i>	vanin 1	0002526 // acute inflammatory response // inferred from direct assay//0002544 // chronic i
NM_001081971		0.042	-2.693		<i>Ankrd63</i>	ankyrin repeat domain 63	
NM_010766		0.001	-2.584		<i>Marco</i>	macrophage receptor with collagenous structure	0002376 // immune system process // inferred from electronic annotation//0006897 // endc
NM_008079//XM_006		0.036	-2.581		<i>Galc</i>	galactosylceramidase	0005975 // carbohydrate metabolic process // inferred from electronic annotation//0006626
NM_001202500//XM_		0.012	-2.537		<i>Armxc4</i>	armadillo repeat containing, X-linked 4	
NM_026516		0.007	-2.444		<i>Tmem178</i>	transmembrane protein 178	0016020 // membrane // inferred from electronic annotation//0016021 // integral compone
NM_054084//XM_006		0.001	-2.372		<i>Calcb</i>	calcitonin-related polypeptide, beta	0005576 // extracellular region // inferred from electronic annotation
NM_029569//XM_006		0.045	-2.360		<i>Asb5</i>	ankyrin repeat and SOCs box-containing 5	0016567 // protein ubiquitination // inferred from electronic annotation//0035556 // intrac
NM_009364//XM_006		0.024	-2.345		<i>Tfpi2</i>	tissue factor pathway inhibitor 2	0007596 // blood coagulation // inferred from electronic annotation//0007599 // hemostasi
NM_008730		0.006	-2.300		<i>Nptx1</i>	neuronal pentraxin 1	0006839 // mitochondrial transport // not recorded//0035865 // cellular response to potassi
NM_153389//NR_003		0.001	-2.291		<i>Atp10d</i>	ATPase, class V, type 10D	0006810 // transport // inferred from electronic annotation//0006812 // cation transport //
NM_022315//XM_006		0.010	-2.287		<i>Smoc2</i>	SPARC related modular calcium binding 2	0007165 // signal transduction // inferred from electronic annotation//0010811 // positive r
NM_053169//XM_006		0.017	-2.262		<i>Trim16</i>	tripartite motif-containing 16	0043966 // histone H3 acetylation // not recorded//0043967 // histone H4 acetylation // not
NM_001111274//NM_		0.008	-2.242		<i>Igf1</i>	insulin-like growth factor 1	0001649 // osteoblast differentiation // inferred from expression pattern//0001775 // cell ac
NM_010140		0.039	-2.202		<i>Epha3</i>	Eph receptor A3	0003197 // endocardial cushion development // inferred from mutant phenotype//0006468
NM_178931//XM_006		0.006	-2.191		<i>Tnfrsf14</i>	tumor necrosis factor receptor superfamily, member 14 (herpesv	0002741 // positive regulation of cytokine secretion involved in immune response // inferred
NM_023186		0.004	-2.189		<i>Chia1</i>	chitinase, acidic 1	0000272 // polysaccharide catabolic process // inferred from electronic annotation//000237
NM_001310659//NM_		0.028	-2.144		<i>Igfbp2</i>	insulin-like growth factor binding protein 2	0001558 // regulation of cell growth // inferred from electronic annotation//0007165 // sign
NM_001164210//NM_		0.002	-2.142		<i>Sptssb</i>	serine palmitoyltransferase, small subunit B	0006629 // lipid metabolic process // inferred from electronic annotation//0006665 // sphin
NM_001289755//NM_		0.004	-2.131		<i>Apoc3</i>	apolipoprotein C-III	0006629 // lipid metabolic process // inferred from electronic annotation//0006641 // trigly
NM_175473//XM_006		0.014	-2.131		<i>Fras1</i>	Fraser syndrome 1 homolog (human)	0002009 // morphogenesis of an epithelium // inferred from mutant phenotype//0003338 //
NM_001293800//NM_		0.048	-2.104		<i>Ocel1</i>	occludin/ELL domain containing 1	
NR_035452		0.002	-2.096		<i>Mir1931</i>	microRNA 1931	
NM_021456		0.007	-2.084		<i>Ces1g</i>	carboxylesterase 1G	0008152 // metabolic process // inferred from electronic annotation//0010468 // regulation
NM_017399		0.016	-2.080		<i>Fabp1</i>	fatty acid binding protein 1, liver	0002230 // positive regulation of defense response to virus by host // not recorded//000681
NM_025748//XM_011		0.045	-2.075		<i>Adat2</i>	adenosine deaminase, tRNA-specific 2	0002100 // tRNA wobble adenosine to inosine editing // inferred from electronic annotation//
NM_001302531//NM_		0.031	-2.029		<i>Esr1</i>	estrogen receptor 1 (alpha)	0001547 // antral ovarian follicle growth // inferred from mutant phenotype//0002064 // ep
NR_015524		0.010	-2.017		<i>Cep83os</i>	centrosomal protein 83, opposite strand	
NM_008689//XM_006		0.000	-2.012		<i>Nfkb1</i>	nuclear factor of kappa light polypeptide gene enhancer in B cells	0000122 // negative regulation of transcription from RNA polymerase II promoter // not recoi
NM_013546//XM_011		0.017	-1.970		<i>Hebp1</i>	heme binding protein 1	0042168 // heme metabolic process // inferred by curator
NM_001081342//NM_		0.042	-1.960		<i>Adgrd1</i>	adhesion G protein-coupled receptor D1	0007166 // G cell surface receptor signaling pathway // inferred from electronic annotation//0
NR_015487//NR_0276		0.000	-1.956		<i>A930005H10Rik</i>	RIKEN cDNA A930005H10 gene	
NM_001252627//NM_		0.007	-1.955		<i>Cdh16</i>	cadherin 16	0007155 // cell adhesion // inferred from electronic annotation//0007156 // homophilic cell
NM_001081328		0.021	-1.953		<i>Chsy3</i>	chondroitin sulfate synthase 3	0008152 // metabolic process // inferred from electronic annotation
NM_001159401//NM_		0.009	-1.953		<i>Upp1</i>	uridine phosphorylase 1	0006218 // uridine catabolic process // inferred from direct assay//0006220 // pyrimidine nu
NM_177303//XM_011		0.010	-1.952		<i>Lrrn4</i>	leucine rich repeat neuronal 4	0007616 // long-term memory // inferred from mutant phenotype//0008542 // visual learni

RefSeq Transcript ID	p	FD Air	Gene Symbol	Gene Title	Gene Ontology
NM_011606	0.005	-1.923	<b>Clec3b</b>	C-type lectin domain family 3, member b	0001501 // skeletal system development // inferred from mutant phenotype//0001503 // os
NM_172757	0.027	-1.897	<b>Heatr3</b>	HEAT repeat containing 3	
NM_001164733//NM_001164733	0.010	-1.890	<b>Mpp6</b>	membrane protein, palmitoylated 6 (MAGUK p55 subfamily mem	0046037 // GMP metabolic process // inferred from sequence or structural similarity//00467
NM_181420//XM_0001113560//NM_001113560	0.029	-1.875	<b>Fn3krp</b>	fructosamine 3 kinase related protein	0016310 // phosphorylation // not recorded
NM_001113560//NM_001113560	0.001	-1.869	<b>Glo1</b>	glyoxalase 1	0005975 // carbohydrate metabolic process // not recorded//0006357 // regulation of trans
NM_172471//XM_0001113560//NM_001113560	0.005	-1.845	<b>Itih5</b>	inter-alpha (globulin) inhibitor H5	0010466 // negative regulation of peptidase activity // inferred from electronic annotation//
NM_175309	0.013	-1.830	<b>Upk3b</b>	uropodin 3B	0010629 // negative regulation of gene expression // not recorded//0046325 // negative reg
NM_172399//XM_0001113560//NM_001113560	0.032	-1.830	<b>Ndnf</b>	neuron-derived neurotrophic factor	0001525 // angiogenesis // not recorded//0001764 // neuron migration // not recorded//0
XR_879970//XR_8799	0.000	-1.806	<b>Tnfsf13os</b>	tumor necrosis factor (ligand) superfamily, member 13, opposite strand	
NM_153127	0.002	-1.803	<b>Mmrrn2</b>	multimerin 2	0001525 // angiogenesis // inferred from electronic annotation//0030948 // negative regula
NM_001109988//NM_001109988	0.002	-1.791	<b>Nrep</b>	neuronal regeneration related protein	0017015 // regulation of transforming growth factor beta receptor signaling pathway // inferr
NM_001166377//NM_001166377	0.023	-1.771	<b>Armxc1</b>	armadillo repeat containing, X-linked 1	0016020 // membrane // inferred from electronic annotation//0016021 // integral compone
NM_001110850//NM_001110850	0.045	-1.770	<b>Creml</b>	cAMP responsive element modulator	0006006 // glucose metabolic process // inferred from electronic annotation//0006351 // tra
NM_010291	0.014	-1.759	<b>Gjb5</b>	gap junction protein, beta 5	0007154 // cell communication // inferred from electronic annotation//0060707 // trophobl
NM_009022	0.046	-1.736	<b>Aldh1a2</b>	aldehyde dehydrogenase family 1, subfamily A2	0001523 // retinoid metabolic process // traceable author statement//0001568 // blood ves
NM_010809	0.000	-1.730	<b>Mmp3</b>	matrix metalloproteinase 3	0006508 // proteolysis // inferred from mutant phenotype//0006508 // proteolysis // not re
NM_008409	0.012	-1.722	<b>Itm2a</b>	integral membrane protein 2A	0005515 // protein binding // inferred from electronic annotation
NM_001198565//NM_001198565	0.014	-1.712	<b>Sulf1</b>	sulfatase 1	0001502 // cartilage condensation // inferred from sequence or structural similarity//000182
NM_001083917//NM_001083917	0.000	-1.710	<b>Scn3b</b>	sodium channel, voltage-gated, type III, beta	0006810 // transport // inferred from electronic annotation//0006811 // ion transport // inf
NM_007562//XM_001111111//NM_001111111	0.018	-1.708	<b>Bnc1</b>	basonuclin 1	0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 //
NM_007984	0.001	-1.705	<b>Fscn1</b>	fascin homolog 1, actin bundling protein (Strongylocentrotus purpuratus)	0007015 // actin filament organization // inferred from electronic annotation//0007043 // ce
NM_001111111//XM_001111111	0.027	-1.700	<b>Atg16l2</b>	autophagy related 16-like 2 (S. cerevisiae)	0000045 // autophagosome assembly // not recorded//0006810 // transport // inferred from
NM_138683//XM_0001025364//NM_001025364	0.029	-1.692	<b>Rspo1</b>	R-spondin 1	0001934 // positive regulation of protein phosphorylation // not recorded//0002090 // regul
NM_001025364//NM_001025364	0.010	-1.686	<b>Rtn2</b>	reticulon 2 (Z-band associated protein)	0046324 // regulation of glucose import // inferred from mutant phenotype//0065002 // int
NM_172793	0.034	-1.684	<b>Btnl9</b>	butyrophilin-like 9	0016020 // membrane // inferred from electronic annotation//0016021 // integral compone
NM_001111051//NM_001111051	0.014	-1.682	<b>Dclk1</b>	doublecortin-like kinase 1	0001764 // neuron migration // inferred from genetic interaction//0006468 // protein phosph
NM_001025564//NR_001025564	0.010	-1.680	<b>Gm15698</b>	transcription elongation factor B (SIII), polypeptide 2 pseudogene	0006368 // transcription elongation from RNA polymerase II promoter // not recorded
NM_001164528//XM_000134102//XM_0001276446//NM_001276446	0.020	-1.679	<b>Ildr2</b>	immunoglobulin-like domain containing receptor 2	0009749 // response to glucose // inferred from mutant phenotype//0030073 // insulin secr
NM_134102//XM_0001276446//NM_001276446	0.000	-1.676	<b>Pla1a</b>	phospholipase A1 member A	0006629 // lipid metabolic process // inferred from electronic annotation//0016042 // lipid c
NM_001276446//NM_001276446	0.001	-1.663	<b>Alad</b>	aminolevulinatase, delta-, dehydratase	0001666 // response to hypoxia // inferred from electronic annotation//0006779 // porphyri
NM_020052	0.043	-1.658	<b>Scube2</b>	signal peptide, CUB domain, EGF-like 2	0005509 // calcium ion binding // inferred from electronic annotation//0042802 // identical
NM_027391	0.045	-1.655	<b>Iyd</b>	iodotyrosine deiodinase	0055114 // oxidation-reduction process // inferred from electronic annotation
NM_001166173//NM_001166173	0.037	-1.654	<b>Dmkn</b>	dermokine	0030154 // cell differentiation // inferred from electronic annotation//1903575 // cornified e
NM_011758	0.012	-1.651	<b>Zfp39</b>	zinc finger protein 39	0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 //
NM_001205369//NM_001205369	0.033	-1.645	<b>Casc4</b>	cancer susceptibility candidate 4	0005794 // Golgi apparatus // not recorded//0016020 // membrane // inferred from electror
NM_013813//XM_0001026864//NM_001026864	0.008	-1.634	<b>Epb41b</b>	erythrocyte membrane protein band 4.1 like 3	0001558 // regulation of cell growth // inferred from electronic annotation//0002175 // prot
NM_026864	0.028	-1.634	<b>Rasl11a</b>	RAS-like, family 11, member A	0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 //
NM_028130//XM_0001029360//NM_001029360	0.017	-1.631	<b>Zfp157</b>	zinc finger protein 157	0006355 // regulation of transcription, DNA-templated // inferred from electronic annotation
NM_029360	0.020	-1.626	<b>Tm4sf5</b>	transmembrane 4 superfamily member 5	0016020 // membrane // inferred from electronic annotation//0016021 // integral compone
NM_175140//XM_0001025949//XM_00010516	0.045	-1.624	<b>Chst8</b>	carbohydrate (N-acetylgalactosamine 4-O) sulfotransferase 8	0005975 // carbohydrate metabolic process // inferred from electronic annotation//000679C
NM_025949//XM_00010516	0.040	-1.624	<b>Rps6ka6</b>	ribosomal protein S6 kinase polypeptide 6	0006417 // regulation of translation // not recorded//0006468 // protein phosphorylation //
NM_010516	0.001	-1.620	<b>Cyr61</b>	cysteine rich protein 61	0001558 // regulation of cell growth // inferred from electronic annotation//0001649 // oste
NM_008083	0.042	-1.619	<b>Gap43</b>	growth associated protein 43	0007275 // multicellular organismal development // inferred from electronic annotation//00
NM_175666	0.002	-1.617	<b>Hist2h2bb</b>	histone cluster 2, H2bb	0006334 // nucleosome assembly // not recorded
NM_001166364//NM_001166364	0.010	-1.612	<b>Fam219b</b>	family with sequence similarity 219, member B	
NM_001024720//XM_001013476	0.007	-1.607	<b>Hmgn1</b>	hemicentin 1	0005509 // calcium ion binding // inferred from electronic annotation
NM_013476	0.010	-1.602	<b>Ar</b>	androgen receptor	0001701 // in utero embryonic development // inferred from mutant phenotype//0003073 /
NM_001313978//NM_001313978	0.019	-1.596	<b>Colec11</b>	collectin sub-family member 11	0007275 // multicellular organismal development // inferred from electronic annotation//00
NM_001017525//NM_001017525	0.010	-1.596	<b>Btbdl1</b>	BTB (POZ) domain containing 11	0006395 // SMAD protein signal transduction // inferred from direct assay
NM_001039536//NM_001039536	0.008	-1.593	<b>Pigl</b>	phosphatidylinositol glycan anchor biosynthesis, class L	0006506 // GPI anchor biosynthetic process // not recorded
NM_028095//XM_0001025208//NM_001025208	0.004	-1.589	<b>Mettl10</b>	methyltransferase like 10	0032259 // methylation // inferred from electronic annotation
NM_001025208//NM_001025208	0.026	-1.584	<b>Gm38417//H2-BI//H2-D4//H2-T3-II</b>	predicted gene, 38417//histocompatibility 2, blastocyst//histoc	0001916 // positive regulation of T cell mediated cytotoxicity // inferred from direct assay//C
NM_001136077//NM_001136077	0.037	-1.584	<b>Enpp2</b>	ectonucleotide pyrophosphatase/phosphodiesterase 2	0001953 // negative regulation of cell-matrix adhesion // not recorded//0006629 // lipid me
NM_013912	0.002	-1.584	<b>Apln</b>	apelin	0002026 // regulation of the force of heart contraction // not recorded//0007165 // signal tr

RefSeq Transcript ID	p	FD Air	Gene Symbol	Gene Title	Gene Ontology
NM_001136260//NM	0.033	-1.580	<b>Slc4a4</b>	solute carrier family 4 (anion exchanger), member 4	0006810 // transport // inferred from electronic annotation//0006811 // ion transport // inf
NM_001141933//NM	0.024	-1.574	<b>Nkain4</b>	Na+/K+ transporting ATPase interacting 4	0002028 // regulation of sodium ion transport // --
NM_011985//XM_00	0.005	-1.574	<b>Mmp23</b>	matrix metalloproteinase 23	0000003 // reproduction // inferred from sequence or structural similarity//0000003 // repr
NM_001081324//XM	0.030	-1.571	<b>Neto2</b>	neuropilin (NRP) and tolloid (TLL)-like 2	2000312 // regulation of kainate selective glutamate receptor activity // inferred from electro
NM_007646	0.011	-1.567	<b>Cd38</b>	CD38 antigen	0001666 // response to hypoxia // not recorded//0007204 // positive regulation of cytosolic
NM_024273//XM_00	0.001	-1.565	<b>Timmdc1</b>	translocase of inner mitochondrial membrane domain containing	0005515 // protein binding // inferred from electronic annotation
NM_009738//XM_01	0.019	-1.562	<b>Bche</b>	butyrylcholinesterase	0006581 // acetylcholine catabolic process // ---//0007268 // synaptic transmission // ---//0
NM_028097//XM_00	0.038	-1.551	<b>Tmem68</b>	transmembrane protein 68	0008152 // metabolic process // inferred from electronic annotation
NM_170778//XM_01	0.031	-1.547	<b>Dpyd</b>	dihydropyrimidine dehydrogenase	0006145 // purine nucleobase catabolic process // not recorded//0006208 // pyrimidine nuc
NM_001308535//NM	0.003	-1.538	<b>Il2rg</b>	interleukin 2 receptor, gamma chain	0010468 // regulation of gene expression // inferred from mutant phenotype//0010628 // p
NM_001165939//NM	0.011	-1.535	<b>Tshb</b>	thyroid stimulating hormone, beta subunit	0033189 // response to vitamin A // inferred from electronic annotation//0043627 // respon
NM_001083912//NM	0.025	-1.530	<b>Plekhg2</b>	pleckstrin homology domain containing, family G (with RhoGef do	0035023 // regulation of Rho protein signal transduction // inferred from electronic annotatio
NM_009778//XM_01	0.004	-1.530	<b>C3</b>	complement component 3	0001798 // positive regulation of type Ila hypersensitivity // inferred from mutant phenotype,
NM_011352//XM_00	0.015	-1.528	<b>Sema7a</b>	sema domain, immunoglobulin domain (Ig), and GPI membrane a	0001649 // osteoblast differentiation // not recorded//0001755 // neural crest cell migratio
NM_018874	0.013	-1.528	<b>Pnliprp1</b>	pancreatic lipase related protein 1	0006629 // lipid metabolic process // inferred from electronic annotation
NM_001310635//NM	0.015	-1.527	<b>Crispld2</b>	cysteine-rich secretory protein LCCL domain containing 2	0030198 // extracellular matrix organization // inferred from direct assay//0030324 // lung c
NM_008727//XM_00	0.001	-1.524	<b>Npr1</b>	natriuretic peptide receptor 1	0006182 // cGMP biosynthetic process // not recorded//0006468 // protein phosphorylation
NM_024472	0.005	-1.523	<b>Cptp</b>	ceramide-1-phosphate transfer protein	0006810 // transport // inferred from electronic annotation//0006869 // lipid transport // in
NM_199446//XM_00	0.010	-1.521	<b>Phkb</b>	phosphorylase kinase beta	0005975 // carbohydrate metabolic process // inferred from electronic annotation//000597
NM_001252563//NM	0.029	-1.519	<b>Matn4</b>	matrilin 4	0048678 // response to axon injury // inferred from direct assay
NM_001033416//XM	0.036	-1.516	<b>Gal3st4</b>	galactose-3-O-sulfotransferase 4	0009058 // biosynthetic process // inferred from electronic annotation//0009101 // glycoprc
NM_021344//XR_387	0.026	-1.515	<b>Tesc</b>	tescalcin	0006810 // transport // inferred from electronic annotation//0006883 // cellular sodium ion
NM_001289780//NM	0.005	-1.514	<b>Pus7</b>	pseudouridylyl synthase 7 homolog (S. cerevisiae)	0001522 // pseudouridine synthesis // inferred from electronic annotation//0001522 // pse
NM_001290457//NM	0.002	-1.512	<b>Relb</b>	avian reticuloendotheliosis viral (v-rel) oncogene related B	0000122 // negative regulation of transcription from RNA polymerase II promoter // not recoi
NM_011823//XM_00	0.036	-1.510	<b>Gpr34</b>	G protein-coupled receptor 34	0007165 // signal transduction // inferred from electronic annotation//0007186 // G-protein
NM_001039201//NM	0.024	-1.510	<b>Hdhd2</b>	haloacid dehalogenase-like hydrolase domain containing 2	0005515 // protein binding // inferred from electronic annotation//0019899 // enzyme bindi
NM_001025373	0.038	-1.507	<b>Zfp943</b>	zinc finger prtoein 943	0006355 // regulation of transcription, DNA-templated // inferred from electronic annotation
NM_008939	0.007	-1.505	<b>Prss12</b>	protease, serine 12 neurotrypsin (motopsin)	0006508 // proteolysis // inferred from direct assay//0006508 // proteolysis // inferred from
NM_0111075//XM_00	0.024	-1.499	<b>Abcb1b</b>	ATP-binding cassette, sub-family B (MDR/TAP), member 1B	0006810 // transport // not recorded//0006855 // drug transmembrane transport // not rec
NM_172947//XM_00	0.002	-1.497	<b>Lsm12</b>	LSM12 homolog (S. cerevisiae)	0000733 // DNA strand renaturation // not recorded//0006338 // chromatin remodeling // r
NM_001290708//NM	0.046	-1.496	<b>Smarca1</b>	SWI/SNF related, matrix associated, actin dependent regulator of	0006355 // regulation of transcription, DNA-templated // inferred from electronic annotation
NM_001008549//XM	0.036	-1.495	<b>Zfp658</b>	zinc finger protein 658	0006810 // transport // inferred from electronic annotation//0006886 // intracellular protein
NM_173781//XM_00	0.028	-1.495	<b>Rab6b</b>	RAB6B, member RAS oncogene family	0055114 // oxidation-reduction process // inferred from electronic annotation
NM_001013785//XR_	0.001	-1.492	<b>Akr1c19</b>	aldo-keto reductase family 1, member C19	0006898 // receptor-mediated endocytosis // ---//0006898 // receptor-mediated endocytosi
NM_138672//XM_00	0.028	-1.489	<b>Stab1</b>	stabilin 1	0006810 // transport // inferred from electronic annotation//0006811 // ion transport // inf
NM_018732//XM_00	0.019	-1.488	<b>Scn3a</b>	sodium channel, voltage-gated, type III, alpha	0006810 // transport // inferred from electronic annotation//0006835 // dicarboxylic acid tr
NM_009199	0.021	-1.488	<b>Slc1a1</b>	solute carrier family 1 (neuronal/epithelial high affinity glutamate	0046579 // positive regulation of Ras protein signal transduction // not recorded
NM_001168505//NM	0.006	-1.486	<b>Shoc2</b>	soc-2 (suppressor of clear) homolog (C. elegans)	0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 /,
NM_013705	0.005	-1.486	<b>Zfp30</b>	zinc finger protein 30	0010951 // negative regulation of endopeptidase activity // inferred from electronic annotati
NM_001243008//NM	0.019	-1.485	<b>Col6a3</b>	collagen, type VI, alpha 3	0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 /,
NM_001110100//NM	0.049	-1.485	<b>Banp</b>	BTG3 associated nuclear protein	0006508 // proteolysis // inferred from electronic annotation
NM_152812//XM_01	0.038	-1.484	<b>Otud6b</b>	OTU domain containing 6B	0006355 // regulation of transcription, DNA-templated // not recorded//0007409 // axonog
NM_001163847//NM	0.042	-1.480	<b>Ntn3//Tbc1d24</b>	netrin 3//TBC1 domain family, member 24	0001702 // gastrulation with mouth forming second // non-traceable author statement//000
NM_001037842//NM	0.007	-1.480	<b>Cml3//Gm1128//Gm4477</b>	camel-like 3//predicted gene 1128//predicted gene 4477	0006810 // transport // inferred from electronic annotation//0008643 // carbohydrate trans
NM_001033633	0.048	-1.480	<b>Slc2a13</b>	solute carrier family 2 (facilitated glucose transporter), member 1	0007520 // myoblast fusion // inferred from direct assay//0007520 // myoblast fusion // infe
NM_023320//XM_00	0.006	-1.480	<b>Plekho1</b>	pleckstrin homology domain containing, family O member 1	0000122 // negative regulation of transcription from RNA polymerase II promoter // inferred
NM_011221	0.005	-1.477	<b>Purb</b>	purine rich element binding protein B	0006508 // proteolysis // inferred from electronic annotation//0007229 // integrin-mediatec
NM_001081401//NM	0.018	-1.477	<b>Adamts3</b>	a disintegrin-like and metalloproteinase (reprolysin type) with thr	0008535 // respiratory chain complex IV assembly // not recorded//0015031 // protein trans
NM_001033310//NM	0.022	-1.474	<b>Cox18</b>	cytochrome c oxidase assembly protein 18	0008152 // metabolic process // inferred from electronic annotation
NM_024257	0.002	-1.472	<b>Hdhd3</b>	haloacid dehalogenase-like hydrolase domain containing 3	0006810 // transport // inferred from electronic annotation//0006811 // ion transport // inf
NM_134160//XM_00	0.004	-1.470	<b>Mcoln3</b>	mucoilin 3	0051443 // positive regulation of ubiquitin-protein transferase activity // not recorded
NM_001042592//NM	0.015	-1.469	<b>Arrdc4</b>	arrestin domain containing 4	0001764 // neuron migration // not recorded//0003407 // neural retina development // infe
NM_001253754//NM	0.029	-1.469	<b>Gpm6a</b>	glycoprotein m6a	0006508 // proteolysis // inferred from direct assay//0008152 // metabolic process // inferre
NM_028279//XM_00	0.009	-1.468	<b>Naalad2</b>	N-acetylated alpha-linked acidic dipeptidase 2	

RefSeq Transcript ID	p	FD Air	Gene Symbol	Gene Title	Gene Ontology
NM_025864	0.006	-1.467	<b>Tmem206</b>	transmembrane protein 206	0009986 // cell surface // not recorded///0016020 // membrane // inferred from electronic annotation
NM_029658	0.008	-1.467	<b>Fam101b</b>	family with sequence similarity 101, member B	0001837 // epithelial to mesenchymal transition // inferred from genetic interaction///00300
NM_001205095///XM_001313897///NM_133972///XM_011	0.014	-1.467	<b>Gm4944</b>	predicted gene 4944	0006355 // regulation of transcription, DNA-templated // not recorded
NM_133972///XM_011	0.008	-1.466	<b>Lta4h</b>	leukotriene A4 hydrolase	0006508 // proteolysis // inferred from electronic annotation///0006691 // leukotriene metal
NM_139063///XM_006	0.044	-1.466	<b>Armc6</b>	armadillo repeat containing 6	0002244 // hematopoietic progenitor cell differentiation // inferred from genetic interaction
NM_026062	0.005	-1.463	<b>Bloc1s5</b>	biogenesis of lysosomal organelles complex-1, subunit 5, muted	0008089 // anterograde axon cargo transport // inferred from mutant phenotype///0016192
NM_019472///XM_006	0.021	-1.462	<b>Fam69a</b>	family with sequence similarity 69, member A	0005515 // protein binding // inferred from physical interaction
NM_026504///XR_387	0.012	-1.461	<b>Myo10</b>	myosin X	0006810 // transport // inferred from electronic annotation///0007165 // signal transduction
NR_045175	0.017	-1.460	<b>Coq5</b>	coenzyme Q5 homolog, methyltransferase (yeast)	0006744 // ubiquinone biosynthetic process // inferred from electronic annotation///0032251
NM_146106///XM_011	0.015	-1.459	<b>Smc2os</b>	structural maintenance of chromosomes 2, opposite strand	
NM_026796///XM_006	0.041	-1.457	<b>Lyplal1</b>	lysophospholipase-like 1	0002084 // protein depalmitoylation // inferred from mutant phenotype///0042997 // negative regulation of transcription from RNA polymerase II promoter // not recorded
NM_008369///XM_006	0.030	-1.457	<b>Smyd2</b>	SET and MYND domain containing 2	0019221 // cytokine-mediated signaling pathway // inferred from electronic annotation
NM_001159564///NM_029494///XM_006	0.010	-1.455	<b>Ii3ra</b>	interleukin 3 receptor, alpha chain	0006954 // inflammatory response // inferred from mutant phenotype///0007155 // cell adhesion
NM_176952///XM_006	0.034	-1.455	<b>Itgb6</b>	integrin beta 6	0006886 // intracellular protein transport // not recorded///0007030 // Golgi organization //
NM_023245	0.015	-1.452	<b>Rab30</b>	RAB30, member RAS oncogene family	0008033 // tRNA processing // inferred from electronic annotation///0008152 // metabolic process
NR_033626	0.033	-1.450	<b>6430573F11Rik</b>	RIKEN cDNA 6430573F11 gene	0008360 // regulation of cell shape // inferred from electronic annotation
NM_001289428///NM_008184///XM_006	0.003	-1.450	<b>Palmd</b>	palmdelphin	0006810 // transport // inferred from electronic annotation///0006811 // ion transport // inferred from mutant phenotype///0002250 // adaptive immune response
NM_008184///XM_006	0.005	1.451	<b>1810010D01Rik</b>	RIKEN cDNA 1810010D01 gene	0001782 // B cell homeostasis // inferred from mutant phenotype///0002250 // adaptive immune response
NM_029152	0.005	1.452	<b>Pira1///Pira2///Pira6///Gm10693///Gm10694</b>	paired-Ig-like receptor A1///paired-Ig-like receptor A2///paired-Ig-like receptor A3	0008152 // metabolic process // inferred from electronic annotation
NM_008030	0.016	1.454	<b>Gstm6</b>	glutathione S-transferase, mu 6	0005509 // calcium ion binding // inferred from electronic annotation
NM_001313712///NM_001040005///XM_153598	0.010	1.462	<b>Fmo3</b>	flavin containing monooxygenase 3	0017144 // drug metabolic process // not recorded///0055114 // oxidation-reduction process
NM_001040005///XM_153598	0.001	1.467	<b>Sp100</b>	nuclear antigen Sp100	0000723 // telomere maintenance // inferred from sequence or structural similarity///000663
NM_001037138///NM_001161667///NM_001002898///NM_0300098///XM_006	0.003	1.469	<b>Rnf213</b>	ring finger protein 213	0008152 // metabolic process // inferred from electronic annotation///0016567 // protein ubiquitination
NM_001161667///NM_001002898///NM_0300098///XM_006	0.006	1.469	<b>Ugt2b34</b>	UDP glucuronosyltransferase 2 family, polypeptide B34	0008152 // metabolic process // inferred from electronic annotation///0009813 // flavonoid biosynthesis
NM_001134399///NM_001161775///NM_011452	0.015	1.471	<b>Cd300lb</b>	CD300 antigen like family member B	0002376 // immune system process // inferred from electronic annotation///0002446 // neutrophil chemotaxis
NM_001161775///NM_011452	0.011	1.472	<b>Acox2</b>	acyl-Coenzyme A oxidase 2, branched chain	0006629 // lipid metabolic process // inferred from electronic annotation///0006631 // fatty acid oxidation
NM_001002898///NM_0300098///XM_006	0.003	1.474	<b>Sirpb1a///Sirpb1b</b>	signal-regulatory protein beta 1-like///signal-regulatory protein beta 1-like	0035556 // intracellular signal transduction // inferred from direct assay///0050766 // positive regulation of transcription from RNA polymerase II promoter
NM_001134399///NM_001161775///NM_011452	0.025	1.481	<b>Rnase6</b>	ribonuclease, RNase A family, 6	0008152 // metabolic process // inferred from electronic annotation///0009305 // nucleic acid metabolic process
NM_001134399///NM_001161775///NM_011452	0.009	1.483	<b>Megf11</b>	multiple EGF-like-domains 11	0010842 // retina layer formation // inferred from mutant phenotype///0034109 // homotypic cell-cell adhesion
NM_001161775///NM_011452	0.012	1.483	<b>Myh11</b>	myosin, heavy polypeptide 11, smooth muscle	0006939 // smooth muscle contraction // inferred from direct assay///0006939 // smooth muscle contraction
NM_008630	0.002	1.487	<b>Serpinh9b</b>	serine (or cysteine) peptidase inhibitor, clade B, member 9b	0010951 // negative regulation of endopeptidase activity // not recorded///0019835 // cytolysis
NM_001205313///NM_001113468///NR_001313970///NM_010734	0.006	1.487	<b>Stat1</b>	signal transducer and activator of transcription 1	0006882 // cellular zinc ion homeostasis // inferred from mutant phenotype///0007263 // nitric oxide production
NM_001113468///NR_001313970///NM_010734	0.000	1.487	<b>Stat1</b>	signal transducer and activator of transcription 1	0000122 // negative regulation of transcription from RNA polymerase II promoter // inferred from mutant phenotype///0007186 // G-protein coupled receptor signaling pathway // inferred from electronic annotation
NM_001113468///NR_001313970///NM_010734	0.002	1.489	<b>Vmn2r29</b>	vomer nasal 2, receptor 29	0007186 // G-protein coupled receptor signaling pathway // inferred from electronic annotation
NM_001313970///NM_010734	0.025	1.490	<b>Ppp1r1b</b>	protein phosphatase 1, regulatory (inhibitor) subunit 1B	0001975 // response to amphetamine // inferred from genetic interaction///0006351 // transcription
NM_001164289///NM_001103156///NM_009999	0.004	1.490	<b>Lst1</b>	leukocyte specific transcript 1	0000902 // cell morphogenesis // inferred from electronic annotation///0002376 // immune response
NM_001164289///NM_001103156///NM_009999	0.000	1.490	<b>Phf11c///Phf11d</b>	PHD finger protein 11C///PHD finger protein 11D	0006351 // transcription, DNA-templated // inferred from electronic annotation///0006355 // transcription
NM_001103156///NM_009999	0.001	1.496	<b>Steap2</b>	six transmembrane epithelial antigen of prostate 2	0006810 // transport // inferred from electronic annotation///0006811 // ion transport // inferred from mutant phenotype///0008202 // steroid metabolic process // not recorded///0008202 // steroid metabolic process
NM_001081029///XR_016681///XM_006	0.016	1.498	<b>Cyp2b10</b>	cytochrome P450, family 2, subfamily b, polypeptide 10	0006805 // xenobiotic metabolic process // not recorded///0008202 // steroid metabolic process
NM_001081029///XR_016681///XM_006	0.000	1.501	<b>Tmem243///Gm31539</b>	transmembrane protein 243, mitochondrial///predicted gene, 31	0016020 // membrane // inferred from electronic annotation///0016021 // integral component of membrane
NM_016681///XM_006	0.029	1.503	<b>Chek2</b>	checkpoint kinase 2	0000077 // DNA damage checkpoint // not recorded///0000086 // G2/M transition of mitotic cell cycle
NM_001291892///NM_001291892///NM_007440///XM_011	0.037	1.503	<b>Lilr4b///Lilrb4a</b>	leukocyte immunoglobulin-like receptor, subfamily B, member 4E	0002250 // adaptive immune response // inferred from electronic annotation///0002376 // interleukin-12 production
NM_001291892///NM_007440///XM_011	0.037	1.503	<b>Lilr4b///Lilrb4a</b>	leukocyte immunoglobulin-like receptor, subfamily B, member 4E	0002250 // adaptive immune response // inferred from electronic annotation///0002376 // interleukin-12 production
NM_029309	0.002	1.504	<b>Alox12</b>	arachidonate 12-lipoxygenase	0006629 // lipid metabolic process // inferred from electronic annotation///0006631 // fatty acid oxidation
NM_001168469///NM_010745	0.047	1.505	<b>Morn5</b>	MORN repeat containing 5	
NM_001168469///NM_010745	0.013	1.506	<b>Ube2m</b>	ubiquitin-conjugating enzyme E2M	0006464 // cellular protein modification process // not recorded///0016567 // protein ubiquitination
NM_172796///XM_006	0.032	1.509	<b>Ly86</b>	lymphocyte antigen 86	0002376 // immune system process // inferred from electronic annotation///0006954 // inflammation
NM_001081957///XM_010185	0.001	1.510	<b>Slf9</b>	schlafen 9	0051607 // defense response to virus // inferred from electronic annotation///2000134 // negative regulation of transcription from RNA polymerase II promoter
NM_001081957///XM_010185	0.049	1.510	<b>Wfdc17</b>	WAP four-disulfide core domain protein 18-like///WAP four-disulfide core domain protein 18-like	0010466 // negative regulation of peptidase activity // inferred from electronic annotation///
NM_001160386///XM_008148	0.009	1.514	<b>Fcer1g</b>	Fc receptor, IgE, high affinity I, gamma polypeptide	0001798 // positive regulation of type I hypersensitivity // inferred from mutant phenotype,
NM_001160386///XM_008148	0.026	1.516	<b>Dnah7b</b>	dynein, axonemal, heavy chain 7B	0003341 // cilium movement // inferred from electronic annotation///0007018 // microtubule cytoskeleton organization
NM_001033444///XM_0005175	0.001	1.520	<b>Gp5</b>	glycoprotein 5 (platelet)	0007160 // cell-matrix adhesion // inferred from mutant phenotype///0007409 // axonogenesis
NM_001033444///XM_0005175	0.005	1.530	<b>Capn13</b>	calpain 13	0006508 // proteolysis // not recorded

RefSeq Transcript ID	p	FD Air	Gene Symbol	Gene Title	Gene Ontology
NM_013478	0.012	1.533	<b>Azgp1</b>	alpha-2-glycoprotein 1, zinc	0001580 // detection of chemical stimulus involved in sensory perception of bitter taste // no
NM_133365//XM_006	0.005	1.535	<b>Dnah5</b>	dynein, axonemal, heavy chain 5	0003341 // cilium movement // inferred from mutant phenotype//0003341 // cilium moverr
NM_022430	0.027	1.536	<b>Ms4a8a</b>	membrane-spanning 4-domains, subfamily A, member 8A	0016020 // membrane // inferred from electronic annotation//0016021 // integral compone
NM_023124//NM_20:	0.017	1.540	<b>H2-Q6//H2-Q8//H2-Q4</b>	histocompatibility 2, Q region locus 6//histocompatibility 2, Q re	0002474 // antigen processing and presentation of peptide antigen via MHC class I // not recc
NM_001001892//NM:	0.013	1.543	<b>H2-D1//H2-K1//H2-L//H2-Q2//H2</b>	histocompatibility 2, D region locus 1//histocompatibility 2, K1, I	0001916 // positive regulation of T cell mediated cytotoxicity // inferred from direct assay//C
NM_001177900//NM:	0.029	1.543	<b>Rd3</b>	retinal degeneration 3	0007601 // visual perception // inferred from electronic annotation//0050896 // response to
NM_001170851//NM:	0.034	1.544	<b>Klra2</b>	killer cell lectin-like receptor, subfamily A, member 2	0007155 // cell adhesion // inferred from electronic annotation
NM_019440	0.001	1.545	<b>Irgm2</b>	immunity-related GTPase family M member 2	0034341 // response to interferon-gamma // inferred from direct assay//0034341 // respons
NM_001081369//XM:	0.029	1.549	<b>Ccdc153</b>	coiled-coil domain containing 153	0005515 // protein binding // inferred from electronic annotation
NM_001039160//NM:	0.001	1.552	<b>Gm4070//Gvin1</b>	predicted gene 4070//GTPase, very large interferon inducible 1	0000166 // nucleotide binding // inferred from electronic annotation//0005525 // GTP bindi
NM_053085//XM_006	0.009	1.552	<b>Tcf23</b>	transcription factor 23	0007275 // multicellular organismal development // inferred from electronic annotation//00
NM_030150	0.007	1.553	<b>Dhx58</b>	DEXH (Asp-Glu-X-His) box polypeptide 58	0002376 // immune system process // inferred from electronic annotation//0008152 // met:
NM_001172207//NM:	0.047	1.555	<b>Lrtm2</b>	leucine-rich repeats and transmembrane domains 2	0007409 // axonogenesis // not recorded//0051965 // positive regulation of synapse assem
NM_001080707//NM:	0.001	1.556	<b>Gpr155</b>	G protein-coupled receptor 155	0035556 // intracellular signal transduction // inferred from electronic annotation//0050890
NM_130452//XM_006	0.006	1.557	<b>Bbox1</b>	butyrobetaine (gamma), 2-oxoglutarate dioxygenase 1 (gamma-b	0045329 // carnitine biosynthetic process // not recorded//0055114 // oxidation-reduction p
NM_009252//XM_011	0.031	1.558	<b>Serpina3n</b>	serine (or cysteine) peptidase inhibitor, clade A, member 3N	0006953 // acute-phase response // inferred from electronic annotation//0010466 // negati
NM_008240//XM_006	0.002	1.561	<b>Foxj1</b>	forkhead box J1	0001122 // negative regulation of transcription from RNA polymerase II promoter // inferred
NM_177546//NM_21:	0.001	1.562	<b>Pcyt1b</b>	phosphate cytidylyltransferase 1, choline, beta isoform	0001541 // ovarian follicle development // inferred from mutant phenotype//0006629 // lipi
NM_021332	0.022	1.563	<b>Glp1r</b>	glucagon-like peptide 1 receptor	0016020 // membrane // inferred from electronic annotation//0016021 // integral compone
NM_027209//XM_011	0.003	1.564	<b>Ms4a6b</b>	membrane-spanning 4-domains, subfamily A, member 6B	
NM_008039	0.000	1.567	<b>Fpr2</b>	formyl peptide receptor 2	0006935 // chemotaxis // inferred from electronic annotation//0007165 // signal transductic
NM_029762	0.015	1.567	<b>Hyls1</b>	hydrolethalus syndrome 1	
NM_009201//XM_006	0.022	1.572	<b>Slc1a5</b>	solute carrier family 1 (neutral amino acid transporter), member 1	0003333 // amino acid transmembrane transport // not recorded//0006810 // transport // i
NM_133990	0.003	1.572	<b>Il13ra1</b>	interleukin 13 receptor, alpha 1	0019221 // cytokine-mediated signaling pathway // inferred from electronic annotation//00:
NM_198095	0.001	1.572	<b>Bst2</b>	bone marrow stromal cell antigen 2	0002376 // immune system process // inferred from electronic annotation//0002737 // neg:
NM_001302338//NM:	0.005	1.573	<b>Nfe2</b>	nuclear factor, erythroid derived 2	0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 //
NM_175467//XM_006	0.032	1.573	<b>Spltc3</b>	serine palmitoyltransferase, long chain base subunit 3	0006629 // lipid metabolic process // inferred from electronic annotation//0006665 // sphin,
NM_001159417//NM:	0.001	1.584	<b>Irf9</b>	interferon regulatory factor 9	0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 //
NM_001204241//NM:	0.030	1.585	<b>Clec4a3</b>	C-type lectin domain family 4, member a3	0006508 // proteolysis // inferred from electronic annotation
NM_001112725//NM:	0.017	1.588	<b>Aldh3a1</b>	aldehyde dehydrogenase family 3, subfamily A1	0001666 // response to hypoxia // not recorded//0006081 // cellular aldehyde metabolic prc
NM_001166376//NM:	0.009	1.590	<b>Ms4a6c//Gm8369</b>	membrane-spanning 4-domains, subfamily A, member 6C//pred	0016020 // membrane // inferred from electronic annotation//0016021 // integral compone
NM_145825	0.014	1.594	<b>Cetn4</b>	centrin 4	0005509 // calcium ion binding // inferred from direct assay//0031683 // G-protein beta/gar
NM_029495//NM_17:	0.000	1.602	<b>Epsti1</b>	epithelial stromal interaction 1 (breast)	
NM_009841	0.013	1.605	<b>Cd14</b>	CD14 antigen	0002237 // response to molecule of bacterial origin // inferred from direct assay//0002376 //
NM_028377//XM_006	0.011	1.609	<b>Bbof1</b>	basal body orientation factor 1	0044458 // motile cilium assembly // inferred from sequence or structural similarity
NM_001110323//NM:	0.004	1.611	<b>Klra7//LOC100862438</b>	killer cell lectin-like receptor, subfamily A, member 7//killer cell	0007155 // cell adhesion // inferred from electronic annotation
NM_007807//XM_006	0.019	1.613	<b>Cybb</b>	cytochrome b-245, beta polypeptide	0006801 // superoxide metabolic process // inferred from mutant phenotype//0006801 // si
NM_008326//XM_006	0.000	1.619	<b>Irgm1</b>	immunity-related GTPase family M member 1	0002376 // immune system process // inferred from electronic annotation//0006914 // auto
NM_029112//XM_006	0.019	1.620	<b>Morn3</b>	MORN repeat containing 3	
NM_001042451//NM:	0.019	1.620	<b>Snca</b>	synuclein, alpha	0001774 // microglial cell activation // inferred from mutant phenotype//0001921 // positiv
NM_029007	0.005	1.632	<b>Fam84a</b>	family with sequence similarity 84, member A	
NM_194336//XM_006	0.000	1.634	<b>Gbp6</b>	guanylate binding protein 6	0006955 // immune response // inferred from mutant phenotype//0008152 // metabolic prc
NM_029383	0.029	1.637	<b>Cldn22</b>	claudin 22	0016338 // calcium-independent cell-cell adhesion via plasma membrane cell-adhesion molec
NM_177753	0.009	1.640	<b>Sox21</b>	SRY (sex determining region Y)-box 21	0001942 // hair follicle development // inferred from mutant phenotype//0006351 // transc
NM_144559	0.001	1.641	<b>Fcgr4</b>	Fc receptor, IgG, low affinity IV	0001866 // NK T cell proliferation // not recorded//0051930 // regulation of sensory percept
NM_019807//NM_20:	0.049	1.646	<b>Acpp</b>	acid phosphatase, prostate	0006144 // purine nucleobase metabolic process // inferred from mutant phenotype//00064
NM_001316689//NM:	0.030	1.647	<b>Ern2</b>	endoplasmic reticulum (ER) to nucleus signalling 2	0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 //
NM_001145948//NM:	0.007	1.649	<b>Ttc39a</b>	tetratricopeptide repeat domain 39A	
NM_021407//XM_006	0.007	1.653	<b>Trem3</b>	triggering receptor expressed on myeloid cells 3	0002374 // cytokine secretion involved in immune response // inferred from genetic interacti
NM_016925//XM_006	0.014	1.653	<b>Fanca</b>	Fanconi anemia, complementation group A	0006281 // DNA repair // inferred from electronic annotation//0006974 // cellular response
NM_009915//XM_006	0.003	1.654	<b>Ccr2</b>	chemokine (C-C motif) receptor 2	0001525 // angiogenesis // traceable author statement//0001974 // blood vessel remodeling
NM_178386	0.014	1.657	<b>Slc25a31</b>	solute carrier family 25 (mitochondrial carrier; adenine nucleotid	0006810 // transport // inferred from electronic annotation//0055085 // transmembrane tr
NM_007417	0.015	1.658	<b>Adra2a</b>	adrenergic receptor, alpha 2a	0001819 // positive regulation of cytokine production // not recorded//0002526 // acute inf
NM_001122635//NM:	0.006	1.662	<b>Cdhr4</b>	cadherin-related family member 4	0007155 // cell adhesion // inferred from electronic annotation//0007156 // homophilic cell

RefSeq Transcript ID	p	FD Air	Gene Symbol	Gene Title	Gene Ontology
NM_028275//XM_006	0.025	1.665	<b>1700112E06Rik</b>	RIKEN cDNA 1700112E06 gene	0030154 // cell differentiation // inferred from electronic annotation//0030318 // melanocyt
NM_029662//XM_006	0.016	1.671	<b>Mfsd2a</b>	major facilitator superfamily domain containing 2A	0006810 // transport // inferred from electronic annotation//0006869 // lipid transport // in
NM_001174053//NM_	0.044	1.679	<b>Camk2b</b>	calcium/calmodulin-dependent protein kinase II, beta	0000082 // G1/S transition of mitotic cell cycle // inferred from mutant phenotype//000203C
NM_011408	0.000	1.681	<b>Slfn2</b>	schlafen 2	0008285 // negative regulation of cell proliferation // inferred from direct assay
NM_0111023	0.036	1.686	<b>Otx1</b>	orthodenticle homolog 1	0006355 // regulation of transcription, DNA-templated // inferred from electronic annotation.
NM_181589//XM_006	0.001	1.689	<b>Ckap2l</b>	cytoskeleton associated protein 2-like	0000922 // spindle pole // inferred from electronic annotation//0005737 // cytoplasm // infe
NM_007689	0.001	1.697	<b>Chad</b>	chondroadherin	0001502 // cartilage condensation // inferred from electronic annotation//00060348 // bone
NM_019948//XM_011	0.044	1.699	<b>Clec4e</b>	C-type lectin domain family 4, member e	0002292 // T cell differentiation involved in immune response // inferred from mutant pheno
NM_145226	0.033	1.700	<b>Oas3</b>	2'-5' oligoadenylate synthetase 3	0002376 // immune system process // inferred from electronic annotation//0006164 // puri
NM_001166627//NM_	0.000	1.702	<b>Dynlt1a//Dynlt1b//Dynlt1c//Dynlt</b>	dynein light chain Tctex-type 1A//dynein light chain Tctex-type 1	0000132 // establishment of mitotic spindle orientation // inferred from mutant phenotype//
NM_001101605//NM_	0.002	1.703	<b>Iift1bl1</b>	interferon induced protein with tetratricopeptide repeats 1B like 1	0051607 // defense response to virus // not recorded//00060337 // type I interferon signaling
NM_001167743//NM_	0.048	1.704	<b>Slfn8</b>	schlafen 8	0051607 // defense response to virus // inferred from electronic annotation//0000134 // neq
NM_024444//XM_006	0.006	1.710	<b>Cyp4f18</b>	cytochrome P450, family 4, subfamily f, polypeptide 18	0000038 // very long-chain fatty acid metabolic process // not recorded//0001676 // long-ch
NM_153094//NR_024	0.003	1.715	<b>Klrb1f</b>	killer cell lectin-like receptor subfamily B member 1F	0004872 // receptor activity // inferred from direct assay//0005515 // protein binding // infe
NM_010654//XM_006	0.019	1.727	<b>Klrd1</b>	killer cell lectin-like receptor, subfamily D, member 1	0002228 // natural killer cell mediated immunity // not recorded
NM_001301353//NM_	0.018	1.731	<b>Apod</b>	apolipoprotein D	0000302 // response to reactive oxygen species // inferred from mutant phenotype//00003C
NM_023785	0.009	1.732	<b>Ppbp</b>	pro-platelet basic protein	0002523 // leukocyte migration involved in inflammatory response // inferred from mutant p
XM_006521609//XM_	0.036	1.734	<b>Fer1l6</b>	fer-1-like 6 (C. elegans)	
NM_001033170//XM_	0.023	1.735	<b>Fam83e</b>	family with sequence similarity 83, member E	0019901 // protein kinase binding // not recorded
NM_001162878//NM_	0.015	1.742	<b>Fam183b</b>	family with sequence similarity 183, member B	
NM_009610	0.032	1.746	<b>Actg2</b>	actin, gamma 2, smooth muscle, enteric	0010628 // positive regulation of gene expression // inferred from sequence or structural sim
NM_010186	0.000	1.754	<b>Fcgr1</b>	Fc receptor, IgG, high affinity I	0001788 // antibody-dependent cellular cytotoxicity // inferred from mutant phenotype//00
NM_011073//XM_006	0.000	1.756	<b>Prf1</b>	perforin 1 (pore forming protein)	0001771 // immunological synapse formation // not recorded//0002357 // defense response
NM_016974//XM_006	0.033	1.765	<b>Dbp</b>	D site albumin promoter binding protein	0001889 // liver development // inferred from electronic annotation//0006351 // transcripti
NM_001033450//NM_	0.026	1.770	<b>Ifi204//Ifi205//Mnda//Mndal</b>	interferon activated gene 204//interferon activated gene 205//	0000122 // negative regulation of transcription from RNA polymerase II promoter // ---//000
NM_001166627//NM_	0.000	1.785	<b>Dynlt1-ps1//Dynlt1a//Dynlt1b//Dy</b>	dynein light chain Tctex-type 1, pseudogene 1//dynein light ch	0000132 // establishment of mitotic spindle orientation // inferred from mutant phenotype//
NM_080457//NM_18:	0.004	1.789	<b>Muc4</b>	mucin 4	0001953 // negative regulation of cell-matrix adhesion // not recorded//0002244 // hemato
NM_001281852//NM_	0.000	1.799	<b>S100a9</b>	S100 calcium binding protein A9 (calgranulin B)	0002376 // immune system process // inferred from electronic annotation//0002523 // leuk
NM_019507	0.001	1.807	<b>Tbx21</b>	T-box 21	0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 /,
NM_011397//XM_011	0.001	1.819	<b>Slc23a1</b>	solute carrier family 23 (nucleobase transporters), member 1	0006810 // transport // inferred from electronic annotation//0006811 // ion transport // inf
NM_001146275//NM_	0.000	1.834	<b>Iigp1</b>	interferon inducible GTPase 1	0002376 // immune system process // inferred from electronic annotation//0008152 // met:
NM_018738	0.000	1.837	<b>Igtp</b>	interferon gamma induced GTPase	0035458 // cellular response to interferon-beta // inferred from direct assay
NM_021475	0.002	1.838	<b>Adamdec1</b>	ADAM-like, decysin 1	0006508 // proteolysis // inferred from electronic annotation
NM_007769//XM_006	0.002	1.841	<b>Dmbt1</b>	deleted in malignant brain tumors 1	0001824 // blastocyst development // inferred from mutant phenotype//0001833 // inner c
NM_001302559//NM_	0.002	1.848	<b>Slfn3//Slfn4</b>	schlafen 3//schlafen 4	0008285 // negative regulation of cell proliferation // inferred from direct assay
NM_145209//XM_006	0.000	1.851	<b>Oas1</b>	2'-5' oligoadenylate synthetase-like 1	0002376 // immune system process // inferred from electronic annotation//0006955 // imm
NM_001081746//XM_	0.001	1.853	<b>Csprs</b>	component of Sp100-rs//predicted pseudogene 15433//predict	0006338 // chromatin remodeling // ---//0006355 // regulation of transcription, DNA-templa
NM_001291066//NM_	0.049	1.858	<b>Adam8</b>	a disintegrin and metallopeptidase domain 8	0000902 // cell morphogenesis // inferred from mutant phenotype//0001525 // angiogenesi
NM_001289492//NM_	0.000	1.866	<b>Gbp3</b>	guanylate binding protein 3	0008152 // metabolic process // inferred from electronic annotation//0035458 // cellular res
NM_009978//XM_006	0.001	1.876	<b>Cst8</b>	cystatin 8 (cystatin-related epididymal spermatogenic)	0010466 // negative regulation of peptidase activity // inferred from electronic annotation//
NM_001139519//NM_	0.000	1.876	<b>Zbp1</b>	Z-DNA binding protein 1	0002376 // immune system process // inferred from electronic annotation//0008152 // met:
NM_008329//XM_006	0.009	1.885	<b>Ifi204//Ifi205//Mnda//Mndal</b>	interferon activated gene 204//interferon activated gene 205//	0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 /,
NM_153590//XM_006	0.000	1.887	<b>Klre1</b>	killer cell lectin-like receptor family E member 1	0002223 // stimulatory C-type lectin receptor signaling pathway // inferred from direct assay/
NM_001110323//NM_	0.049	1.896	<b>Klra7//LOC100862438</b>	killer cell lectin-like receptor, subfamily A, member 7//killer cell l	0007155 // cell adhesion // inferred from electronic annotation
NM_0008489	0.001	1.899	<b>Lbp</b>	lipopolysaccharide binding protein	0001889 // liver development // inferred from electronic annotation//0002232 // leukocyte
NM_001142706//NM_	0.000	1.899	<b>Cfb</b>	complement factor B	0002376 // immune system process // inferred from electronic annotation//0006508 // prot
NM_008611	0.001	1.906	<b>Mmp8</b>	matrix metallopeptidase 8	0006508 // proteolysis // not recorded//0030574 // collagen catabolic process // inferred fr
NM_139198//XM_011	0.000	1.932	<b>Plac8</b>	placenta-specific 8	0008284 // positive regulation of cell proliferation // inferred from direct assay//0009409 //
NM_178594	0.013	1.934	<b>Vtcn1</b>	V-set domain containing T cell activation inhibitor 1	0001562 // response to protozoan // inferred from mutant phenotype//0002250 // adaptive
NM_013650	0.000	1.942	<b>S100a8</b>	S100 calcium binding protein A8 (calgranulin A)	0002376 // immune system process // inferred from electronic annotation//0002523 // leuk
NM_001136068//NM_	0.026	1.945	<b>Klrc1</b>	killer cell lectin-like receptor subfamily C, member 1	0023024 // MHC class I protein complex binding // not recorded
NM_001270495//NM_	0.009	1.952	<b>Tmem254a//Tmem254b//Tmem254</b>	transmembrane protein 254a//transmembrane protein 254b//transmembrane protein 254c	
NM_001198560//NM_	0.006	1.955	<b>H2-D4//H2-Q7//H2-Q9</b>	histocompatibility 2, D region locus 4//histocompatibility 2, Q re	0001916 // positive regulation of T cell mediated cytotoxicity // inferred from direct assay//C
NM_011909	0.000	1.958	<b>Usp18</b>	ubiquitin specific peptidase 18	0006508 // proteolysis // inferred from electronic annotation//0006511 // ubiquitin-depend

RefSeq Transcript ID	p	FD Air	Gene Symbol	Gene Title	Gene Ontology
NM_001037713//NM_001270495//NM_026630	0.000 0.009 0.014	1.967 1.985 1.990	<b>Xaf1</b> <b>Tmem254a</b> /// <b>Tmem254b</b> /// <b>Tmem254</b> <b>Gtsf1</b>	XIAP associated factor 1 transmembrane protein 254a//transmembrane protein 254b//transmembrane protein 254c gametocyte specific factor 1-like	0006915 // apoptotic process // inferred from electronic annotation//0031333 // negative re 0046872 // metal ion binding // inferred from electronic annotation
NM_001281845//NM_010501//XM_011	0.040 0.000	1.994 2.012	<b>Anxa8</b> <b>Ifi3</b>	annexin A8 interferon-induced protein with tetratricopeptide repeats 3	0007596 // blood coagulation // inferred from electronic annotation//0007599 // hemostasi: 0002376 // immune system process // inferred from electronic annotation//0008285 // neg:
NM_021274	0.016	2.018	<b>Cxcl10</b>	chemokine (C-X-C motif) ligand 10	0002690 // positive regulation of leukocyte chemotaxis // not recorded//0006935 // chemot
NM_009363	0.015	2.022	<b>Tff2</b>	trefoil factor 2 (spasmolytic protein 1)	0008284 // positive regulation of cell proliferation // inferred from genetic interaction//0008
NM_013653	0.001	2.029	<b>Ccl5</b>	chemokine (C-C motif) ligand 5	0000165 // MAPK cascade // not recorded//0002230 // positive regulation of defense respor
NM_011150	0.000	2.055	<b>Lgals3bp</b>	lectin, galactoside-binding, soluble, 3 binding protein	0006898 // receptor-mediated endocytosis // inferred from sequence or structural similarity/
NM_001081746//NM_001033632	0.002 0.012	2.059 2.059	<b>Csprs</b> <b>lftm6</b>	component of Sp100-rs//predicted pseudogene 15433//predict interferon induced transmembrane protein 6	0006338 // chromatin remodeling // ---//0006355 // regulation of transcription, DNA-templa 0009607 // response to biotic stimulus // inferred from electronic annotation
NM_016675//XM_006	0.001	2.069	<b>Cldn2</b>	claudin 2	0016338 // calcium-independent cell-cell adhesion via plasma membrane cell-adhesion molec
NM_001145164//NM_010172	0.000 0.005	2.094 2.098	<b>Tgtp1</b> /// <b>Tgtp2</b> <b>F7</b>	T cell specific GTPase 1//T cell specific GTPase 2 coagulation factor VII	0006955 // immune response // non-traceable author statement//0009615 // response to vi 0002690 // positive regulation of leukocyte chemotaxis // not recorded//0006508 // proteol
NM_020002//XM_006	0.048	2.103	<b>Rec8</b>	REC8 meiotic recombination protein	0000724 // double-strand break repair via homologous recombination // inferred from geneti
NM_001161621//NM_001204910//XM_134157	0.043 0.047 0.022	2.105 2.111 2.150	<b>Aoc1</b> <b>Al607873</b> <b>Atp6v1b1</b>	amine oxidase, copper-containing 1 expressed sequence Al607873 ATPase, H+ transporting, lysosomal V1 subunit B1	0006812 // cation transport // ---//0009308 // amine metabolic process // inferred from elec 0000122 // negative regulation of transcription from RNA polymerase II promoter // --- 0001503 // ossification // not recorded//0001503 // ossification // inferred from sequence o
NM_029796	0.002	2.192	<b>Lrg1</b>	leucine-rich alpha-2-glycoprotein 1	0001938 // positive regulation of endothelial cell proliferation // inferred from mutant pheno
NM_001277944//NM_001101620//NM_023386//XM_006	0.003 0.011 0.000	2.205 2.209 2.221	<b>Apoc2</b> /// <b>Apoc4-apoc2</b> <b>Klra21</b> /// <b>Klra3</b> /// <b>Klra8</b> /// <b>Klra9</b> <b>Rtp4</b>	apolipoprotein C-II//Apoc4-Apoc2 readthrough killer cell lectin-like receptor subfamily A, member 21//killer cell receptor transporter protein 4	0006629 // lipid metabolic process // inferred from electronic annotation//0006810 // trans 0007155 // cell adhesion // inferred from electronic annotation//0009615 // response to vir 0001580 // detection of chemical stimulus involved in sensory perception of bitter taste // no
NM_001304551//NM_130878	0.029 0.000	2.234 2.236	<b>Stil</b> <b>Cdhr1</b>	Scf/Tal1 interrupting locus cadherin-related family member 1	0000578 // embryonic axis specification // inferred from mutant phenotype//0001701 // in t 0007155 // cell adhesion // inferred from electronic annotation//0007156 // homophilic cell
NM_001033207//XM_145600	0.000 0.047	2.253 2.267	<b>Nlr5</b> <b>Zfp330</b>	NLR family, CARD domain containing 5 zinc finger protein 330	0002376 // immune system process // inferred from electronic annotation//0032088 // neg: 0008270 // zinc ion binding // inferred from electronic annotation//0046872 // metal ion bin
NM_001033384//NM_001289604//NM_010846//NR_003	0.003 0.004 0.000	2.271 2.279 2.300	<b>Pydc4</b> <b>Klra3</b> /// <b>Klra9</b> <b>Mx1</b>	pyrin domain containing 4 killer cell lectin-like receptor, subfamily A, member 3//killer cell MX dynamin-like GTPase 1	0000122 // negative regulation of transcription from RNA polymerase II promoter // --- 0007155 // cell adhesion // inferred from electronic annotation 0002376 // immune system process // inferred from electronic annotation//0008152 // met:
NM_029499//XM_006	0.001	2.305	<b>Ms4a4c</b>	membrane-spanning 4-domains, subfamily A, member 4C	0005887 // integral component of plasma membrane // inferred from electronic annotation//
NM_001033409//XM_010362	0.018 0.001	2.307 2.316	<b>Lgr6</b> <b>Gsto1</b>	leucine-rich repeat-containing G protein-coupled receptor 6 glutathione S-transferase omega 1	0007165 // signal transduction // inferred from electronic annotation//0007186 // G-protein 0006749 // glutathione metabolic process // not recorded//0008152 // metabolic process //
NM_008331	0.000	2.325	<b>Ifi1</b>	interferon-induced protein with tetratricopeptide repeats 1	0002376 // immune system process // inferred from electronic annotation//0009615 // resp
NM_146050//XM_006	0.040	2.337	<b>Oit1</b>	oncoprotein induced transcript 1	0046676 // negative regulation of insulin secretion // not recorded//0046676 // negative reg
NM_001136059//NM_145838//XM_006	0.009 0.002	2.357 2.396	<b>Cyp1a1</b> <b>St8sia6</b>	cytochrome P450, family 1, subfamily a, polypeptide 1 ST8 alpha-N-acetyl-neuraminidase alpha-2,8-sialyltransferase 6	0001666 // response to hypoxia // inferred from electronic annotation//0001889 // liver dev 0001574 // ganglioside biosynthetic process // inferred from direct assay//0006486 // protei
NM_026671//XM_006	0.010	2.427	<b>Lypd2</b>	Ly6/Plaur domain containing 2	0005576 // extracellular region // ---//0005886 // plasma membrane // inferred from electro
NM_175026	0.004	2.427	<b>Pyhin1</b>	pyrin and HIN domain family, member 1	0000122 // negative regulation of transcription from RNA polymerase II promoter // ---//003
NM_153576	0.001	2.430	<b>Cxcl17</b>	chemokine (C-X-C motif) ligand 17	0001525 // angiogenesis // inferred from electronic annotation//0006935 // chemotaxis // ir
NM_013542	0.000	2.441	<b>Gzmb</b>	granzyme B	0001913 // T cell mediated cytotoxicity // inferred from mutant phenotype//0006508 // pro
XM_011238903//XM_015783//XR_168	0.041 0.000	2.560 2.611	<b>Gm37416</b> /// <b>Gm39743</b> /// <b>Gm40611</b> /// <b>Gm9706</b> /// <b>Isg15</b>	predicted gene, 37416//predicted gene, 39743//predicted gene predicted gene 9706//ISG15 ubiquitin-like modifier	0006278 // RNA-dependent DNA replication // inferred from electronic annotation//000815: 0019941 // modification-dependent protein catabolic process // inferred from direct assay//
NM_027399	0.007	2.612	<b>Steap1</b>	six transmembrane epithelial antigen of the prostate 1	0006810 // transport // inferred from electronic annotation//0006811 // ion transport // inf
NM_011407	0.008	2.635	<b>Slfn1</b>	schlafen 1	0000122 // negative regulation of transcription from RNA polymerase II promoter // inferred
NM_145227//XM_006	0.000	2.656	<b>Oas2</b>	2'-5' oligoadenylate synthetase 2	0002376 // immune system process // inferred from electronic annotation//0006164 // puri
NM_010370	0.000	2.669	<b>Gzma</b>	granzyme A	0006508 // proteolysis // inferred from electronic annotation//0006915 // apoptotic process
NM_001281830//NM_015783//XR_168	0.030 0.000	2.683 2.852	<b>Ifi272a</b> <b>Gm9706</b> /// <b>Isg15</b>	interferon, alpha-inducible protein 27 like 2A predicted gene 9706//ISG15 ubiquitin-like modifier	0007568 // aging // inferred from direct assay//0009615 // response to virus // inferred from
NM_001001179	0.001	2.933	<b>BC048546</b>	cDNA sequence BC048546	0010466 // negative regulation of peptidase activity // inferred from electronic annotation//
NM_001162883//NM_001081180//XM_145423	0.000 0.020	2.948 3.086	<b>Apol9a</b> /// <b>Apol9b</b> <b>Spink5</b>	apolipoprotein L 9a//apolipoprotein L 9b serine peptidase inhibitor, kazal type 5	0006869 // lipid transport // inferred from electronic annotation//0042157 // lipoprotein me 0002787 // negative regulation of antibacterial peptide production // inferred from mutant pl
NM_016771	0.043	3.187	<b>Slc5a8</b>	solute carrier family 5 (iodide transporter), member 8	0006810 // transport // inferred from electronic annotation//0006811 // ion transport // inf
NM_018751	0.037 0.000	3.249 3.269	<b>Sult1d1</b> <b>Sult1c1</b>	sulfotransferase family 1D, member 1 sulfotransferase family, cytosolic, 1C, member 1	0000103 // sulfate assimilation // inferred from direct assay//0006584 // catecholamine met 0006790 // sulfur compound metabolic process // inferred from direct assay

RefSeq Transcript ID	p	FD Air	Gene Symbol	Gene Title	Gene Ontology
NM_001252600//NM_0011854//XM_001010243	0.000	3.343	<b>Irf7</b>	interferon regulatory factor 7	0002376 // immune system process // inferred from electronic annotation//0002819 // regu
NM_011854//XM_001010243	0.000	3.351	<b>Oasl2</b>	2'-5' oligoadenylate synthetase-like 2	0002376 // immune system process // inferred from electronic annotation//0006164 // puri
NM_010243	0.007	3.358	<b>Fut9</b>	fucosyltransferase 9	0006486 // protein glycosylation // inferred from direct assay//0007399 // nervous system d
NM_177406	0.042	3.418	<b>Cyp4a12a</b>	cytochrome P450, family 4, subfamily a, polypeptide 12a	0006631 // fatty acid metabolic process // inferred from sequence or structural similarity//01
NM_028801//XM_001021384//XM_011145211//XM_001027416	0.000	3.518	<b>Muc5b</b>	mucin 5, subtype B, tracheobronchial	0042742 // defense response to bacterium // inferred from mutant phenotype//0043030 //
NM_021384//XM_011145211//XM_001027416	0.000	3.553	<b>Rsad2</b>	radical S-adenosyl methionine domain containing 2	0001503 // ossification // not recorded//0002376 // immune system process // inferred from
NM_145211//XM_001027416	0.000	3.660	<b>Oasl1a</b>	2'-5' oligoadenylate synthetase 1A	0002376 // immune system process // inferred from electronic annotation//0006164 // puri
NM_027416	0.044	3.685	<b>Calml3</b>	calmodulin-like 3	0005509 // calcium ion binding // inferred from electronic annotation//0005515 // protein b
NM_054037//NM_17133238	0.044	3.847	<b>Scgb3a1</b>	secretoglobin, family 3A, member 1	1901741 // positive regulation of myoblast fusion // inferred from mutant phenotype
NM_133238	0.009	4.009	<b>Cd209a</b>	CD209a antigen	0006897 // endocytosis // inferred from electronic annotation//0010468 // regulation of ger
NM_001033767//XM_011238903//XM_133871//XM_001009244//XM_001011783	0.000	4.068	<b>Gm4951</b>	predicted gene 4951	0035458 // cellular response to interferon-beta // inferred from direct assay
XM_011238903//XM_133871//XM_001009244//XM_001011783	0.022	4.822	<b>Gm37416//Gm39743//Gm40611//Gm40611</b>	predicted gene, 37416//predicted gene, 39743//predicted gene, 37416//predicted gene, 39743	0006278 // RNA-dependent DNA replication // inferred from electronic annotation//000815:
NM_133871//XM_001009244//XM_001011783	0.000	5.044	<b>Ifi44</b>	interferon-induced protein 44	0005737 // cytoplasm // inferred from electronic annotation
NM_009244//XM_001011783	0.011	5.159	<b>Serpina1b</b>	serine (or cysteine) preptidase inhibitor, clade A, member 1B	0001701 // in utero embryonic development // inferred from mutant phenotype//0006487 /
NM_011783	0.002	5.455	<b>Agr2</b>	anterior gradient 2	0010628 // positive regulation of gene expression // not recorded//0010811 // positive regu
NM_017474//XM_001001302559//NM_011315	0.010	5.554	<b>Clca1//Clca3a1//Clca2//Clca3a2</b>	chloride channel accessory 1//chloride channel accessory 3A1//	0006508 // proteolysis // inferred from electronic annotation//0006810 // transport // infer
NM_001302559//NM_011315	0.000	6.148	<b>Slfn4//Slfn3</b>	schlafen 4//schlafen 3	0008285 // negative regulation of cell proliferation // inferred from direct assay
NM_011315	0.000	6.202	<b>Saa3</b>	serum amyloid A 3	0006953 // acute-phase response // inferred from electronic annotation//0007252 // I-kapp:
XM_011238903//XM_031367	0.046	6.504	<b>Gm3579//Gm40514//Gm40814//Gm40814</b>	predicted gene 3579//predicted gene, 40514//predicted gene, 40514//predicted gene, 40514	0015074 // DNA integration // inferred from electronic annotation//0090502 // RNA phosph
NM_031367	0.000	8.278	<b>Ifi44l</b>	interferon-induced protein 44 like	0006955 // immune response // inferred from direct assay
NM_001012392//NM_025989//XM_001011260	0.016	8.872	<b>Bpifb1</b>	BPI fold containing family B, member 1	0002227 // innate immune response in mucosa // not recorded//0002376 // immune system
NM_025989//XM_001011260	0.000	10.017	<b>Gp2</b>	glycoprotein 2 (zymogen granule membrane)	0002412 // antigen transcytosis by M cells in mucosal-associated lymphoid tissue // inferred f
NM_011260	0.00421	25.756	<b>Reg3g</b>	regenerating islet-derived 3 gamma	0002755 // MyD88-dependent toll-like receptor signaling pathway // inferred from mutant pt



Table S6. Nfk1b-dependently modulated lung genes after ozone (0.3 ppm, 48 hr) exposure.

Selected genes varied >1.5-fold between Nfk1b-WT and Nfk1b-KO mice (positive-higher in KO-O3, negative-lower in KO-O3, compared to WT-O3).

Afymetrix\_GeneChip\_Mouse430\_2\_2-Way ANOVA (p<0.05). Order by fold difference (FD) between WT and KO. FC=fold change by O3 in each genotype.

RefSeq	Transcript ID	p (Genotype)	p (Genotype-Exposure)	Z (p Exposure)	FC WT/O3	FC KO/O3	FC Air WT/KO	FC O3 WT/KO	Gene Symbol	Gene Title	Gene Ontology Biological Process
NM_028216		2.08E-04	0.002125263	4.99E-04	8.88	1.24	-1.51	-10.87	<i>Pcco</i>	prostate stem cell antigen	
NM_007394		0.003934348	0.013873396	0.004998094	5.31	1.19	-1.27	-5.70	<i>Ptpa2</i>	fructose biphosphatase 2	0005975 // carbohydrate metabolic process // inferred from electronic annotation//0006004 // gluconeogenesis, 0001558 // regulation of cell growth // not recorded//0006281 // DNA repair // inferred from electronic annotation
NM_001131054//NM_0113911//NM_006533515//NM_006533516					-2.12	-1.70	-3.51	-2.81	<i>Pttg1</i>	pituitary tumor-transforming gene 1	0008152 // metabolic process // inferred from electronic annotation
NM_001081328					3.07	2.21	-1.95	-2.71	<i>Chsy3</i>	chondroitin sulfate synthase 3	0002100 // tRNA wobble adenosine to inosine editing // inferred from electronic annotation//0006400 // tRNA m 0018149 // peptide cross-linking // not recorded//0003216 // keratinocyte differentiation // not recorded//00331
NM_025748//NM_011243200					1.98	1.56	-2.07	-2.63	<i>Adot2</i>	adenosine deaminase, tRNA-specific 2	
NM_009264		0.31510517	0.002185997	7.96E-07	21.03	5.00	1.67	-2.52	<i>Spr1a</i>	small proline-rich protein 1A	
NM_013069//NM_1		1.26E-04	0.005971318	0.008376999	1.83	-1.09	-1.26	-2.51	<i>Nxpe2</i>	neurexophilin and PC-esterase domain family, member 2	
NM_172301//NM_1		0.27635863	0.026451888	0.03953187	3.23	-1.15	1.52	-2.44	<i>Ccnb1</i>	cyclin B1	0000278 // mitotic cell cycle // inferred from electronic annotation//0001556 // oocyte maturation // not recorded
NM_001177544//NM_1		0.06527217	0.045352243	0.01881624	2.88	1.23	-1.03	-2.42	<i>Histh2oo//Histh2op</i>	histone cluster 1, H2ao//histone cluster 1, H2ap	0006325 // chromatin organization // not recorded//0006342 // chromatin silencing // not recorded//0008285 //
NM_010295//NM_1		1.68E-04	0.003448708	0.004016006	1.97	1.07	-1.30	-2.38	<i>Gic</i>	glutamate-cysteine ligase, catalytic subunit	0006534 // cysteine metabolic process // not recorded//0006535 // glutamate metabolic process // not recorded, 0001889 // liver development // inferred from electronic annotation//0006351 // transcription, DNA-templated, 0006463 // protein complex assembly // not recorded//0006468 // protein phosphorylation // inferred from direct
NM_007659		0.19335605	0.042050056	0.056642193	2.77	-1.04	1.32	-2.18	<i>Cdk1</i>	cyclin-dependent kinase 1	0002548 // monocytic chemotaxis // --//0006935 // chemotaxis // traceable author statement//0006954 // infla 0002244 // hematopoietic progenitor cell differentiation // inferred from genetic interaction//0006275 // regulat
NM_011332//NM_1		0.25220744	0.015234006	1.71E-05	4.96	2.29	1.01	-2.16	<i>Ccl17</i>	chemokine (C-C motif) ligand 17	0002029 // protein polyubiquitination // not recorded//0006511 // ubiquitin-dependent protein catabolic process
NM_028039		0.3708932	0.043021165	0.06698847	2.62	-1.07	1.35	-2.07	<i>Esco2</i>	establishment of cohesion 1 homolog 2 (S. cerevisiae)	0001656 // metanephros development // inferred from mutant phenotype//0006810 // transport // inferred from
NM_026785		0.10046281	0.006311119	0.12935555	1.96	-1.23	1.18	-2.04	<i>Ube2c</i>	ubiquitin-conjugating enzyme E2C	0007596 // blood coagulation // inferred from electronic annotation//0005759 // hemostasis // inferred from ele 0000070 // mitotic sister chromatid segregation // --//0007049 // cell cycle // inferred from electronic annotatio
NM_010910		4.43E-04	0.003642625	1.30E-04	2.13	1.15	-1.09	-2.02	<i>Sic1a1</i>	solute carrier family 5 (sodium/glucose cotransporter), member 1	0006508 // proteolysis // inferred from mutant phenotype//0006508 // proteolysis // not recorded//0010727 //
NM_009364//NM_006505043//NM_006505044//NM_011241055//NM_0011					2.14	2.49	-2.34	-2.02	<i>Tjp2</i>	tissue factor pathway inhibitor 2	0001012 // negative regulation of transcription from RNA polymerase II promoter // not recorded//0005978 // gh 0000079 // regulation of cyclin-dependent protein serine/threonine kinase activity // inferred from electronic annot
NM_010809		0.170261	0.041151717	0.01817487	2.44	1.01	1.22	-1.98	<i>Ccna8</i>	cell division cycle-associated 8	0000086 // G2/M transition of mitotic cell cycle // not recorded//0001212 // negative regulation of transcription
NM_010104		0.007884334	0.020289894	0.14191255	1.62	-1.05	-1.16	-1.96	<i>Edn1</i>	endothelin 1	0001212 // negative regulation of transcription from RNA polymerase II promoter // not recorded//0001501 // sk 0002548 // monocytic chemotaxis // --//0006935 // chemotaxis // inferred from electronic annotation//0006955
NM_009137		0.002550701	0.022045342	0.032397464	1.60	-1.07	-1.14	-1.96	<i>Ccl22</i>	chemokine (C-C motif) ligand 22	0008543 // fibroblast growth factor receptor signaling pathway // inferred from mutant phenotype//2000177 // r 0000278 // mitotic cell cycle // inferred from electronic annotation//0001556 // oocyte maturation // not recorded
NM_011369		0.07999367	0.01631937	0.001532258	2.69	1.18	1.16	-1.95	<i>Shcp1</i>	Shc SH2-domain binding protein 1	0001012 // negative regulation of transcription from RNA polymerase II promoter // not recorded//0001818 // ne 0016310 // phosphorylation // inferred from electronic annotation
NM_172301//NM_1		0.22189107	0.0355218	0.03068305	2.35	-1.07	1.30	-1.95	<i>Ccnb1//Gm5593</i>	cyclin B1//predicted gene 5593	0000070 // mitotic sister chromatid segregation // not recorded//0000086 // G2/M transition of mitotic cell cycle 0001549 // osteoblast differentiation // not recorded//0007155 // cell adhesion // inferred from electronic annot 0000077 // DNA damage checkpoint // inferred from mutant phenotype//0000723 // telomere maintenance // uni 0008152 // metabolic process // inferred from electronic annotation
NM_008689//NM_006501106//NM_006501107					-1.08	-1.05	-2.01	-1.94	<i>Nfk1b</i>	nuclear factor of kappa light polypeptide gene enhancer in B cells 1, p105	0001568 // blood vessel development // inferred from mutant phenotype//0003158 // endothelium development 0007049 // cell cycle // inferred from electronic annotation//0007059 // chromosome segregation // not recorded
NM_177351		3.61E-04	0.03394541	0.7943103	1.21	-1.24	-1.29	-1.94	<i>Hykk</i>	hydroxylysine kinase 1	0000070 // mitotic sister chromatid segregation // not recorded//0000086 // G2/M transition of mitotic cell cycle
NM_145434		0.14153165	0.012387881	0.001671302	1.20	-2.64	-1.14	-1.94	<i>Nfk1a1</i>	nuclear receptor subfamily 1, group D, member 1	0001568 // blood vessel development // inferred from mutant phenotype//0003158 // endothelium development
NM_009328		0.102943716	0.006373226	0.001945413	2.53	1.11	1.20	-1.90	<i>C22</i>	cyclin A2	0000086 // G2/M transition of mitotic cell cycle // not recorded//0001212 // negative regulation of transcription
NM_008021//NM_1		0.08395548	0.013229165	0.04609279	1.93	-1.15	1.20	-1.86	<i>Foxm1</i>	forkhead box M1	0002376 // immune system process // inferred from electronic annotation//0006897 // endocytosis // inferred fr 0000226 // microtubule cytoskeleton organization // inferred from electronic annotation//0000910 // cytokinesis
NM_010766					2.15	2.98	-2.58	-1.86	<i>Marco</i>	macrophage receptor with collagenase structure	0001817 // activation of MAPK activity // not recorded//0001696 // gastric acid secretion // not recorded//0001 0010951 // negative regulation of endopeptidase activity // inferred from electronic annotation
NM_00128599//NM_1		0.11426556	0.011221865	0.005312019	2.29	1.02	1.21	-1.85	<i>Prc1</i>	protein regulator of cytokinesis 1	0001913 // T cell mediated cytotoxicity // --//0002839 // positive regulation of immune response to tumor cell //
NM_00128640//NM_1		0.01847303	0.028604146	0.014477238	1.79	1.02	1.03	-1.81	<i>Ghr1</i>	ghrelin	0000070 // mitotic sister chromatid segregation // not recorded//0000086 // G2/M transition of mitotic cell cycle
NM_001243008//NM_001243009//NM_009935					-1.21	-1.48	-1.48	-1.81	<i>Col6a3</i>	collagen, type VI, alpha 3	0001549 // osteoblast differentiation // not recorded//0007155 // cell adhesion // inferred from electronic annot 0000086 // G2/M transition of mitotic cell cycle // not recorded//0001212 // negative regulation of transcription
NM_010400					1.51	1.03	-1.23	-1.80	<i>H60a</i>	histocompatibility 60a	0001568 // blood vessel development // inferred from mutant phenotype//0003158 // endothelium development 0007049 // cell cycle // inferred from electronic annotation//0007059 // chromosome segregation // not recorded
NM_011121		0.2916006	0.021945084	0.010812664	2.06	1.01	1.13	-1.80	<i>PK1</i>	polo-like kinase 1	0000070 // mitotic sister chromatid segregation // not recorded//0000086 // G2/M transition of mitotic cell cycle
NM_011607//NM_00653774//NM_00653775//NM_00653776//NM_00653777//NM_00653778//NM_00653779//NM_00653780//NM_00653781//NM_00653782//NM_00653783//NM_00653784//NM_00653785//NM_00653786//NM_00653787//NM_00653788//NM_00653789//NM_00653790//NM_00653791//NM_00653792//NM_00653793//NM_00653794//NM_00653795//NM_00653796//NM_00653797//NM_00653798//NM_00653799//NM_00653800//NM_00653801//NM_00653802//NM_00653803//NM_00653804//NM_00653805//NM_00653806//NM_00653807//NM_00653808//NM_00653809//NM_00653810//NM_00653811//NM_00653812//NM_00653813//NM_00653814//NM_00653815//NM_00653816//NM_00653817//NM_00653818//NM_00653819//NM_00653820//NM_00653821//NM_00653822//NM_00653823//NM_00653824//NM_00653825//NM_00653826//NM_00653827//NM_00653828//NM_00653829//NM_00653830//NM_00653831//NM_00653832//NM_00653833//NM_00653834//NM_00653835//NM_00653836//NM_00653837//NM_00653838//NM_00653839//NM_00653840//NM_00653841//NM_00653842//NM_00653843//NM_00653844//NM_00653845//NM_00653846//NM_00653847//NM_00653848//NM_00653849//NM_00653850//NM_00653851//NM_00653852//NM_00653853//NM_00653854//NM_00653855//NM_00653856//NM_00653857//NM_00653858//NM_00653859//NM_00653860//NM_00653861//NM_00653862//NM_00653863//NM_00653864//NM_00653865//NM_00653866//NM_00653867//NM_00653868//NM_00653869//NM_00653870//NM_00653871//NM_00653872//NM_00653873//NM_00653874//NM_00653875//NM_00653876//NM_00653877//NM_00653878//NM_00653879//NM_00653880//NM_00653881//NM_00653882//NM_00653883//NM_00653884//NM_00653885//NM_00653886//NM_00653887//NM_00653888//NM_00653889//NM_00653890//NM_00653891//NM_00653892//NM_00653893//NM_00653894//NM_00653895//NM_00653896//NM_00653897//NM_00653898//NM_00653899//NM_00653900//NM_00653901//NM_00653902//NM_00653903//NM_00653904//NM_00653905//NM_00653906//NM_00653907//NM_00653908//NM_00653909//NM_00653910//NM_00653911//NM_00653912//NM_00653913//NM_00653914//NM_00653915//NM_00653916//NM_00653917//NM_00653918//NM_00653919//NM_00653920//NM_00653921//NM_00653922//NM_00653923//NM_00653924//NM_00653925//NM_00653926//NM_00653927//NM_00653928//NM_00653929//NM_00653930//NM_00653931//NM_00653932//NM_00653933//NM_00653934//NM_00653935//NM_00653936//NM_00653937//NM_00653938//NM_00653939//NM_00653940//NM_00653941//NM_00653942//NM_00653943//NM_00653944//NM_00653945//NM_00653946//NM_00653947//NM_00653948//NM_00653949//NM_00653950//NM_00653951//NM_00653952//NM_00653953//NM_00653954//NM_00653955//NM_00653956//NM_00653957//NM_00653958//NM_00653959//NM_00653960//NM_00653961//NM_00653962//NM_00653963//NM_00653964//NM_00653965//NM_00653966//NM_00653967//NM_00653968//NM_00653969//NM_00653970//NM_00653971//NM_00653972//NM_00653973//NM_00653974//NM_00653975//NM_00653976//NM_00653977//NM_00653978//NM_00653979//NM_00653980//NM_00653981//NM_00653982//NM_00653983//NM_00653984//NM_00653985//NM_00653986//NM_00653987//NM_00653988//NM_00653989//NM_00653990//NM_00653991//NM_00653992//NM_00653993//NM_00653994//NM_00653995//NM_00653996//NM_00653997//NM_00653998//NM_00653999//NM_00654000//NM_00654001//NM_00654002//NM_00654003//NM_00654004//NM_00654005//NM_00654006//NM_00654007//NM_00654008//NM_00654009//NM_00654010//NM_00654011//NM_00654012//NM_00654013//NM_00654014//NM_00654015//NM_00654016//NM_00654017//NM_00654018//NM_00654019//NM_00654020//NM_00654021//NM_00654022//NM_00654023//NM_00654024//NM_00654025//NM_00654026//NM_00654027//NM_00654028//NM_00654029//NM_00654030//NM_00654031//NM_00654032//NM_00654033//NM_00654034//NM_00654035//NM_00654036//NM_00654037//NM_00654038//NM_00654039//NM_00654040//NM_00654041//NM_00654042//NM_00654043//NM_00654044//NM_00654045//NM_00654046//NM_00654047//NM_00654048//NM_00654049//NM_00654050//NM_00654051//NM_00654052//NM_00654053//NM_00654054//NM_00654055//NM_00654056//NM_00654057//NM_00654058//NM_00654059//NM_00654060//NM_00654061//NM_00654062//NM_00654063//NM_00654064//NM_00654065//NM_00654066//NM_00654067//NM_00654068//NM_00654069//NM_00654070//NM_00654071//NM_00654072//NM_00654073//NM_00654074//NM_00654075//NM_00654076//NM_00654077//NM_00654078//NM_00654079//NM_00654080//NM_00654081//NM_00654082//NM_00654083//NM_00654084//NM_00654085//NM_00654086//NM_00654087//NM_00654088//NM_00654089//NM_00654090//NM_00654091//NM_00654092//NM_00654093//NM_00654094//NM_00654095//NM_00654096//NM_00654097//NM_00654098//NM_00654099//NM_00654100//NM_00654101//NM_00654102//NM_00654103//NM_00654104//NM_00654105//NM_00654106//NM_00654107//NM_00654108//NM_00654109//NM_00654110//NM_00654111//NM_00654112//NM_00654113//NM_00654114//NM_00654115//NM_00654116//NM_00654117//NM_00654118//NM_00654119//NM_00654120//NM_00654121//NM_00654122//NM_00654123//NM_00654124//NM_00654125//NM_00654126//NM_00654127//NM_00654128//NM_00654129//NM_00654130//NM_00654131//NM_00654132//NM_00654133//NM_00654134//NM_00654135//NM_00654136//NM_00654137//NM_00654138//NM_00654139//NM_00654140//NM_00654141//NM_00654142//NM_00654143//NM_00654144//NM_00654145//NM_00654146//NM_00654147//NM_00654148//NM_00654149//NM_00654150//NM_00654151//NM_00654152//NM_00654153//NM_00654154//NM_00654155//NM_00654156//NM_00654157//NM_00654158//NM_00654159//NM_00654160//NM_00654161//NM_00654162//NM_00654163//NM_00654164//NM_00654165//NM_00654166//NM_00654167//NM_00654168//NM_00654169//NM_00654170//NM_00654171//NM_00654172//NM_00654173//NM_00654174//NM_00654175//NM_00654176//NM_00654177//NM_00654178//NM_00654179//NM_00654180//NM_00654181//NM_00654182//NM_00654183//NM_00654184//NM_00654185//NM_00654186//NM_00654187//NM_00654188//NM_00654189//NM_00654190//NM_00654191//NM_00654192//NM_00654193//NM_00654194//NM_00654195//NM_00654196//NM_00654197//NM_00654198//NM_00654199//NM_00654200//NM_00654201//NM_00654202//NM_00654203//NM_00654204//NM_00654205//NM_00654206//NM_00654207//NM_00654208//NM_00654209//NM_00654210//NM_00654211//NM_00654212//NM_00654213//NM_00654214//NM_00654215//NM_00654216//NM_00654217//NM_00654218//NM_00654219//NM_00654220//NM_00654221//NM_00654222//NM_00654223//NM_00654224//NM_00654225//NM_00654226//NM_00654227//NM_00654228//NM_00654229//NM_00654230//NM_00654231//NM_00654232//NM_00654233//NM_00654234//NM_00654235//NM_00654236//NM_00654237//NM_00654238//NM_00654239//NM_00654240//NM_00654241//NM_00654242//NM_00654243//NM_00654244//NM_00654245//NM_00654246//NM_00654247//NM_00654248//NM_00654249//NM_00654250//NM_00654251//NM_00654252//NM_00654253//NM_00654254//NM_00654255//NM_00654256//NM_00654257//NM_00654258//NM_00654259//NM_00654260//NM_00654261//NM_00654262//NM_00654263//NM_00654264//NM_00654265//NM_00654266//NM_00654267//NM_00654268//NM_00654269//NM_00654270//NM_00654271//NM_00654272//NM_00654273//NM_00654274//NM_00654275//NM_00654276//NM_00654277//NM_00654278//NM_00654279//NM_00654280//NM_00654281//NM_00654282//NM_00654283//NM_00654284//NM_00654285//NM_00654286//NM_00654287//NM_00654288//NM_00654289//NM_00654290//NM_00654291//NM_00654292//NM_00654293//NM_00654294//NM_00654295//NM_00654296//NM_00654297//NM_00654298//NM_00654299//NM_00654300//NM_00654301//NM_0065											

RefSeq	Transcript ID	p (Genotype)	: p (Genotype-Exposure)	Z	p (Exposure)	FC WT:KO	FC KO Air:O3	FC Air:WT:KO	FC O3:WT:KO	Gene Symbol	Gene Title	Gene Ontology Biological Process
NM_010225		0.007460019	0.014400821	0.22995287	1.10	-1.21	-1.10	-1.46	<b>Foxf2</b>	forkhead box F2	0006351 // transcription, DNA-templated // inferred from electronic annotation // 0006355 // regulation of trans	
NM_009610		0.404168	0.009947431	0.023610901	1.10	-2.31	1.75	-1.46	<b>Actg2</b>	actin, gamma 2, smooth muscle, enteric	0010628 // positive regulation of gene expression // inferred from sequence or structural similarity // 0090131 // r	
NM_001159564	NM_0213599	0.006498808	0.006498809	0.006498809	1.64	1.64	-1.45	-1.45	<b>Irgb6</b>	cytokine beta 6	0006954 // inflammatory response // inferred from mutant phenotype // 0007155 // cell adhesion // inferred from	
NM_001004140	NR_03142748	0.039913804	0.09432041	1.53	-1.13	-1.19	-1.45	<b>Cxcp2</b>	integrin beta associated protein 2	0000284 // mitotic cytokinesis // not recorded // 0006915 // apoptotic process // inferred from electronic annota		
NM_001083917	NR_001286648	0.153521	0.178227	0.00650	-1.86	-1.58	-1.71	-1.45	<b>Kcnzb1</b>	sodium channel, voltage-gated, type II, beta	0008310 // transport // inferred from electronic annotation // 0006811 // ion transport // inferred from electronic	
NM_133774	NR_00625694	0.011246851	1.29	1.14	-1.28	-1.45	<b>Star4d</b>	STAR-related lipid transfer (START) domain containing 4	0006810 // transport // inferred from electronic annotation // 0006869 // lipid transport // inferred from electroni			
NM_001025779	NR_08211958	0.034671698	1.82E-04	4.13	1.73	1.65	-1.45	<b>Cdc6</b>	cell division cycle 6	0006260 // DNA replication // inferred from electronic annotation // 0006270 // DNA replication initiation // infer		
NM_001308327	NR_001308329	0.0088113	0.006512597	0.006512597	1.41	1.15	-1.18	-1.45	<b>Enpp1</b>	ectonucleotide pyrophosphatase/phosphodiesterase 1	0006091 // generation of precursor metabolites and energy // inferred from mutant phenotype // 0006796 // phosphate-containi	
NM_008842	NR_009017425	0.03932411	0.004323326	1.09	1.54	1.02	-1.45	<b>Pim1</b>	provinil integration site 1	0006488 // protein phosphorylation // not recorded // 0007346 // regulation of mitotic cell cycle // not recorded //		
NM_134117	NR_011246234	0.008962023	0.03866082	0.03866082	-1.44	-1.06	1.07	-1.45	<b>Pknox</b>	protein kinase domain containing, cytoplasmic	0001501 // skeletal system development // inferred from mutant phenotype // 0001503 // ossification // inferred f	
NM_178911	NR_011243975	0.006525353	0.006525353	0.006525353	-1.25	-1.11	1.29	-1.45	<b>Plid4</b>	phospholipase D family, member 4	0002244 // hematopoietic progenitor cell differentiation // inferred from mutant phenotype // 0006629 // lipid me	
NM_001033308	NR_011250230	0.00252347	0.4994762	0.4994762	-1.60	-1.38	1.26	-1.46	<b>Themis2</b>	thymocyte selection associated family member 2	0002376 // immune system process // inferred from electronic annotation // 0006954 // inflammatory response //	
NM_022358	NR_022718892	0.00252347	0.4994762	0.4994762	1.21	1.73	1.02	-1.46	<b>Zfp36</b>	zinc finger protein 36	0001122 // negative regulation of transcription from RNA polymerase II promoter // inferred from mutant phenot	
NM_029084	NR_022718892	0.00252347	0.4994762	0.4994762	-1.32	1.30	-1.18	-1.46	<b>Slmfb</b>	SLAMF family member 8	0003860 // regulation of NAD(P)H oxidase activity // inferred from mutant phenotype // 00035690 // cellular resp	
NM_023738	NR_022718892	0.00252347	0.4994762	0.4994762	-1.28	-1.03	-1.18	-1.47	<b>Uba7</b>	ubiquitin-like modifier activating enzyme 7	0006464 // cellular protein modification process // not recorded // 0006974 // cellular response to DNA damage st	
NM_001278269	NR_0118151	0.006519982	0.006519983	0.006519983	-1.35	-1.31	1.43	-1.48	<b>Fyb</b>	FYB binding protein	0006955 // immune response // inferred from electronic annotation // 0004576 // mast cell activation // inferred f	
NM_001289755	NR_040118688	0.026309016	0.6852822	0.6852822	-2.03	1.56	-2.13	-1.48	<b>ApoC3</b>	apolipoprotein C-III	0006629 // lipid metabolic process // inferred from electronic annotation // 0006641 // triglyceride metabolic pro	
NM_134133	NR_000701278	0.025884103	0.71766454	0.71766454	-1.21	1.26	-1.03	-1.48	<b>Slim3</b>	small integral membrane protein 3	0002412 // antigen transcytosis by M cells in mucosal-associated lymphoid tissue // inferred from direct assay // 0	
NM_025989	NR_008962023	0.03866082	0.03866082	0.03866082	-1.06	-7.17	10.02	-1.48	<b>Gp2</b>	glycoprotein 2 (zymogen granule membrane)	0002376 // immune system process // inferred from electronic annotation // 0006954 // inflammatory response //	
NM_009780	NR_006523531	0.006525353	0.006525353	0.006525353	-1.23	-1.16	1.40	-1.48	<b>Ccb2</b>	complement component 4B (Chido blood group) // complement C4-B	0001773 // myeloid dendritic cell activation // not recorded // 0002218 // activation of innate immune response //	
NM_020984	NR_022718892	0.00252347	0.4994762	0.4994762	-1.43	-1.05	-1.49	-1.49	<b>Pycard</b>	PKD and CARD domain containing	0001502 // cartilage condensation // inferred from electronic annotation // 00060348 // bone development // infer	
NM_020769	NR_022718892	0.00252347	0.4994762	0.4994762	-1.98	-2.24	1.70	-1.50	<b>Chad</b>	chondroatherin	0006801 // superoxide metabolic process // not recorded // 0006979 // response to oxidative stress // inferred fr	
NM_008706	NR_017970597	0.04884449	0.08275565	0.08275565	-1.07	1.36	1.03	-1.50	<b>Nqo1</b>	NAD(P)H dehydrogenase, quinone 1	0002690 // positive regulation of leukocyte chemotaxis // not recorded // 0006508 // proteolysis // inferred fr	
NM_010172	NR_006510132	0.011242445	0.011242445	0.011242445	1.89	1.35	2.10	-1.50	<b>F7</b>	coagulation factor VII	0006508 // proteolysis // inferred from electronic annotation // 0006898 // receptor-mediated endocytosis // infe	
NM_001013373	NR_006510132	0.011242445	0.011242445	0.011242445	-1.66	-1.49	1.34	-1.50	<b>Trmpss13</b>	transmembrane protein, serine 13	0002376 // immune system process // inferred from electronic annotation // 0002819 // regulation of adaptive im	
NM_001159393	NR_020029576	0.032851394	0.090463966	0.090463966	-1.04	1.49	-1.03	-1.50	<b>Irf1</b>	interferon regulatory factor 1	0002376 // immune system process // inferred from electronic annotation // 0002819 // regulation of adaptive im	
NM_001029841	NR_0091912	0.006520668	0.011245530	0.011245530	1.15	1.51	1.15	-1.50	<b>Sia</b>	src-like adaptor	0007155 // cell adhesion // inferred from electronic annotation // 0019221 // cytokine-mediated signaling pathwa	
NM_001252651	NR_913E-04	0.018762708	0.020152634	0.020152634	-1.39	1.00	1.09	-1.51	<b>Csf3r</b>	colony stimulating factor 3 receptor (granulocyte)	0001875 // activation of MAPK activity // not recorded // 0001570 // vasculogenesis // inferred from mutant phen	
NM_0011562	NR_011242957	0.01662339	0.11330092	0.11330092	1.15	1.60	1.08	-1.51	<b>Tgfb1</b>	transforming growth factor beta 1	0001502 // cartilage condensation // inferred from electronic annotation // 00060348 // bone development // infer	
NM_001164708	NR_011390411	0.01662339	0.11330092	0.11330092	-1.52	1.21	-1.22	-1.51	<b>Hspb2</b>	heat shock protein 2	0006801 // superoxide metabolic process // not recorded // 0006979 // response to oxidative stress // inferred fr	
NM_020557	NR_381188	0.006507471	0.01167828	0.01167828	-1.39	-1.16	1.27	-1.53	<b>Cmpk2</b>	cytidine monophosphate (UMP-CMP) kinase 2, mitochondrial	0006801 // superoxide metabolic process // not recorded // 0006979 // response to oxidative stress // inferred fr	
NM_009099	NR_006507471	0.01167828	0.01167828	0.01167828	-1.58	-1.24	1.21	-1.53	<b>Trim30a</b>	tripartite motif-containing 30A // tripartite motif-containing 30D	0006351 // transcription, DNA-templated // inferred from electronic annotation // 0006355 // regulation of transc	
NM_001081029	NR_868243	0.00654631	0.00654632	0.00654632	1.86	1.91	1.50	-1.54	<b>Tmem243</b>	transmembrane protein 243, mitochondrial	0006351 // transcription, DNA-templated // inferred from electronic annotation // 0006355 // regulation of transc	
NM_029495	NR_178825	0.011244910	0.011244910	0.011244910	-1.19	-1.24	1.60	-1.55	<b>Eps11</b>	epithelial stromal interaction 1 (breast)	0006898 // receptor-mediated endocytosis // inferred from sequence or structural similarity // 0006898 // recept	
NM_011150	NR_109E-05	0.020499367	0.02188839	0.02188839	-1.01	-1.31	2.06	-1.55	<b>Lgals3bp</b>	lectin, galactoside-binding, soluble, 3 binding protein	0006351 // transcription, DNA-templated // inferred from electronic annotation // 0006355 // regulation of transc	
NM_001164289	NR_001164323	0.006518862	0.006518862	0.006518862	-1.26	-1.21	1.49	-1.55	<b>Pph1d</b>	PHD finger protein 11C // PHD finger protein 11D	0006898 // receptor-mediated endocytosis // inferred from sequence or structural similarity // 0006898 // recept	
NM_001164625	NR_011242957	0.01662339	0.11330092	0.11330092	-1.57	-1.29	1.28	-1.56	<b>Tatd1</b>	thiosulfate sulfurtransferase (rhodanese)-like domain containing 1	0006898 // receptor-mediated endocytosis // inferred from sequence or structural similarity // 0006898 // recept	
NM_001159738	NR_016960	0.006496447	0.006496448	0.006496448	1.45	1.16	-1.16	-1.56	<b>Cd200</b>	chemokine (C-C motif) ligand 20	0002376 // immune system process // inferred from electronic annotation // 0006508 // proteolysis // inferred fr	
NM_007686	NR_0082811646	0.046391945	0.3154507	0.3154507	-1.19	1.35	-1.02	-1.56	<b>Cj</b>	complement component factor Cj	0008152 // metabolic process // inferred from electronic annotation	
NM_026601	NR_C_068584606	0.040043514	0.5474951	0.5474951	-1.20	1.46	-1.12	-1.57	<b>Hyl</b>	hydroxypruvate isomerase homolog (E. coli)	0008152 // metabolic process // inferred from electronic annotation	
NM_001040005	NR_006534631	0.006534632	0.006534632	0.006534632	-1.23	-1.15	1.47	-1.57	<b>Rnf213</b>	ring finger protein 213	0008152 // metabolic process // inferred from electronic annotation // 0016567 // protein ubiquitination // not r	
NM_001160711	NR_536E-05	0.010786352	0.061238483	0.061238483	-1.30	1.00	1.21	-1.57	<b>Cd300g</b>	CD300 antigen like family member G	0002376 // immune system process // inferred from electronic annotation // 0002414 // immunoglobulin transcyt	
NM_016780	NR_006532312	0.011248766	0.011248766	0.011248766	-1.44	-1.18	1.29	-1.58	<b>Irgb3</b>	integrin beta 3	0001938 // positive regulation of endothelial cell proliferation // not recorded // 0001954 // positive regulation of	
NM_007421	NR_0181965	0.033065483	0.001208518	0.001208518	1.22	2.02	-1.05	-1.58	<b>Adsl1</b>	adenylosuccinate synthetase like 1	0006613 // purine nucleotide metabolic process // inferred from direct assay // 0006164 // purine nucleotide bios	
NM_013640	NR_0004284681	0.001395478	0.06894126	0.06894126	-1.23	1.44	-1.12	-1.58	<b>Psmo10</b>	proteasome (synthetase, macropain) subunit, beta type 10	0000902 // cell morphogenesis // inferred from mutant phenotype // 0006508 // proteolysis // inferred from elect	
NM_0013132	NR_001313714	0.001313714	0.001313714	0.001313714	-1.46	-1.34	1.47	-1.60	<b>Sp100</b>	nuclear antigen Sp100	0000723 // telomere maintenance // inferred from sequence or structural similarity // 0006338 // chromatin rem	
NM_011530	NR_573E-04	0.05744587	0.05744587	0.05744587	1.21	1.42	-1.07	-1.60	<b>Tsp2</b>	transporter 2, ATP-binding cassette, sub-family B (MDR/TAP)	0001916 // positive regulation of cell mediated cytotoxicity // inferred from direct assay // 0001916 // positive r	
NM_013612	NR_006495773	0.006495774	0.006495774	0.006495774	-1.19	-1.01	1.36	-1.61	<b>Ski1a1</b>	solute carrier family 11 (proton-coupled divalent metal ion transporters), member 1	0000050 // protein import into nucleus, translocation // inferred from mutant phenotype // 0000165 // MAPK casc	
NM_001170853	NR_006495971	0.006495971	0.006495971	0.006495971	-1.64	-1.59	1.57	-1.61	<b>R204a</b>	retinoic acid receptor 204 // 205 // myeloid cell nuclear differentiation antigen 2	0001012 // negative regulation of transcription from RNA polymerase II promoter // - // 0003038 // negative re	
NM_011452	NR_006495971	0.006495971	0.006495971	0.006495971	1.41	1.53	1.49	-1.61	<b>Serp1n9b</b>	serpin (or cysteine) activated inhibitor, class B, member 9b	0001951 // negative regulation of endopeptidase activity // not recorded // 0001935 // cytotoxicity // inferred fr	
NM_001254744	NR_0005418789	0.028454479	0.06375431	0.06375431	-1.06	1.37	1.11	-1.62	<b>E03003006Rik</b>	RIKEN cDNA E03003006 gene	0007049 // cell cycle // inferred from electronic annotation // 0042127 // regulation of cell proliferation // infer	
NM_007281	NR_01870459	0.01870459	0.01903932	0.01903932	-1.17	-1.13	1.62	-1.62	<b>Mettl21e</b>	methyltransferase like 21E	0003259 // methylation // inferred from electronic annotation	
NM_198095	NR_011248766	0.011248766	0.011248766	0.011248766	-1.24	-1.18	1.57	-1.64	<b>Bst2</b>	bone marrow stromal cell antigen 2	0002376 // immune system process // inferred from electronic annotation // 0002737 // negative regulation of pla	
NM_029847	NR_006517456	0.006517456	0.006517456	0.006517456	-1.46	-1.02	1.16	-1.65	<b>Arsk</b>	arylsulfatase K	0008152 // metabolic process // inferred from electronic annotation	
NM_028801	NR_006506653	0.006506653	0.006506653	0.006506653	-2.91	-6.20	3.52	-1.65	<b>Muc5b</b>	mucin 5, subtype B, tracheobronchial	0042742 // defense response to bacterium // inferred from mutant phenotype // 00043030 // regulation of macrop	
NM_183249	NR_0034024853	0.011973868	0.37563986	0.37563986	1.28	1.48	1.44	-1.66	<b>Wf4c21</b>	WAP-four disulfide core domain 21	0010466 // negative regulation of peptidase activity // inferred from electronic annotation // 0003496 // response	
NM_008360	NR_034024853	0.011973868	0.37563986	0.37563986	-1.21	1.58	-1.15	-1.66	<b>I18</b>	interleukin 18	0000165 // MAPK cascade // not recorded // 0001525 // angiogenesis // not recorded // 0001525 // angiogenesis, i	
NM_013930	NR_011973868	0.011973868	0.37563986	0.37563986	-1.91	-1.36	1.18	-1.66	<b>Aass</b>	aminoadipate-semialdehyde synthase	0006091 // generation of precursor metabolites and energy // traceable author statement // 0008152 // metabolic	
NM_008611	NR_011973868	0.011973868	0.37563986	0.37563986	1.38	1.21	1.91	-1.67	<b>Mmp8</b>	matrix metalloproteinase 8	0006508 // proteolysis // not recorded // 00030574 // collagen catabolic process // inferred from electronic anat	
NM_023785	NR_011973868	0.011973868	0.37563986	0.37563986	-1.89	-1.94	1.73	-1.69	<b>Pbbp</b>	pro-platelet basic protein	0002523 // leukocyte migration involved in inflammatory response // inferred from mutant phenotype // 0002690	
NM_010734	NR_011973868	0.011973868	0.37563986	0.37563986	-1.56	-1.38	1.49	-1.69	<b>Lst1</b>	leukocyte specific transcript 1	0000902 // cell morphogenesis // inferred from electronic annotation // 0002376 // immune system process // inf	
NM_011517	NR_06025549	0.04851214	0.54293686	0.54293686	-1.80	1.27	-1.34	-1.71	<b>Syp3</b>	synaptonemal complex protein 3	0000711 // meiotic DNA repair synthesis // inferred from genetic interaction // 0007049 // cell cycle // inferred fr	
NM_001317105	NR_133862	0.005208184	0.245E-04	0.245E-04	1.37	1.48	1.59	-1.71	<b>Pig</b>	fibronectin gamma chain	0002250 // adaptive immune response // inferred from electronic annotation // 0002376 // immune system proces	
NM_001291892	NR_001291893	0.001291893	0.001291893	0.001291893	1.56	1.77						

RefSeq Transcript ID (p (Genotype)   (p (Genotype-Exposure)   (p (Exposure)   FC WT:KO   FC KO Air:O3   FD Air WT:KO   FD O3 WT:KO   Gene Symbol   Gene Title   Gene Ontology Biological Process										
NM_017373//XM.J	0.15306924	0.002679221	4.19E-05	1.48	3.96	-1.34	2.00	<b>Nfj13</b>	nuclear factor, interleukin 3, regulated	0000122 // negative regulation of transcription from RNA polymerase II promoter // not recorded//0006351 // tr
NM_025416	0.020313757	0.042609792	0.08676615	-1.10	1.72	1.10	2.08	<b>Them5</b>	thioesterase superfamily member 5	0006629 // lipid metabolic process // inferred from electronic annotation//0006631 // fatty acid metabolic proce
NM_010247//XM.J	2.24E-05	0.002021546	0.09661372	-1.14	1.55	1.17	2.08	<b>Psmb8</b>	proteasome (prosome, macropain) subunit, beta type 8 (large multifunctional peptidase 7)	0002376 // immune system process // inferred from electronic annotation//0006508 // proteolysis // inferred fro
NM_001310640//X	0.00892747	0.026918758	2.12E-05	2.09	4.28	2.01	2.08	<b>Pmva</b>	phosphomevalonate kinase	0006629 // lipid metabolic process // inferred from electronic annotation//0006694 // steroid biosynthetic proce
NM_028967//XM.J	6.63E-04	0.013054218	0.014988259	-1.04	1.80	1.12	2.11	<b>Raf2</b>	basic leucine zipper transcription factor, ATF-like 2	0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 // regulation of transc
NM_001271005//X	6.43E-05	0.011145398	0.96271	-1.21	1.36	1.30	2.14	<b>H2-123</b>	histocompatibility 2, T region locus 23	0001916 // positive regulation of T cell mediated cytotoxicity // inferred from direct assay//0001915 // positive r
NM_010531//XM.I	6.64E-05	0.001810247	0.001231183	1.09	1.78	1.32	2.16	<b>I18bp</b>	interleukin 18 binding protein	0004208 // T-helper 1 type im
NM_001037713//X	0.001291513//XM_006533567//XM_006533568//XM_			-1.24	-1.12	1.97	2.19	<b>Xaf1</b>	XIAP associated factor 1	0006915 // apoptotic process // inferred from electronic annotation//0031333 // negative regulation of protein c
NM_027209//XM_011247337				-1.66	-1.18	1.56	2.20	<b>Msa6b</b>	membrane-spanning 4-domains, subfamily A, member 6B	
NM_015783//XR_188557//XJ_397495				-1.27	-1.62	2.85	2.24	<b>Isg15</b>	ISG15 ubiquitin-like modifier	
NM_153590//XM_006506121//XM_006506122//XM_006				-1.54	-1.28	1.89	2.26	<b>Kir1</b>	killer cell lectin-like receptor family E member 1	0019941 // modification-dependent protein catalytic process // inferred from direct assay//0031397 // negative
NM_001302559//X	1.27E-06	8.77E-04	1.11E-05	-1.66	-4.51	6.15	2.27	<b>Sjfn4//Sjfn3</b>	schlafen 4//schlafen 3	0002223 // stimulatory C-type lectin receptor signaling pathway // inferred from direct assay//0002859 // negati
NM_001305935//X	0.03148155	0.012993463	0.24723457	-1.92	-1.48	-1.18	2.40	<b>Nctd4b</b>	branched chain ketoacid dehydrogenase E1, beta polypeptide	0008285 // negative regulation of cell proliferation // inferred from direct assay
NM_008331				-1.78	-1.76	2.43	2.45	<b>Pyha1</b>	pyrin and NIN domain family, member 1	0001152 // metabolic process // inferred from electronic annotation//0009063 // cellular amino acid catabolic pr
NM_001080941//X	0.033015296	0.047486916	0.3625288	-1.97	1.24	1.06	2.60	<b>Zfp429</b>	interferon-induced protein with tetratricopeptide repeats 1	0002376 // immune system process // inferred from electronic annotation//0009615 // response to virus // infer
NM_011073//XM.J	2.40E-06	0.013736106	0.49245003	-1.33	1.12	1.76	2.61	<b>Prf1</b>	zinc finger protein 429	0006355 // regulation of transcription, DNA-templated // inferred from electronic annotation
NM_001314054//NM_031168				5.31	11.59	1.20	2.60	<b>I6</b>	perforin 1 (pore forming protein)	0001771 // immunological synapse formation // not recorded//0002357 // defense response to tumor cell // infe
NM_011403				-2.95	-1.40	1.28	2.69	<b>Sic1a1</b>	interleukin 6	0001781 // neutrophil apoptotic process // inferred from direct assay//0001781 // neutrophil apoptotic process //
NM_139198//XM_011249430				-1.70	-1.21	1.93	2.72	<b>Ploc8</b>	solute carrier family 4 (anion exchanger), member 1	0006810 // transport // inferred from electronic annotation//0006811 // ion transport // inferred from electronic
NM_029499//XM_006527250//XM_006527251				-1.85	-1.55	2.31	2.75	<b>Msa4c</b>	placenta-specific 8	0008284 // positive regulation of cell proliferation // inferred from direct assay//0009409 // response to cold // ir
NM_001143686				-2.40	-1.78	2.05	2.76	<b>Apol11b</b>	membrane-spanning 4-domains, subfamily A, member 4C	
NM_013855//XM.I	1.19E-05	5.73E-04	0.5460914	-1.50	1.52	1.23	2.80	<b>Psmb9</b>	apolipoprotein L11b	0008689 // lipid transport // inferred from electronic annotation//0041217 // lipoprotein metabolic process // inf
NM_028386//XM_006522491				-1.57	-1.23	2.22	2.83	<b>Rtp4</b>	proteasome (prosome, macropain) subunit, beta type 9 (large multifunctional peptidase 2)	0002376 // immune system process // inferred from electronic annotation//0006508 // proteolysis // inferred fro
NM_001161730//X	6.23E-06	7.33E-04	0.080780625	-1.29	1.70	1.32	2.90	<b>Tap1</b>	receptor transporter protein 4	0001580 // detection of chemical stimulus involved in sensory perception of bitter taste // not recorded//0006611
NM_137869	0.002842786	0.025394054	0.031699836	-1.03	2.22	1.28	2.94	<b>Sfp21a</b>	transporter 1, ATP-binding cassette, subfamily B (MDR/TPA)	0002250 // adaptive immune response // inferred from electronic annotation//0002376 // immune system proce
NM_001281830//NM_029803				-2.98	-2.64	2.68	3.02	<b>Ifi271a</b>	stefin A2 like 1	0010951 // negative regulation of endopeptidase activity // inferred from electronic annotation
NM_010654//XM_006505655//XM_006505656				-2.08	-1.19	1.73	3.03	<b>Kir1d1</b>	interferon, alpha-inducible protein 27 like 2A	0007568 // aging // inferred from direct assay//000615 // response to virus // inferred from direct assay
NM_172777//XM.J	7.16E-05	1.21E-04	0.010784728	-2.16	1.44	-1.03	3.04	<b>Gbp9</b>	killer cell lectin-like receptor, subfamily D, member 1	0002228 // natural killer cell mediated immunity // not recorded
NM_001205313//X	1.71E-06	9.54E-04	0.1928924	-1.26	1.65	1.49	3.08	<b>Stat1</b>	signal transducer and activator of transcription 1	0008152 // metabolic process // inferred from electronic annotation//0042832 // defense response to protozoan
NM_001252600//NM_001252601//NM_016850//XM_006536214				-1.35	-1.46	3.34	3.09	<b>Irf7</b>	interferon regulatory factor 7	0002376 // immune system process // inferred from electronic annotation//0002819 // regulation of adaptive im
NM_008326//XM.I	4.82E-07	0.001143392	6.02E-04	1.04	1.99	1.62	3.09	<b>Irgm1</b>	immunity-related GTPase family M member 1	0002376 // immune system process // inferred from electronic annotation//0006914 // autophagy // inferred fro
NM_145211//XM.J	9.80E-09	0.03495188	1.72E-05	-1.43	-1.68	3.66	3.10	<b>Oas1a</b>	2'-5' oligoadenylate synthetase 1A	0002376 // immune system process // inferred from electronic annotation//0006164 // purine nucleotide biosynt
NM_001139519//X	1.96E-06	0.021276742	0.010490653	-1.01	1.65	1.88	3.11	<b>Zbp1</b>	Z-DNA binding protein 1	0002376 // immune system process // inferred from electronic annotation//0008152 // metabolic process // inf
NM_001162883//NM_001168660//NM_173743//NM_173786//XM_00652				-1.48	-1.38	2.95	3.15	<b>ApoB9//ApoBb</b>	apolipoprotein L9a//apolipoprotein L9b	0006869 // lipid transport // inferred from electronic annotation//0042157 // lipoprotein metabolic process // inf
NM_144559	3.09E-06	0.00304968	0.002918902	-1.04	1.89	1.64	3.21	<b>Fcgr4</b>	Fc receptor, IgG, low affinity IV	0001866 // NK T cell proliferation // not recorded//0051930 // regulation of sensory perception of pain // not rec
NM_011854//XM_006530314//XM_006530315//XM_006530316				-1.39	-1.38	3.35	3.37	<b>Oas1z</b>	2'-5' oligoadenylate synthetase-like 2	0002376 // immune system process // inferred from electronic annotation//0006164 // purine nucleotide biosynt
NM_001293690//X	0.003732	0.00231509	0.021634238	-1.29	2.66	1.00	3.43	<b>Irf1</b>	indoleamine 2,3-dioxygenase 1	0002376 // immune system process // inferred from electronic annotation//0002534 // cytokine production invol
NM_029509//XM.J	0.025589565	0.007223136	0.11731671	-1.48	2.60	-1.11	3.45	<b>Gbp8</b>	guanylate-binding protein 8	0008152 // metabolic process // inferred from electronic annotation//0071346 // cellular response to interferon-g
NM_173886	1.03E-04	0.011639653	0.06928708	-1.16	1.80	1.66	3.45	<b>Sic2s3a1</b>	solute carrier family 25 (mitochondrial carrier; adenine nucleotide translocator), member 31	0006810 // transport // inferred from electronic annotation//0005085 // transmembrane transport // inferred fr
NM_010260	5.92E-05	1.37E-04	0.80003136	-1.75	2.04	1.01	3.59	<b>Gbp2</b>	guanylate binding protein 2	0008152 // metabolic process // inferred from electronic annotation//0035458 // cellular response to interferon-I
NM_175449	0.002981814	0.044325806	0.6242128	-1.50	1.62	1.52	3.70	<b>Fam26f</b>	family with sequence similarity 26, member F	0006810 // transport // inferred from electronic annotation//0006811 // ion transport // inferred from electronic
NM_011315				4.04	2.44	6.20	3.74	<b>Saa3</b>	serum amyloid A 3	0006953 // acute-phase response // inferred from electronic annotation//0007252 // I-kappaB phosphorylation //
NM_001271676//X	1.75E-06	7.61E-05	0.052070796	-1.42	2.20	1.36	4.24	<b>Ifi47</b>	interferon gamma inducible protein 47	0006952 // defense response // inferred from mutant phenotype//0007165 // signal transduction // inferred fro
NM_024253	4.18E-04	0.038715716	0.90266514	-1.64	1.48	1.75	4.25	<b>Nkg7</b>	natural killer cell group 7 sequence	
NM_001039160//X	3.29E-07	5.64E-05	0.29797998	-1.50	1.92	1.55	4.47	<b>Ovin1</b>	GTPase, very large interferon inducible 1	0001503 // ossification // not recorded//0002376 // immune system process // inferred from electronic annotatio
NM_021384//NM_011243886				-1.82	-1.44	3.55	4.48	<b>Rasd2</b>	radical S-adenosyl methionine domain containing 2	0001666 // response to hypoxia // inferred from electronic annotation//0001889 // liver development // infer
NM_001136059//NM_009092//XM_006510810				-6.59	-3.43	2.36	4.53	<b>Cypl1a1</b>	cytochrome P450, family 1, subfamily A, polypeptide 1	0009396 // muscle contraction // not recorded//0008152 // metabolic process // inferred from electronic anot
NM_030679//NM.I	0.9685817	0.034358054	0.9833375	-4.93	4.86	-4.93	4.87	<b>Myh1//Myh4</b>	myosin, heavy polypeptide 1, skeletal muscle, adult//myosin, heavy polypeptide 4, skeletal muscle	0008152 // metabolic process // inferred from electronic annotation//0042832 // defense response to protozoan
NM_001083312//X	1.08E-05	3.38E-04	0.22118247	-1.58	2.29	1.36	4.93	<b>Gbp7</b>	guanylate binding protein 7	0001913 // T cell mediated cytotoxicity // inferred from mutant phenotype//0006508 // proteolysis // inferred fr
NM_013542	4.09E-07	0.007064547	0.08473857	-1.69	1.23	2.44	5.07	<b>Gamb</b>	granzyme B	0002376 // immune system process // inferred from electronic annotation//0032088 // negative regulation of NF
NM_001033207//X	3.61E-06	0.012560561	0.24143435	-1.29	1.75	2.25	5.08	<b>Nlr3</b>	NLR family, CARD domain containing 5	0004341 // response to interferon-gamma // inferred from direct assay//0034341 // response to interferon-gamm
NM_019440	1.35E-06	1.46E-04	0.035187297	-1.41	2.39	1.55	5.20	<b>Irgm2</b>	immunity-related GTPase family M member 2	0006955 // immune response // non-traceable author statement//000615 // response to virus // inferred from d
NM_001145164//X	3.88E-07	6.50E-04	0.00193326	-1.06	2.44	2.09	5.42	<b>Tgtp1//Tgtp2</b>	T cell specific GTPase 1//T cell specific GTPase 2	0006955 // immune response // not recorded//0007165 // signal transduction // not recorded//0007166 // cell
NM_021893//XM.J	3.39E-05	3.35E-04	5.14E-04	-1.07	4.44	1.23	5.88	<b>Ccl27a</b>	CD274 antigen	0035458 // cellular response to interferon-beta // inferred from direct assay
NM_018738	1.79E-07	3.68E-05	0.02253012	-1.51	2.59	1.84	7.20	<b>Igtg</b>	interferon gamma induced GTPase	0008152 // metabolic process // inferred from electronic annotation//0035458 // cellular response to interferon-I
NM_001289492//X	2.14E-06	4.39E-04	0.07993907	-2.35	1.66	1.87	7.28	<b>Gbp3</b>	guanylate binding protein 3	0002376 // immune system process // inferred from electronic annotation//0008152 // metabolic process // infer
NM_001146275//X	4.10E-06	6.57E-04	0.057767134	-1.47	2.75	1.83	7.39	<b>Hgp1</b>	interferon inducible GTPase 1	
NM_133871//XM_006502485//XM_006502486				-2.92	-1.92	5.04	7.66	<b>Ifi44</b>	interferon-induced protein 44	
NM_010370	2.06E-06	0.004724333	0.00905636	-2.57	1.16	2.67	7.98	<b>Gzma</b>	granzyme A	0006508 // proteolysis // inferred from electronic annotation//0006915 // apoptotic process // inferred from elec
NM_194336//XM.I	7.76E-07	3.69E-05	0.37096202	-2.64	2.32	1.63	10.01	<b>Gbp6</b>	guanylate binding protein 6	0006955 // immune response // inferred from mutant phenotype//0008152 // metabolic process // inferred fro
NM_001033767//X	4.80E-06	0.043635536	0.7827524	-1.50	1.72	4.07	10.48	<b>Gm4951</b>	predicted gene 4951	0035458 // cellular response to interferon-beta // inferred from direct assay

Table S7. Common genes altered by O3 in Tnfr- and Nfkb1-dependent manner (n=341)

Venn Diagram analysis of Tnfr-dependent genes (n=2180, pooled from 24, 48, and 72 hr O3) and Nfkb1-dependent genes (n=2397). Fold difference (FD); Positive-higher in KO-O3, negative-lower in KO-O3, compared to corresponding WT-O3.

RefSeq	Transcript ID	p Tnfr 24 hr	p Tnfr 48hr	p Tnfr 72 hr	p Nfkb1	FD Tnfr 24 hr	FD Tnfr 48 hr	FD Nfkb1	Gene Symbol	Gene Title	Gene Ontology	
NM_010370		0.031957				-1.27	-1.89	-1.36	<b>7.98</b> <i>Gzma</i>	granzyme A	0006508 // proteolysis // inferred from electronic annotation//0006915 // apoptotic process // inferred from electro	
NM_001136059//NM_009992//X		0.021329				-1.64	<b>1.21</b>	-1.57	<b>4.53</b> <i>Cyp11a1</i>	cytochrome P450, family 1, subfamily a, polypeptide 1	0001666 // response to hypoxia // inferred from electronic annotation//0001889 // liver development // inferred from	
NM_024253		0.0126742				-1.03	-1.48	-1.30	<b>4.25</b> <i>Nkg7</i>	natural killer cell group 7 sequence	0005515 // protein binding // inferred from electronic annotation	
NM_001293690//NM_008324		0.0474173				-1.02	-1.31	-1.08	<b>3.43</b> <i>Id1</i>	indoleamine 2,3-dioxygenase 1	0002376 // immune system process // inferred from electronic annotation//0002534 // cytokine production involved	
NM_144559		0.0320214				0.3202	<b>1.04</b>	-1.07	<b>3.21</b> <i>Fcgr4</i>	FC receptor, IgG, low affinity IV	0001866 // NK T cell proliferation // not recorded//0051930 // regulation of sensory perception of pain // not record	
NM_013585//NM_006523730//X		0.0428359				0.4284	<b>1.16</b>	-1.25	<b>1.14</b> <b>2.80</b> <i>Psmb9</i>	proteasome (prosome, macropain) subunit, beta type 9 (large multifunctional pep	0002376 // immune system process // inferred from electronic annotation//0006508 // proteolysis // inferred from e	
NM_029499//NM_001		0.0458086				0.04581	<b>1.26</b>	-1.02	<b>2.75</b> <i>Ms404c</i>	membrane-spanning 4-domains, subfamily A, member 4C	0005887 // integral component of plasma membrane // inferred from electronic annotation//0016020 // membrane,	
NM_139198//NM_001		0.0379849				0.03798	<b>1.85</b>	-1.21	<b>1.44</b> <b>2.72</b> <i>Plac8</i>	placenta-specific 8	0002884 // positive regulation of cell proliferation // inferred from direct assay//0009409 // response to cold // infer	
NM_001314054//NM_00109972						0.011	<b>1.78</b>	-1.17	-1.01	<b>2.63</b> <i>Irf6</i>	interleukin 6	0001781 // neutrophil apoptotic process // inferred from direct assay//0001781 // neutrophil apoptotic process // inf
NM_001271005//NM_010398//X		0.0493594				0.04936	<b>1.02</b>	-1.46	-1.13	<b>2.14</b> <i>H2-T23</i>	Riken cDNA C920025E04 gene//histocompatibility 2, T region locus 23	0001916 // positive regulation of T cell mediated cytotoxicity // inferred from direct assay//0001916 // positive regul
NM_017373//NM_006516875//X		0.0236738				0.02367	-1.31	-1.09	-1.34	<b>2.00</b> <i>Nfj3</i>	nuclear factor, interleukin 3, regulated	0001222 // negative regulation of transcription from RNA polymerase II promoter // not recorded//0006351 // trans
NM_010234		0.0392224				0.03392	<b>2.51</b>	<b>1.06</b>	<b>1.09</b> <b>1.97</b> <i>Fos</i>	FB1 osteosarcoma oncogene	0001661 // conditioned taste aversion // inferred from electronic annotation//0006355 // regulation of transcription,	
NM_015767//NM_001		0.0470459				0.04705	-1.19	-1.07	<b>1.03</b> <b>1.96</b> <i>Tpa</i>	tocopherol (alpha) transfer protein	0001890 // placenta development // inferred from mutant phenotype//0001892 // embryonic placenta development	
NM_001164059//NM_00140566						0.01406	<b>1.72</b>	-1.04	-1.05	<b>1.91</b> <i>Sell</i>	selectin, lymphocyte	0001755 // cell adhesion // inferred from electronic annotation//0032198 // response to ATP // inferred from direct:
NM_001111059//NM_00477121						0.04771	-1.83	-1.03	-1.41	<b>1.78</b> <i>Cdkn1a</i>	cyclin-dependent kinase inhibitor 1A [P21]	0000079 // regulation of cyclin-dependent protein serine/threonine kinase activity // inferred from mutant phenotype,
NM_021718		0.0186814				0.01868	<b>1.52</b>	<b>1.11</b>	-1.09	<b>1.77</b> <i>Ms404b</i>	membrane-spanning 4-domains, subfamily A, member 4B	0005887 // integral component of plasma membrane // inferred from direct assay//0016020 // membrane // inferred
NM_001291892//NM_0090002		0.0301939				0.03019	<b>1.65</b>	<b>1.52</b>	<b>1.02</b> <b>1.71</b> <i>Lilr4b</i>	leukocyte immunoglobulin-like receptor, subfamily B, member 4B//Lilr4a	0002250 // adaptive immune response // inferred from electronic annotation//0002376 // immune system process //	
NM_010734		0.0188023				0.01888	<b>1.27</b>	-1.13	-1.09	<b>1.69</b> <i>Lst1</i>	leukocyte specific transcript 1	0000902 // cell morphogenesis // inferred from electronic annotation//0002376 // immune system process // infer
NM_008611		0.0280208				0.02802	<b>1.07</b>	-1.02	<b>1.04</b> <b>1.67</b> <i>Mmp8</i>	matrix metalloproteinase 8	0006508 // proteolysis // not recorded//0030574 // collagen catabolic process // inferred from electronic annotation	
NM_183249		0.0327021		0.0431278		0.0327	<b>1.24</b>	<b>1.38</b>	<b>1.26</b> <b>1.66</b> <i>Wfdc21</i>	WAP four-disulfide core domain 21	0010466 // negative regulation of peptidase activity // inferred from electronic annotation//0032496 // response to I	
NM_001159738//NM_00021256		0.0141236		0.0087143		0.01412	-1.33	-1.18	-1.22	<b>1.56</b> <i>Ccl20</i>	chemokine (C-C motif) ligand 20	0002548 // monocyte chemotaxis // --//0006935 // chemotaxis // not recorded//0006954 // inflammatory respons
NM_029495//NM_17		0.0158681				0.01587	<b>1.09</b>	-1.07	-1.03	<b>1.55</b> <i>Epst11</i>	epithelial stromal interaction 1 (breast)	
NM_001252651//NM_00126991						0.0127	<b>1.24</b>	-1.23	-1.21	<b>1.51</b> <i>Csf3r</i>	colony stimulating factor 3 receptor (granulocyte)	
NM_001013373//NM_006510132		0.0305592				0.03056	-1.12	-1.21	-1.18	<b>1.50</b> <i>Tmprss13</i>	transmembrane protease, serine 13	
NM_0010172		0.0051493		8.73E-04		0.00172	<b>1.18</b>	<b>1.22</b>	<b>1.02</b> <b>1.50</b> <i>F7</i>	coagulation factor VII		
NM_009780//NM_001		0.0110776		0.0215402		0.02154	-1.21	-1.11	-1.11	<b>1.48</b> <i>C4b</i>	complement component 4B (Chido blood group)//complement C4-B	
NM_025989//NM_006508121//X		0.0297162				0.02972	-1.11	<b>1.00</b>	<b>1.06</b> <b>1.48</b> <i>Gp2</i>	glycoprotein 2 (zymogen granule membrane)		
NM_134133//NM_006525481//X		0.0145036				0.0145	-1.23	<b>1.00</b>	-1.03	<b>1.48</b> <i>Smlm3</i>	small integral membrane protein 3	
NM_001278269//NM_00166895						0.01669	<b>1.40</b>	-1.05	-1.10	<b>1.48</b> <i>Fyb</i>	FYN binding protein	
NM_011756		0.0041983				0.0042	<b>1.46</b>	<b>1.08</b>	<b>1.13</b> <b>1.46</b> <i>Zfp36</i>	zinc finger protein 36		
NM_178911//NM_001		0.032975				0.0033	<b>1.50</b>	-1.10	-1.05	<b>1.45</b> <i>Pld4</i>	phospholipase D family, member 4	
NM_008842		0.0062451				0.00625	<b>1.29</b>	-1.11	<b>1.01</b> <b>1.45</b> <i>Pim1</i>	proliferal integration site 1		
NM_007440//NM_011248676//X		0.0202748				0.02027	-1.04	-1.25	-1.01	<b>1.42</b> <i>Alox12</i>	arachidonate 12-lipoxygenase	
NM_010501//NM_001		0.048251				0.04825	<b>1.29</b>	-1.08	<b>1.28</b> <b>1.41</b> <i>Ifit3</i>	interferon-induced protein with tetratricopeptide repeats 3		
NM_009396//NM_006515792//X		0.0045507				0.00455	<b>1.09</b>	-1.20	<b>1.02</b> <b>1.40</b> <i>Tnfrsf2</i>	tumor necrosis factor, alpha-induced protein 2		
NM_001127348//NM_00269581						0.02696	<b>1.07</b>	<b>1.03</b>	<b>1.37</b> <i>Srs10</i>	springerovirus 10		
NM_138683//NM_006502862		0.0042547				0.00425	-1.05	-1.21	-1.09	<b>1.37</b> <i>Rgs19</i>	Rgspondin 1	
NM_019521		4.51E-04		0.0107763		0.01078	-1.25	-1.16	<b>1.04</b> <b>1.36</b> <i>Gas6</i>	growth arrest specific 6		
NM_025427		0.0063318				0.00633	-1.65	-1.27	-1.05	<b>1.35</b> <i>Rgcc</i>	regulator of cell cycle	
NM_009151//NM_001		0.0478234				0.04784	<b>1.21</b>	-1.01	-1.06	<b>1.35</b> <i>Selp1g</i>	selectin, platelet (alpha-selectin) ligand	
NM_013599//NM_001		0.0026953				0.0027	<b>1.07</b>	-1.29	-1.46	<b>1.34</b> <i>Mmp9</i>	matrix metalloproteinase 9	
NM_026835		0.0483779				0.04838	<b>1.14</b>	<b>1.58</b>	<b>1.15</b> <b>1.33</b> <i>Ms404d</i>	membrane-spanning 4-domains, subfamily A, member 6D		
NM_153071//NM_001		0.0285745				0.02857	-1.10	-1.02	-1.07	<b>1.33</b> <i>Gprc6a</i>	G protein-coupled receptor, family C, group 6, member 6A	
NM_001033301//NM_001205355		0.02936				0.02936	-1.57	-1.60	-1.14	<b>1.31</b> <i>Fhd1</i>	FHD domain containing 1	
NM_015786		0.0114646				0.01146	-1.04	-1.37	-1.14	<b>1.31</b> <i>Hist1h1c</i>	histone cluster 1, H1c	
NM_001001892//NM_001267808		0.0411866				0.04119	<b>1.05</b>	-1.18	-1.08	<b>1.30</b> <i>H2-D1</i>	histocompatibility 2, D region locus 1//histocompatibility 2, H1c, K region//histoc	
NM_145953//NM_006500815		0.0206117				0.02061	-1.24	<b>1.33</b>	-1.05	<b>1.29</b> <i>Chc</i>	cystathionase (cystathionine gamma-lyase)	
NM_001164885//NM_00081215		0.0186868				0.01869	-1.24	-1.06	<b>1.16</b> <b>1.27</b> <i>Lpin2</i>	lipin 2		
NM_001160163//NM_001160164		0.03408				0.03408	-1.02	-1.23	-1.05	<b>1.26</b> <i>Neu2</i>	neuraminidase 2	
NM_013566//NM_001		0.0116526				0.01165	<b>1.31</b>	-1.13	-1.16	<b>1.25</b> <i>Irbp7</i>	integrin beta 7	
NM_016675//NM_001		0.0374343				0.03743	<b>1.14</b>	<b>1.00</b>	-1.01	<b>1.25</b> <i>Cldn2</i>	claudin 2	
NM_029688		0.0112739				0.01127	<b>1.15</b>	<b>1.06</b>	-1.03	<b>1.24</b> <i>Srxn1</i>	sulfiredoxin 1 homolog (S. cerevisiae)	
NM_001252479//NM_00489366		0.0276464				0.04894	<b>1.19</b>	-1.07	-1.19	<b>1.24</b> <i>Cntm7</i>	CKLF-like MARVEL transmembrane domain containing 7	
NM_001316372//NM_008796//X		0.03876				0.02765	<b>1.06</b>	<b>1.08</b>	<b>1.07</b> <b>1.24</b> <i>Pctp</i>	phosphatidylcholine transfer protein		
NM_011401//NM_001		0.0387578				0.03876	<b>1.08</b>	-1.29	-1.11	<b>1.23</b> <i>Slc23a3</i>	solute carrier family 2 (facilitated glucose transporter), member 3	
NM_001001009//NM_00357954						0.0358	<b>1.05</b>	<b>1.06</b>	<b>1.15</b> <b>1.23</b> <i>Srp54a</i>	signal recognition particle 54B//signal recognition particle 54B//signal recognitio		
NM_011189		0.0427805				0.04278	<b>1.22</b>	<b>1.05</b>	<b>1.31</b> <b>1.22</b> <i>Psmc1</i>	proteasome (prosome, macropain) activator subunit 1 (PA28 alpha)		
NM_001037859//NM_00779//X		0.0395433				0.03954	<b>1.03</b>	-1.12	-1.02	<b>1.22</b> <i>Csf1r</i>	colony stimulating factor 1 receptor	
NM_007802//NM_006500974		0.046115				0.04611	<b>1.08</b>	<b>1.26</b>	<b>1.04</b> <b>1.21</b> <i>Ctsk</i>	cathespain K		
NM_02233//NM_001		1.41E-04				0.02233	-1.56	-1.12	-1.09	<b>1.21</b> <i>Hspud1</i>	homocysteine-inducible, endoplasmic reticulum stress-inducible, ubiquitin-like don	
NM_025510		4.81E-04		0.0113849		0.01138	<b>1.15</b>	-1.17	-1.10	<b>1.21</b> <i>Pilo</i>	paired immunoglobulin-like type 2 receptor alpha	
NM_010550//NM_001		0.03030509		0.0411284		0.04113	<b>1.20</b>	-1.20	-1.20	<b>1.11</b> <i>Irf2</i>	interleukin 1 receptor, type II	
NM_181821		0.0450951				0.0451	-1.12	-1.06	<b>1.01</b> <b>1.20</b> <i>Hcf1r1</i>	host cell factor C1 regulator 1 (XPO1-dependent)		
NM_00111015//NM_013681//X		0.0076582		0.0071612		0.00766	-1.04	-1.14	-1.13	<b>1.20</b> <i>Syn2</i>	synapsin II	
NM_001177945//NM_00309111						0.0309	-1.10	-1.01	-1.02	<b>1.19</b> <i>Aardc</i>	adipogenesis associated Mth938 domain containing	
NM_001286037//NM_00069666						0.0067	<b>1.45</b>	<b>1.09</b>	-1.14	<b>1.19</b> <i>Ncf1</i>	neutrophil cytosolic factor 1	
NM_008490		6.30E-05				6.30E-05	<b>1.01</b>	-1.12	-1.03	<b>1.19</b> <i>Lcat</i>	lecithin cholesterol acyltransferase	
NM_001113248//NM_00299019						0.0299	<b>1.29</b>	<b>1.08</b>	<b>1.00</b> <b>1.19</b> <i>Sin3b</i>	transcriptional regulator, SIN3 (yeast)		
NM_001290525//NM_00023673						0.00237	<b>1.19</b>	-1.20	-1.20	<b>1.19</b> <i>Blvrb</i>	biliverdin reductase B (flavin reductase (NADPH))	
NM_010476//NM_001		0.0374562				0.03746	<b>1.23</b>	<b>1.21</b>	<b>1.03</b> <b>1.18</b> <i>Hsd17b7</i>	hydroxysteroid (17-beta) dehydrogenase 7		
NM_001310705//NM_00397513						0.03975	-1.20	-1.13	-1.14	<b>1.18</b> <i>Slc16a4</i>	solute carrier family 16 (monocarboxylic acid transporters), member 4	
NM_001253751//NM_0006113		0.0114804				0.01148	<b>1.59</b>	<b>1.76</b>	<b>1.46</b> <b>1.17</b> <i>Fdps</i>	farnesyl diphosphate synthetase		
NM_009999		0.0400147				0.04001	-1.22	-1.24	<b>1.26</b> <b>1.17</b> <i>Cyp2b10</i>	cytochrome P450, family 2, subfamily B, polypeptide 10		
NM_028024		0.0497831				0.04978	<b>1.15</b>	<b>1.02</b>	<b>1.03</b> <b>1.17</b> <i>Nkiras2</i>	NFKB inhibitor interacting Ras-like protein 2		

RefSeq	Transcript ID	p Tnfr 24 hr	p Tnfr 48hr	p Tnfr 72 hr	p Nfk1	( FD Tnfr 24 hr (	FD Tnfr 48 hr (	FD Tnfr 72 hr (	FD Nfk1	Gene Symbol	Gene Title	Gene Ontology
NM_008304	0.022382				0.02238	-1.07	1.12	1.12	1.14	<i>Sdc2</i>	syndecan 2	0007399 // nervous system development // inferred from electronic annotation // 0016477 // cell migration // not rec
NM_021472//NM_20	0.0040024	0.0497113			0.04971	-1.12	-1.02	-1.01	1.13	<i>Rnase4</i>	ribonuclease, RNase A family 4	0001525 // angiogenesis // inferred from electronic annotation // 0001525 // angiogenesis // -- // 0001525 // angiogenesis
NM_001039373//NM	0.0017875	0.0108495	0.010648		0.01085	-1.12	-1.05	-1.05	1.13	<i>Cmc4//Mtcp1</i>	C-x(9)-C motif containing // mature T cell proliferation 1	0005739 // mitochondrion // inferred from direct assay // 0005739 // mitochondrion // not recorded
NM_00117833//NM	0.0479175				0.04792	-1.08	-1.06	-1.12	1.13	<i>Smox</i>	serpinine oxidase	0006598 // polyamine catabolic process // not recorded // 00046208 // spermine catabolic process // inferred from dir
NM_019814//NM_006512201//X	0.0321375				0.03214	-1.03	1.11	1.04	1.12	<i>Higd1a</i>	HIG1 domain family, member 1A	0006810 // transport // inferred from electronic annotation // 00042149 // cellular response to glucose starvation // inf
NM_001039373//NM	0.0017875	0.0108495	0.010648		0.01085	-1.12	-1.05	-1.05	1.12	<i>Mtcp1//Cmc4</i>	mature T cell proliferation 1 // C-x(9)-C motif containing 4	0005739 // mitochondrion // inferred from direct assay // 0005739 // mitochondrion // not recorded
XM_011238903//XM_011238926//	0.0332051				0.03321	2.61	3.75	3.71	1.12	<i>Gm37416//Gm39743//Gm40611//Gm408</i>	predicted gene, 37416 // predicted gene, 39743 // predicted gene, 40611 // predicted gene, 408	0006278 // RNA-dependent DNA replication // inferred from electronic annotation // 0008152 // metabolic process // 0000122 // negative regulation of transcription from RNA polymerase II promoter // not recorded // 0001570 // vas
NM_008416	0.001622				0.00162	1.90	1.19	1.03	1.12	<i>Junb</i>	jun B proto-oncogene	0000678 // transcription, DNA-templated // inferred from electronic annotation // 0006355 // regulation of transcript
NM_001289476//NM	0.0021963				0.0022	1.24	1.19	-1.05	1.12	<i>Psmo7</i>	proteasome (prosome, macropain) subunit, alpha type 7	0006508 // proteolysis // inferred from electronic annotation // 0006511 // ubiquitin-dependent protein catabolic pro
NM_011794//NM_006497159//X	0.0120047	0.0153885			0.012	-1.20	1.09	1.16	1.12	<i>Bpnt1</i>	biphosphate 3'-nucleotidase 1	0006139 // nucleobase-containing compound metabolic process // not recorded // 0006470 // protein dephosphoryla
NM_001038587//NM	0.0499708				0.04997	1.31	1.19	1.09	1.12	<i>Ador</i>	adenosine deaminase, RNA-specific	0001649 // osteoblast differentiation // inferred from mutant phenotype // 0001701 // in utero embryonic developme
NM_019777//NM_00	0.0031129				0.00311	1.08	1.03	-1.07	1.12	<i>Ibke</i>	inhibitor of kappaB kinase epsilon	0006468 // protein phosphorylation // not recorded // 0006974 // cellular response to DNA damage stimulus // infer
NM_153059//NM_00	0.043095				0.04305	1.03	-1.04	-1.14	1.14	<i>Tmem5</i>	transmembrane protein 5	0006486 // protein glycosylation // inferred from electronic annotation // 0035269 // protein O-linked mannosylation
NM_008086	0.00454716	0.0028526			0.00285	-1.00	-1.12	-1.06	1.10	<i>Gp1</i>	growth arrest specific 1	0002053 // positive regulation of mesenchymal cell proliferation // inferred from mutant phenotype // 0007049 // cell
NM_029796	0.0029807	0.0054629			0.00546	2.00	1.45	-1.04	1.10	<i>Lrg1</i>	leucine-rich alpha-2-glycoprotein 1	0001938 // positive regulation of endothelial cell proliferation // inferred from mutant phenotype // 0003511 // posit
NM_001136077//NM	0.0211292				0.02113	-1.06	-1.00	1.04	1.10	<i>Emp2</i>	nucleotide pyrophosphatase/phosphodiesterase 2	0001953 // negative regulation of cell-matrix adhesion // not recorded // 0006629 // lipid metabolic process // infer
NM_010902//NR_131	0.0178916				0.01789	-1.17	1.13	1.15	1.10	<i>Nfe2l2//LOC105244211</i>	ectonuclear factor, erythroid derived 2, like 2 // uncharacterized LOC105244211	0006351 // transcription, DNA-templated // inferred from electronic annotation // 0006355 // regulation of transcript
NM_025912//NM_006500059	0.0208285				0.02083	1.02	-1.01	-1.09	1.10	<i>Fam210b</i>	family with sequence similarity 210, member B	0016020 // membrane // inferred from electronic annotation // 0016021 // integral component of membrane // infer
NM_007435	0.0338033				0.0338	1.17	-1.04	1.12	1.10	<i>Abcd1</i>	ATP-binding cassette, sub-family D (ALD), member 1	0006635 // fatty acid beta-oxidation // inferred from mutant phenotype // 0006635 // fatty acid beta-oxidation // not
NM_001101430//NM	0.0037818				0.00378	1.18	1.10	-1.14	1.10	<i>Psmg4</i>	proteasome (prosome, macropain) assembly chaperone 4	0043248 // proteasome assembly // inferred from electronic annotation
NM_020906//NM_133908//XR_8	0.026953	0.0095988			0.02695	1.04	-1.12	-1.10	1.10	<i>Rito1//Gm38465</i>	RBP1 interacting and tubulin associated 1 // predicted gene, 38465	0007219 // Notch signaling pathway // inferred from electronic annotation // 0007399 // nervous system development
NM_145156//NM_006527097//X	0.0138662				0.01386	1.12	-1.09	-1.11	1.10	<i>Slc25a28</i>	solute carrier family 25, member 28	0006810 // transport // inferred from electronic annotation // 0006811 // ion transport // inferred from electronic an
NM_175309	0.0163726				0.01637	1.05	-1.14	1.18	1.09	<i>Upk3b</i>	uroplakin 3B	0010629 // negative regulation of gene expression // not recorded // 00046325 // negative regulation of glucose import
NM_00116769//NM	0.0088986				0.0089	1.11	1.01	-1.11	1.09	<i>Lmo4</i>	LIM domain only 4	0001843 // neural tube closure // inferred from mutant phenotype // 0003281 // ventricular septum development // li
NM_001177594//NM_001177595	0.0282329				0.02823	-1.01	-1.10	1.04	1.09	<i>Slc8b1</i>	solute carrier family 8 (sodium/lithium/calcium exchanger), member 81	0006810 // transport // inferred from electronic annotation // 0006811 // ion transport // inferred from electronic an
NM_024432//NM_006524796	0.0342473				0.03425	1.02	-1.11	-1.08	1.09	<i>Ubxm6</i>	UBX domain protein 6	0005634 // nucleus // not recorded // 0005730 // nucleus // not recorded // 0005737 // cytoplasm // inferred from e
NM_021789//XR_870	0.0358103	0.0389616			0.03896	-1.07	-1.10	-1.14	1.08	<i>Trappc4</i>	trafficking protein particle complex 4	0006810 // transport // inferred from electronic annotation // 0006888 // ER to Golgi vesicle-mediated transport // no
NM_001314013//NM_0530669//X	0.0303102	0.0273162			0.03031	1.06	1.10	1.15	1.07	<i>Atg5</i>	autophagy related 5	0000045 // autophagosome assembly // inferred from mutant phenotype // 0000422 // mitophagy // not recorded //
NM_001045544//NM	0.0013916				0.00139	1.28	-1.18	-1.07	1.07	<i>Akna</i>	AT-hook transcription factor	0006351 // transcription, DNA-templated // inferred from electronic annotation // 0006355 // regulation of transcript
NM_008344	0.0206806	0.0259694			0.02597	1.09	-1.19	-1.07	1.06	<i>Igf6p6</i>	insulin-like growth factor binding protein 6	0001558 // regulation of cell growth // inferred from electronic annotation // 0043567 // regulation of insulin-like gro
NM_053159	0.0137382	9.06E-04			0.01373	1.13	-1.13	-1.01	1.06	<i>Mrp13</i>	mitochondrial ribosomal protein L3	0006412 // translation // not recorded
NM_001291503//NM	0.0243809				0.02438	-1.17	-1.05	1.07	1.06	<i>Birc2</i>	baculoviral IAP repeat-containing 2	0002029 // protein polyubiquitination // not recorded // 0001666 // response to hypoxia // not recorded // 0001890 //
NM_007621//NM_00	0.0096765	0.0158171			0.01582	-1.03	-1.10	1.26	1.05	<i>Cbr2</i>	carboxyl reductase 2	0006116 // NADH oxidation // traceable author statement // 0008152 // metabolic process // 0001890 //
NM_153516//NM_00	0.0107404				0.01074	1.12	1.11	1.07	1.05	<i>Bcl2l13</i>	BCL2-like 13 (apoptosis facilitator)	0006915 // apoptotic process // inferred from reviewed computational analysis // 0042981 // regulation of apoptotic i
NM_009052//NM_00	0.0017031				0.00107	1.40	1.06	1.08	1.05	<i>Rasa3</i>	RAS p21 protein activator 3	0007165 // signal transduction // inferred from electronic annotation // 0034605 // cellular response to heat // not rec
NM_001248	0.0389777	0.03898			0.03898	1.06	1.12	1.09	1.05	<i>Lamtor2</i>	late endosomal/lysosomal adaptor, MAPK and MTOR activator 2	0001886 // activation of MAPK activity // inferred from direct assay // 0016049 // cell growth // not recorded // 00032
NM_023232	0.0192033				0.0192	1.06	1.13	1.05	1.13	<i>Diablo</i>	diablo homolog (Drosophila)	0006915 // apoptotic process // inferred from electronic annotation // 0006919 // activation of cysteine-type endopep
NM_026124	0.0058328				0.00583	1.15	-1.03	-1.07	1.04	<i>1110008F13Rik</i>	RIKEN cDNA 1110008F13 gene	0005739 // mitochondrion // inferred from direct assay
NM_011512//NM_00	0.0020724				0.00207	1.10	1.05	1.18	1.03	<i>Surf1</i>	surflet gene 4	0007030 // Golgi organization // not recorded // 0010638 // positive regulation of organelle organization // not recor
NM_031381//NM_01	0.0018739				0.00187	-1.13	-1.11	-1.02	1.03	<i>Tax13</i>	testis expressed gene 13	0006915 // apoptotic process // inferred from electronic annotation // 0006919 // activation of cysteine-type endopep
NM_139197//NM_006497918//X	0.0320381				0.03204	1.00	-1.20	-1.14	1.03	<i>Gbp1</i>	globoside alpha-1,3-N-acetylgalactosaminyltransferase 1	0005975 // carbohydrate metabolic process // inferred from electronic annotation // 0006486 // protein glycosylation
NM_175263//NM_006534494//X	0.0257043	0.0320829			0.0257	-1.03	-1.26	-1.16	1.03	<i>Notum</i>	notum pectinacetyltransferase homolog (Drosophila)	0006507 // GPI anchor release // inferred from direct assay // 0016055 // Wnt signaling pathway // inferred from elc
NM_001206367//NM	0.0299643				0.02996	-1.21	-1.21	-1.01	1.02	<i>Gsn</i>	gelsolin	0006911 // phagocytosis, engulfment // inferred from mutant phenotype // 0006915 // apoptotic process // not recor
NM_001037940//NM_01037941	0.0184684				0.01847	-1.06	-1.08	1.05	1.02	<i>Onaj6</i>	DnaI (Hsp40) homolog, subfamily B, member 6	0006457 // protein folding // not recorded // 0030036 // actin cytoskeleton organization // inferred from mutant ph
NM_145513//NM_00	0.0471327				0.04713	-1.07	1.04	1.12	1.01	<i>Tjpr1</i>	TIP41, TOR signalling pathway regulator-like (S. cerevisiae)	0000077 // DNA damage checkpoint // not recorded // 0034048 // negative regulation of protein phosphatase type 2
NM_001290437//NM_033134//X	0.0400683	0.0426836			0.04007	-1.01	-1.03	1.01	1.01	<i>Inpp5e</i>	inositol polyphosphatase 5-phosphatase E	0006470 // transport // inferred from direct assay // 0006470 // protein dephosphorylation // infer
NM_001048057//NM_001048058	0.0323493				0.03235	-1.01	1.10	1.04	1.01	<i>Rpl38</i>	ribosomal protein L38	0001501 // skeletal system development // inferred from mutant phenotype // 0001501 // skeletal system developme
NM_053068	0.0047056				0.00471	1.21	1.02	1.02	1.01	<i>Chrac1</i>	chromatin accessibility complex 1	0008152 // metabolic process // inferred from electronic annotation // 0071897 // DNA biosynthetic process // infer
NM_008403//NM_00	0.0161564				0.01616	1.14	1.08	-1.02	-1.01	<i>Ihg1b1p1</i>	integrin beta 1 binding protein 1	0001525 // angiogenesis // inferred from electronic annotation // 0002043 // blood vessel endothelial cell proliferation
NM_013536	0.0155215	0.0396649			0.03966	1.12	1.18	1.21	-1.01	<i>Emp1</i>	EMG1 nuclear protein homolog (S. cerevisiae)	0001824 // blastocyst development // inferred from mutant phenotype // 0006364 // rRNA processing // inferred from
NM_145404//NM_00	0.0270387				0.02704	1.08	1.03	-1.04	-1.01	<i>Prrt7</i>	protein arginine N-methyltransferase 7	0000387 // spliceosomal snRNP assembly // not recorded // 0006349 // regulation of gene expression by genetic imp
NM_001033201	0.0271104				0.02711	1.03	1.12	1.05	-1.02	<i>Ncbp1</i>	nuclear cap binding protein subunit 1	0000184 // nuclear-transcribed mRNA catabolic process, nonsense-mediated decay // not recorded // 0006370 // 7-m
NM_026113//NM_00	0.0459785	0.0056938			0.00569	1.14	1.30	1.08	-1.02	<i>Gtf3c6</i>	general transcription factor IIIc, polypeptide 6, alpha	0006351 // transcription, DNA-templated // not recorded // 0006383 // transcription from RNA polymerase III promot
NM_026526//NM_00	0.0444804	0.0311002			0.0311	1.06	1.11	-1.02	-1.02	<i>N6amt2</i>	N-6 adenine-specific DNA methyltransferase 2 (putative)	0032259 // methylation // inferred from electronic annotation
NM_030109//NM_006531771	0.0383358				0.03834	1.03	1.09	1.21	-1.02	<i>Sfb3b</i>	splicing factor 3b, subunit 2	0000398 // mRNA splicing, via spliceosome // not recorded
NM_025919//NM_00	0.0015412				0.00154	1.22	1.15	1.04	-1.02	<i>Rpl11</i>	ribosomal protein L11	0000027 // ribosomal large subunit assembly // -- // 0006364 // rRNA processing // not recorded // 0006412 // trans
NM_001159354//NM	0.0272379	0.039371			0.03937	1.44	1.40	1.47	-1.03	<i>Magi3</i>	membrane associated guanylate kinase, WW and PDZ domain containing 3	0007165 // signal transduction // inferred from electronic annotation // 0016310 // phosphorylation // inferred from e
NM_001166506//NM	0.0202679				0.02027	-1.18	-1.02	1.06	-1.02	<i>Sec14l1</i>	SEC14-like lipid binding 1	0006810 // transport // inferred from electronic annotation
NM_018874	0.0080419	0.0112728			0.01127	-1.04	-1.06	1.01	-1.03	<i>Plnpp1</i>	pancreatic lipase related protein 2A	0006629 // lipid metabolic process // inferred from electronic annotation
NM_008409	0.0482514				0.04825	1.13	1.11	1.12	-1.03	<i>Htm2a</i>	integral membrane protein 2A	0005515 // protein binding // inferred from electronic annotation
NM_001110251//NM	0.0225508				0.02251	1.24	1.20	1.01	-1.04	<i>Hmb5</i>	hydroxymethylbilane synthase	0001666 // response to hypoxia // inferred from electronic annotation // 0006779 // porphyrin-containing compound
NM_001102455//NM	0.0055096				0.00551	-1.06	1.10	1.10	1.10	<i>Aplp2</i>	amyloid beta (A4) precursor-like protein 2	0001967 // sucking behavior // inferred from genetic interaction // 0006878 // cellular copper ion homeostasis // infe
NM_011483//NM_00	0.0106377				0.01064	1.09	1.20	1.20	-1.04	<i>LOC100862468//Nhp21</i>	NHP2-like protein 1 // NHP2 non-histone chromosome protein 2-like 1 (S. cerevisiae)	0006397 // mRNA processing // inferred from electronic annotation // 0007338 // single fertilization // inferred from c
NM_026030	0.02303	0.0230266			0.02303	1.01	1.10	1.01	-1.04	<i>Ejfs2</i>	eukaryotic translation initiation factor 2, subunit 2 (beta)	0001701 // in utero embryonic development // inferred from mutant phenotype // 0002216 // male germ cell prolifer
NM_001098277//NM	0.0280175				0.02807	-1.01	1.14	1.09	-1.05	<i>Sd19p</i>	syndecan binding protein 1	0007265 // Ras protein signal transduction // inferred from physical interaction // 0007266 // synaptic transmission //
NM_001033481//NM	0.0375939				0.03759	-1.12	1.01	1.09	-1.05	<i>Myp1</i>	myelin regulatory factor	0006351 // transcription, DNA-templated // inferred from electronic annotation // 0006355 // regulation of transcript
NM_001081392//NM_133874//X	0.0393782				0.03938	-1.03	1.02	-1.05	-1.05	<i>Mdn1</i>	midasin homolog (yeast)	0

RefSeq	Transcript ID	p Tnfr 24 hr	p Tnfr 48hr	p Tnfr 72 hr	p Nfk1b	( FD Tnfr 24 hr	( FD Tnfr 48 hr	( FD Tnfr 72 hr	( FD Nfk1b	Gene Symbol	Gene Title	Gene Ontology
NM_145940		0.0444011	0.0444	-1.03	-1.07	1.02	-1.07	1.02	-1.07	<i>Wip1</i>	WD repeat domain, phosphoinositide interacting 1	0000045 // autophagosome assembly // not recorded//0000422 // mitophagy // not recorded//0006497 // protein
NM_019447//XM_0010164451		0.016451	0.01645	-1.17	-1.16	1.03	-1.07	1.03	-1.07	<i>Hgfoc</i>	hepatocyte growth factor activator	0006508 // proteolysis // inferred from electronic annotation
NM_0110172		0.0362128	1.26	1.05	-1.13	-1.07	-1.07	1.05	-1.07	<i>Pfn1</i>	profilin 1	0001843 // neural tube closure // inferred from genetic interaction//0006357 // regulation of transcription from RNA
NM_001110310//NM_001110311, 0.0153699		0.01537	1.03	1.08	1.06	-1.07	-1.07	1.08	1.06	<i>Snx12</i>	sorting nexin 12	0006810 // transport // inferred from electronic annotation//0006899 // endocytosis // not recorded//0010629 // r
NM_008638//XM_001030243, 0.0035288		0.00353	1.09	1.12	-1.14	-1.07	-1.07	1.12	-1.14	<i>Mthfd2</i>	methylene-tetrahydrofolate dehydrogenase (NAD-dependent), methylenetetrahydr	0006730 // one-carbon metabolic process // not recorded//0008152 // metabolic process // inferred from electronic
NM_011952		0.0407381	1.00	1.07	1.21	-1.07	-1.07	1.07	1.21	<i>Mapk3</i>	mitogen-activated protein kinase 3	0000165 // MAPK cascade // not recorded//0000189 // MAPK import into nucleus // not recorded//0001934 // posi
NM_001252332//NM_001033312		0.03331	1.02	1.18	1.16	-1.07	-1.07	1.18	1.16	<i>8-Sep</i>	septin 8	0000166 // nucleotide binding // inferred from electronic annotation//0005515 // protein binding // inferred from ete
NM_019426//XM_001066639		0.01666	1.31	-1.02	1.06	-1.07	-1.07	1.31	-1.02	<i>Atf7ip</i>	activating transcription factor 7 interacting protein	0000122 // negative regulation of transcription from RNA polymerase II promoter // inferred from direct assay//000
NM_009503		0.0176248	0.01762	1.19	1.13	1.00	-1.07	1.19	1.13	<i>Vcp</i>	valosin containing protein	0006281 // DNA repair // inferred from electronic annotation//0006302 // double-strand break repair // not recorde
NM_010617//XM_006516861//X, 0.0273545		0.02735	-1.08	1.13	1.10	-1.08	-1.08	1.13	1.10	<i>Kif13a</i>	kinesin family member 13A	0000910 // cytokinesis // not recorded//0006810 // transport // inferred from electronic annotation//0006886 // in
NM_001145034		0.0461378	1.29	-1.21	-1.20	-1.08	-1.08	1.29	-1.21	<i>Gm13889</i>	predicted gene 13889	
NM_029416//XM_0010297776	0.030468	0.0099994	0.03047	-1.06	-1.04	-1.18	-1.08	1.07	-1.18	<i>Klf17</i>	Kruppel-like factor 17	0000122 // negative regulation of transcription from RNA polymerase II promoter // inferred from direct assay//0006
NM_009226		0.0290011	0.029	1.15	1.53	1.17	-1.08	1.15	1.53	<i>Snrpd1</i>	small nuclear ribonucleoprotein D1	0000245 // spliceosomal complex assembly // not recorded//0000387 // spliceosomal snRNP assembly // not recorde
NM_019427//XM_001022712		0.022712	0.02271	-1.20	-1.11	1.15	-1.08	1.15	-1.11	<i>Eps1144b</i>	erythrocyte membrane protein band 4.1 like 4b	0010628 // positive regulation of gene expression // not recorded//0031032 // actomyosin structure organization // i
NM_025578		0.0099199	0.00992	-1.02	-1.12	1.00	-1.08	1.00	-1.12	<i>Mpsp25</i>	mitochondrial ribosomal protein S25	0032543 // mitochondrial translation // inferred by curator
NM_001039184//NM_001031606		0.03166	0.03161	-1.23	-1.02	1.16	-1.09	1.16	-1.09	<i>Cpsp20</i>	centrosomal protein 350	0034453 // microtubule anchoring // inferred from electronic annotation
NM_023773//XM_006519640//X, 0.042539	0.0209159	0.04254	-1.02	-1.05	-1.11	-1.09	-1.09	1.02	-1.05	<i>Aphosphp8</i>	M-phase phosphoprotein 8	0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 // regulation of transcripti
NM_001190804//NM_001190805, 0.0188629		0.01886	-1.06	1.23	-1.03	-1.09	-1.09	1.23	-1.03	<i>Dnajp11</i>	Dnaj (Hsp40) homolog, subfamily B, member 11	0006457 // protein folding // inferred from electronic annotation//0016556 // mRNA modification // inferred from di
NM_001081196//NM_0104187		0.01482	-1.12	1.02	1.18	-1.09	-1.09	1.18	-1.09	<i>Hnrnpul2</i>	heterogeneous nuclear ribonucleoprotein U-like 2	0005515 // protein binding // inferred from physical interaction//0044822 // poly(A) RNA binding // not recorde
NM_001163662//NM_00439748		0.04397	-1.11	1.03	1.07	-1.09	-1.09	1.03	1.07	<i>Nucb1</i>	nucleobindin 1	0072718 // response to cisplatin // inferred from electronic annotation//1903533 // regulation of protein targeting //
NM_001306143//NM_0038381		0.03838	1.13	1.09	-1.17	-1.10	-1.10	1.13	1.09	<i>Mbd3</i>	methyl-CpG binding domain protein 3	0000122 // negative regulation of transcription from RNA polymerase II promoter // inferred from direct assay//0001
NM_001081144//NM_0006173		0.00617	-1.10	-1.06	-1.10	-1.10	-1.10	1.10	-1.10	<i>Zfp518b</i>	zinc finger protein 518B	0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 // regulation of transcripti
NM_001305284//NM_00350286, 0.0499463		0.04995	-1.28	1.09	1.06	-1.10	-1.10	1.09	1.06	<i>Mpdz</i>	multiple PDZ domain protein	0007155 // cell adhesion // inferred from direct assay//0042552 // myelination // not recorded
NM_001161782//NM_001041009		0.04101	-1.22	-1.09	1.13	-1.10	-1.10	1.13	-1.10	<i>Trim32</i>	tripartite motif-containing 32	0002029 // protein polyubiquitination // not recorded//0001894 // tissue homeostasis // inferred from mutant phen
NM_026514//XM_006524295	0.003048	0.00305	-1.08	-1.24	-1.08	-1.10	-1.10	1.08	-1.24	<i>Cdc42ep3</i>	CDC42 effector protein (Rho GTPase binding) 3	0007266 // Rho protein signal transduction // not recorded//0008360 // regulation of cell shape // not recorded//00
NM_010485//XM_006508698	0.0330496	0.03305	-1.02	1.20	1.15	-1.10	-1.10	1.20	1.15	<i>Elav1</i>	ELAV (embryonic lethal, abnormal vision)-like 1 (Hu antigen R)	0006417 // regulation of translation // not recorded//0045727 // positive regulation of translation // inferred from di
NM_144918		0.0236148	0.012548	1.14	1.10	-1.00	-1.10	1.14	1.10	<i>Smyd5</i>	SET and MYND domain containing 5	0032259 // methylation // inferred from electronic annotation
NM_133933		0.01294	0.0129	-1.06	1.18	-1.12	-1.10	1.18	-1.12	<i>Rpn1</i>	ribophorin 1	0006486 // protein glycosylation // inferred from electronic annotation//0018279 // protein N-linked glycosylation vi
NM_172015//XM_006516826	0.0330718	0.03307	-1.05	1.08	1.02	-1.10	-1.10	1.08	1.02	<i>Iars</i>	isoleucine-tRNA synthetase	0001649 // osteoblast differentiation // not recorded//0006412 // translation // inferred from electronic annotation//
NM_133895//XM_006504271//X, 0.0200086		0.02001	-1.04	1.14	1.08	-1.10	-1.10	1.14	1.08	<i>Slc15a4</i>	solute carrier family 15, member 4	0006810 // transport // inferred from electronic annotation//0006657 // oligopeptide transport // inferred from elec
NM_001163513//NM_0039438	0.0068113	0.03944	1.09	1.22	1.22	-1.10	-1.10	1.22	1.22	<i>Dlg5</i>	discs, large homolog 5 (Drosophila)	0006461 // protein complex assembly // inferred from mutant phenotype//0003089 // polarized epithelial cell differe
NM_134010//XM_006513018	0.0363082	0.03631	1.09	1.12	1.08	-1.11	-1.11	1.09	1.12	<i>Nup107</i>	nucleoporin 107	0000973 // posttranscriptional tethering of RNA polymerase II gene DNA at nuclear periphery // --//0006355 // regul
NM_001286040//NM_0015112		0.01511	-1.15	-1.12	1.00	-1.11	-1.11	1.00	-1.11	<i>Anks1</i>	ankyrin repeat and SAM domain containing 1	0006929 // substrate-dependent cell migration // inferred from direct assay//0016322 // neuron remodeling // infer
NM_011966//XM_001260604	0.0334973	2.60E-04	1.20	1.36	1.21	-1.11	-1.11	1.20	1.36	<i>Psmo4</i>	proteasome (prosome, macropain) subunit, alpha type 4	0006508 // proteolysis // inferred from electronic annotation//0006511 // ubiquitin-dependent protein catabolic pro
NM_00113470//NM_146012	0.0247841	0.02478	1.16	1.03	1.04	-1.11	-1.11	1.16	1.03	<i>Ctdsp2</i>	CTD (carboxy-terminal domain, RNA polymerase II, polypeptide A) small phosphat	0001933 // negative regulation of protein phosphorylation // inferred from direct assay//0006470 // protein dephos
NM_001290486//NM_0103366//N, 0.0072765		0.00728	-1.21	1.06	-1.06	-1.11	-1.11	1.06	-1.06	<i>Lpar1</i>	lyso-phosphatidic acid receptor 1	0000187 // activation of MAPK activity // inferred from direct assay//0007165 // signal transduction // inferred from
NM_001311790//NM_0099822//X, 0.0318398	0.0362418	0.03184	1.09	1.20	1.14	-1.11	-1.11	1.09	1.20	<i>Ctsc</i>	cathepsin C	0001913 // T cell mediated cytotoxicity // inferred from genetic interaction//0006508 // proteolysis // inferred from
NM_009538		0.0410006	0.04104	-1.44	-1.10	-1.13	-1.11	1.44	-1.10	<i>Plagl1</i>	pliomorphic adenoma gene-like 1	0006351 // transcription, DNA-templated // inferred from electronic annotation//0006357 // regulation of transcripti
XR_378553//NR_040558//XR_862	0.030526	0.03053	-1.18	-1.18	-1.04	-1.11	-1.11	1.18	-1.18	<i>1500002F19RIK</i>	RIKEN cDNA 1500002F19 gene	
NM_00763//XM_001026375	0.0214593	0.02146	1.03	1.15	1.08	-1.11	-1.11	1.03	1.15	<i>Ctcs1</i>	chaperonin containing Tcp1, subunit 5 (epsilon)	0006457 // protein folding // inferred from electronic annotation//0007339 // binding of sperm to zona pellucida // i
NM_007591		0.0175542	0.01755	-1.11	1.25	1.22	-1.11	1.25	1.22	<i>Calr</i>	calreticulin	0000122 // negative regulation of transcription from RNA polymerase II promoter // not recorded//0002502 // pepti
NM_132942//XM_0010158775	0.015887	0.01588	-1.14	1.11	1.07	-1.11	-1.11	1.11	1.07	<i>Plekha1</i>	pleckstrin homology domain containing, family A (phosphoinositide binding specifi	0001553 // ubiquitination // inferred from genetic interaction//0007283 // spermatogenesis // inferred from mutan
NM_001039351//NM_001039352, 0.0012504		0.00125	1.07	1.24	1.30	-1.12	-1.12	1.07	1.24	<i>Nok1</i>	nucleolar and colled-body phosphoprotein 1	0007000 // nucleolus organization // inferred from direct assay
NM_026554		0.0129665	0.01297	-1.01	1.26	1.16	-1.12	1.26	1.16	<i>Ncbp2</i>	nuclear cap binding protein subunit 2	0000184 // nuclear-transcribed mRNA catabolic process, nonsense-mediated decay // not recorded//0000399 // mR
NM_011594		0.0493615	0.04936	1.02	1.08	1.13	-1.12	1.02	1.08	<i>Temp</i>	tissue inhibitor of metalloproteinase 2	0007417 // central nervous system development // inferred from electronic annotation//0007568 // aging // inferre
NM_017376//NM_15_00071118	0.0109324	0.01093	1.11	1.11	1.14	-1.12	-1.12	1.11	1.14	<i>Tcfp2</i>	thyrotroph embryonic factor 2	0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 // regulation of transcripti
NM_011119		0.035631	0.03563	1.08	1.01	1.17	-1.12	1.08	1.01	<i>Pa2g4</i>	proliferation-associated 264	0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 // regulation of transcripti
NM_198885//XM_0010320757	0.03208	0.03208	-1.04	1.01	-1.07	-1.13	-1.13	1.01	-1.07	<i>Scx</i>	scleraxis	0001707 // mesoderm formation // inferred from mutant phenotype//0001894 // tissue homeostasis // inferred from
NM_001080126//NM_00209222	0.02092	0.02092	1.24	1.15	1.17	-1.13	-1.13	1.24	1.15	<i>Casp8</i>	caspase 8	0001525 // angiogenesis // inferred from mutant phenotype//0001841 // neural tube formation // inferred from mut
NM_001253857//NM_00490024	0.049	0.049	-1.09	-1.11	-1.09	-1.13	-1.13	1.09	-1.11	<i>Tet1</i>	tet methylcytosine dioxygenase 1	0001826 // inner cell mass cell differentiation // inferred from mutant phenotype//0006351 // transcription, DNA-tem
NM_001177371//NM_001174665	0.01175	0.01175	1.09	-1.07	-1.12	-1.13	-1.13	1.09	-1.07	<i>Dbn1</i>	drebrin 1	0007015 // actin filament organization // inferred from direct assay//0007275 // multicellular organismal developme
NM_001290817//NM_009242	0.0465537	0.04655	-1.15	1.02	1.00	-1.13	-1.13	1.02	1.00	<i>Sparc</i>	secreted acidic cysteine rich glycoprotein	0001503 // ossification // inferred from electronic annotation//0001937 // negative regulation of endothelial cell pro
NM_001290696//NM_00054834	0.00548	0.00548	-1.04	1.02	1.05	-1.13	-1.13	1.02	1.05	<i>Foxj3</i>	forkhead box J3	0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 // regulation of transcripti
NM_018826		0.0260593	0.02606	-1.10	-1.27	-1.14	-1.14	1.10	-1.27	<i>Irx5</i>	Iroquois related homeobox 5 (Drosophila)	0002027 // regulation of heart rate // inferred from mutant phenotype//0006351 // transcription, DNA-templated //
NM_001040690//NM_00455639	0.04556	0.04556	1.04	1.17	1.14	-1.14	-1.14	1.04	1.17	<i>Rap1gds1</i>	RAP1, GTP-GDP dissociation stimulator 1	0000060 // small import into nucleus, translocation // not recorded//0006606 // protein import into nucleus // infe
NM_026532//NR_033574//X, 0.0396536	0.02483	0.02483	1.02	1.22	1.29	-1.14	-1.14	1.02	1.22	<i>Nut2//Nut2-ps1//Nut2-ps2</i>	nuclear transport factor 2//nuclear transport factor 2, pseudogene 1//nuclear tr	0005515 // protein binding // inferred from electronic annotation
NM_001168672//NM_001411733	0.04117	0.04117	-1.03	-1.04	-1.05	-1.14	-1.14	1.03	-1.04	<i>Gtse1</i>	G two 5 phase expressed protein 1	0006508 // proteolysis // inferred from electronic annotation//0008283 // cell proliferation // not recorded//00164
NM_001291818//NM_00134002	0.0134	0.0134	-1.02	-1.11	-1.02	-1.14	-1.14	1.02	-1.11	<i>Rhbdf1</i>	rhomboid family 1 (Drosophila)	0006355 // regulation of transcription, DNA-templated // inferred from electronic annotation
NM_001166029//NM_004581806	0.04582	0.04582	-1.15	1.09	1.06	-1.14	-1.14	1.15	1.09	<i>Zfp275</i>	zinc finger protein 275	0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 // regulation of transcripti
NM_001038625//NM_021372//X, 0.013385	0.0183489	0.01835	1.26	1.04	1.08	-1.14	-1.14	1.26	1.04	<i>Sertad2</i>	SERTA domain containing 2	0006457 // protein folding // inferred from electronic annotation//0007339 // binding of sperm to zona pellucida // i
NM_009840		0.013385	-1.10	1.27	1.31	-1.15	-1.15	1.27	1.31	<i>Cct8</i>	chaperonin containing Tcp1, subunit 8 (theta)	0006281 // DNA repair // inferred from electronic annotation//0006974 // cellular response to DNA damage stimulus
NM_001081225//NM_944E-04	9.44E-04	9.44E-04	-1.40	-1.08	1.12	-1.15	-1.15	1.40	-1.08	<i>Fam178a</i>	family with sequence similarity 178, member A	0000122 // negative regulation of transcription from RNA polymerase II promoter // inferred from mutant phenotype//
NM_001085492//XM_317E-04	3.17E-04	3.17E-04	1.03	1.03	1.34	-1.15	-1.15	1.03	1.03	<i>Rere</i>	arginine glutamic acid dipeptide (REG) repeats	0007010 // cytoskeleton organization // inferred from mutant phenotype//0030855 // epithelial cell differentiation //
NM_011526		0.0031575	1.02	1.61	1.41	-1.15	-1.15	1.02	1.61	<i>Tcpin</i>	collagen, type XVIII, alpha 1	00

RefSeq	Transcript ID	p Tnfr 24 hr	p Tnfr 48hr	p Tnfr 72 hr	p Nfkb1	( FD Tnfr 24 hr (	FD Tnfr 48 hr (	FD Tnfr 72 hr (	FD Nfkb1	Gene Symbol	Gene Title	Gene Ontology
NM_001080819	/NM_00110352				0.01104	-1.01	1.02	1.17	-1.19	<i>Arid1a</i>	AT rich interactive domain 1A (SWI-like)	0000122 // negative regulation of transcription from RNA polymerase II promoter // inferred from direct assay // 0001
NM_008491		0.004128		0.0110278	0.01103	1.67	1.43	1.37	-1.20	<i>Lcn2</i>	lipocalin 2	0002376 // immune system process // inferred from electronic annotation // 0006810 // transport // inferred from elec
NM_001122958	/NM_001122959			0.0142584	0.01426	-1.04	1.01	-1.01	-1.20	<i>Rad54l</i>	RAD54 like (S. cerevisiae)	0000724 // double-strand break repair via homologous recombination // inferred from genetic interaction // 0000724
NM_001039537	/NM_00103169				0.03317	1.17	-1.05	-1.08	-1.20	<i>Lif</i>	leukemia inhibitory factor	0001974 // blood vessel remodeling // inferred from genetic interaction // 0006955 // immune response // inferred fr
NM_011063	/NM_00108294				0.01083	-1.08	1.24	1.13	-1.21	<i>Pea15a</i>	phosphoprotein enriched in astrocytes 15A	0000077 // DNA damage checkpoint // inferred from electronic annotation // 0006810 // transport // inferred from el
NM_001267622	/NM_00262599		0.0426134		0.04261	-1.08	-1.15	1.02	-1.21	<i>Ttc28</i>	tetratricopeptide repeat domain 28	0007049 // cell cycle // inferred from electronic annotation // 0007067 // mitotic nuclear division // inferred from elec
NM_008057		0.0300766			0.03008	-1.01	-1.03	1.15	-1.21	<i>Fzd7</i>	frizzled homolog 7 (Drosophila)	0006355 // regulation of transcription, DNA-templated // not recorded // 0007165 // signal transduction // inferred fr
NM_007392	/NM_00652606		0.0490329		0.04903	-1.13	1.38	1.12	-1.22	<i>Acta2</i>	actin, alpha 2, smooth muscle, aorta	0006936 // muscle contraction // not recorded // 0008217 // regulation of blood vessel development // inferred from mutant ph
NM_178595	/XR_374	0.044167			0.04417	1.10	1.04	-1.10	-1.23	<i>Pthr1</i>	peptidyl-L-histidylase 1 homolog (S. cerevisiae)	0008152 // metabolic process // inferred from electronic annotation
NM_022022	/NM_00354374				0.03544	1.05	-1.06	-1.09	-1.23	<i>Ube4b</i>	ubiquitin factor E4B	0002009 // protein polyubiquitination // inferred from direct assay // 0000209 // protein polyubiquitination // inferre
NM_001079686	/NM_0008956				0.00896	-1.12	-1.00	1.06	-1.23	<i>Syne1</i>	spectrin repeat containing, nuclear envelope 1	0007030 // Golgi organization // not recorded // 0040023 // establishment of nucleus localization // inferred from mu
NM_016966	/NR_031	0.0299773			0.02998	1.30	1.03	1.36	-1.23	<i>Gm0896</i> // <i>Phgdh</i>	3-phosphoglycerate dehydrogenase pseudogene // 3-phosphoglycerate dehydrog	0006541 // glutamine metabolic process // inferred from mutant phenotype // 0008544 // glycine metabolic process /
NM_001146707	/NM_015781	0.0012336	0.0369231		0.00123	-1.06	-1.09	-1.03	-1.23	<i>Gm4204</i> // <i>Nap11</i>	nucleosome assembly protein 1-like 1 pseudogene // nucleosome assembly protei	0006334 // nucleosome assembly // inferred from electronic annotation // 0014010 // Schwann cell proliferation // in
NM_021457		0.0017932			0.00179	1.05	1.16	1.16	-1.23	<i>Fzd1</i>	frizzled homolog 1 (Drosophila)	0001934 // positive regulation of protein phosphorylation // inferred from mutant phenotype // 0003149 // membran
NM_011416	/NM_020351283				0.03513	-1.10	1.23	1.18	-1.24	<i>Smarca2</i>	SMH/SNF related, matrix associated, actin dependent regulator of chromatin, subf	0006325 // chromatin organization // traceable author statement // 0006334 // nucleosome assembly // traceable au
NM_133229		0.0442596			0.04426	-1.18	-1.34	-1.16	-1.24	<i>Riply3</i>	ripply3 homolog (zebrafish)	0000122 // negative regulation of transcription from RNA polymerase II promoter // inferred from direct assay // 0006
NM_021288	/NR_000040	0.014	0.020285	0.0216754	0.014	-1.02	1.01	1.21	-1.24	<i>Ttms</i> // <i>Ttms-ps</i>	thymidylate synthase // thymidylate synthase, pseudogene	0006206 // pyrimidine nucleobase metabolic process // inferred from electronic annotation // 0006231 // dTMP biosy
NM_009697	/NM_183261	0.0330305			0.03303	1.05	-1.03	1.06	-1.24	<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 // 0000
NM_001163847	/NM_00118024				0.0118	1.11	-1.03	-1.09	-1.25	<i>Ntn3</i> // <i>Tbc1d24</i>	netrin 3 // TBC1 domain family, member 24	0006355 // regulation of transcription, DNA-templated // not recorded // 0007409 // axonogenesis // traceable aut
NM_001039129	/NM_00105077				0.00323	1.53	1.18	1.20	-1.25	<i>Hnmpa1</i>	heterogeneous nuclear ribonucleoprotein A1 pseudogene	0000380 // alternative mRNA splicing, via spliceosome // inferred from direct assay // 0006397 // mRNA processing //
NM_133218	/NM_0010087123	0.0344265			0.03443	-1.24	-1.06	-1.26	-1.26	<i>Zfp704</i>	zinc finger protein 704	0046872 // metal ion binding // inferred from electronic annotation
NM_029682	/NM_0010475493				0.04755	1.03	-1.10	-1.09	-1.27	<i>Stambp1</i>	STAM binding protein like 1	0006508 // proteolysis // inferred from electronic annotation
NM_001276408	/NM_0007884	0.0043191			0.00432	1.22	1.24	1.16	-1.27	<i>Fn1</i>	fibronectin 1	0001525 // angiogenesis // inferred from electronic annotation // 0001775 // cell activation // not recorded // 000193
NM_197999	/NM_001017728				0.00177	-1.11	1.06	1.12	-1.27	<i>Ces2g</i>	carboxylesterase 2G	0008152 // metabolic process // inferred from electronic annotation
NM_001110443	/NM_001111044	0.0108745			0.01087	-1.57	1.20	1.02	-1.29	<i>Serpinh1</i>	serine (or cysteine) peptidase inhibitor, clade H, member 1	0003433 // chondrocyte development involved in endochondral bone morphogenesis // inferred from mutant phenot
NM_023850	/NM_006500388	0.0050417			0.00504	-1.03	-1.24	-1.06	-1.30	<i>Chst1</i>	carbohydrate (keratan sulfate Gal-6) sulfotransferase 1	0005975 // carbohydrate metabolic process // inferred from electronic annotation // 0006012 // galactose metabolic
NM_133918	/NM_001024689				0.02469	1.14	1.07	-1.06	-1.30	<i>Emilin1</i>	elastin microfibril interfacer 1	0007155 // cell adhesion // inferred from electronic annotation // 0010811 // positive regulation of cell-substrate adh
NM_008250		0.0036699			0.00367	1.54	1.09	-1.30	-1.31	<i>Hlx</i>	H2.0-like homeobox	0001889 // liver development // inferred from mutant phenotype // 0006351 // transcription, DNA-templated // infer
NM_009363		0.0242412			0.02424	-1.01	1.59	1.12	-1.31	<i>Tfj2</i>	trefoil factor 2 (spasmolytic protein 1)	0008284 // positive regulation of cell proliferation // inferred from genetic interaction // 0008284 // positive regulati
NM_001136086	/NM_001291455	0.0243615			0.02436	-1.07	1.16	1.10	-1.31	<i>Dpysl3</i>	dihydropyrimidinase-like 3	0007399 // nervous system development // inferred from direct assay // 0008152 // metabolic process // inferred fro
NM_028232	/NM_0010261336	0.0267846			0.02678	-1.06	-1.06	1.07	-1.32	<i>Sgol1</i>	shugoshin-like 1 (S. pombe)	0007049 // cell cycle // inferred from electronic annotation // 0007059 // chromosome segregation // not recorded //
NM_001122733	/NM_00134443	0.0438303	0.0482141		0.04383	1.33	1.34	1.50	-1.33	<i>Kat</i>	kit oncogene	0000187 // activation of MAPK activity // not recorded // 0001541 // ovarian follicle development // inferred from mu
NM_001171187	/NM_00034257				0.00343	1.38	1.26	1.10	-1.35	<i>Mil</i>	myelin and lymphocyte protein, T cell differentiation protein	0042552 // myelination // not recorded // 13902043 // positive regulation of extrinsic apoptotic signaling pathway via d
NM_007743		0.0392629			0.03926	-1.12	1.19	1.01	-1.36	<i>Col1a2</i>	collagen, type I, alpha 2	0001501 // skeletal system development // not recorded // 0001568 // blood vessel development // not recorded //
NM_008861	/NM_0010468099				0.04681	-1.20	-1.13	1.08	-1.37	<i>Pkad2</i>	polycystic kidney disease 2	0001658 // branching involved in ureteric bud morphogenesis // inferred from electronic annotation // 0001822 // kid
NM_172924	/NM_006511167	0.0201199			0.02012	1.09	1.19	-1.05	-1.37	<i>Peak1</i>	pseudopodium-enriched atypical classin 1	0006468 // protein phosphorylation // not recorded // 0016310 // phosphorylation // inferred from electronic annota
NM_026555	/NM_006540986	0.0247598			0.02476	-1.03	1.13	-1.24	-1.41	<i>Rcn3</i>	reticulocalbin 3, EF-hand calcium binding domain	0005509 // calcium ion binding // inferred from electronic annotation // 0005515 // protein binding // inferred from el
NM_012012	/NM_006496862	0.0195294			0.01953	1.04	1.10	-1.06	-1.41	<i>Exo1</i>	exonuclease 1	0002376 // immune system process // inferred from electronic annotation // 0002455 // humoral immune response //
NM_134102	/NM_001031144	0.0477859			0.03111	1.15	-1.07	1.07	-1.43	<i>Pls1a</i>	phospholipase A1 member A	0006629 // lipid metabolic process // inferred from electronic annotation // 0001604 // lipid catabolic process // infer
NM_009791	/NM_00184453				0.01845	-1.32	-1.22	1.12	-1.44	<i>Aspm</i>	asp (abnormal spindle)-like, microcephaly associated (Drosophila)	0001764 // neuron migration // inferred from genetic interaction // 0001764 // neuron migration // inferred from mul
NM_001308327	/NM_001308329	0.0079678			0.00797	1.13	-1.10	-1.15	-1.45	<i>Enp1</i>	ectonucleotide pyrophosphatase/phosphodiesterase 1	0006091 // generation of precursor metabolites and energy // not recorded // 0006796 // phosphate-containing com
NM_001159564	/NM_021359	0.0385212			0.03852	1.35	1.58	1.44	-1.45	<i>Htb6</i>	integrin beta 6	0006954 // inflammatory response // inferred from mutant phenotype // 0007155 // cell adhesion // inferred from elec
NM_009610		0.0093985	0.037104		0.0094	-1.14	1.42	1.19	-1.46	<i>Actg2</i>	actin, gamma 2, smooth muscle, enteric	0010628 // positive regulation of gene expression // inferred from sequence or structural similarity // 0009031 // mes
NM_026014		0.0059587			0.00596	1.24	1.12	1.00	-1.46	<i>Cdt1</i>	chromatin licensing and DNA replication factor 1	0000076 // DNA replication checkpoint // inferred from direct assay // 0000076 // DNA replication checkpoint // not r
NM_013811	/NM_006523588	0.0173194			0.01732	1.05	-1.06	-1.04	-1.47	<i>Dnah8</i>	dynein, axonemal, heavy chain 8	0000178 // microtubule-based movement // inferred from electronic annotation // 0008152 // metabolic process // in
NM_001289780	/NM_00351398	0.0019182			0.00192	1.05	1.21	1.04	-1.47	<i>Pus7</i>	pseudouridylylase 7 homolog (S. cerevisiae)	0001522 // pseudouridine synthesis // inferred from electronic annotation // 0001522 // pseudouridine synthesis // --
NM_010721		0.0280595			0.02806	1.10	1.16	1.03	-1.47	<i>Lmnb1</i>	lamin B1	0031662 // positive regulation of cyclin-dependent protein serine/threonine kinase activity involved in G2/M transiti
NM_013462	/NM_006508987	0.03375			0.03375	1.05	-1.40	-1.17	-1.48	<i>Adrb3</i>	adrenergic receptor, beta 3	0002024 // diet induced thermogenesis // inferred from genetic interaction // 0002025 // vasodilation by norepinephr
NM_001308535	/NM_00404131				0.04041	1.20	1.12	1.15	-1.49	<i>Il2rg</i>	interleukin 2 receptor, gamma chain	0010468 // regulation of gene expression // inferred from mutant phenotype // 0010628 // positive regulation of gene
NM_010516		4.41E-04			0.01051	2.94	1.10	1.08	-1.49	<i>Cyrl6</i>	cysteine rich protein 61	0001558 // regulation of cell growth // inferred from electronic annotation // 0007059 // chromosome segregation // not rec
NM_030707	/XR_871926	0.0498891			0.04989	-1.11	1.38	1.50	-1.51	<i>D17H6556E.5</i>	DNA segment, Chr 17, human D6556E 5	0019058 // viral life cycle // inferred from electronic annotation
NM_001033217	/NM_006520264	0.0161053			0.01611	1.22	-1.28	1.24	-1.54	<i>Prickle1</i>	prickle homolog 1 (Drosophila)	0001843 // neural tube closure // not recorded // 0006606 // protein import into nucleus // not recorded // 0031398 //
NM_001159299	/NM_00073735				0.00737	1.45	1.53	1.02	-1.59	<i>Hth4</i>	inter alpha-trypsin inhibitor, heavy chain 4	0006953 // acute-phase response // inferred from electronic annotation // 0010466 // negative regulation of peptidas
NM_019568	/NM_0039746				0.03975	1.84	1.60	1.11	-1.65	<i>Cxcl14</i>	chemokine (C-X-C motif) ligand 14	0006955 // immune response // inferred from electronic annotation // 0045662 // negative regulation of myoblast dif
NM_010790	/NM_006537640	0.0169902			0.01699	1.16	1.28	1.07	-1.68	<i>Melk</i>	maternal embryonic leucine zipper kinase	0006468 // protein phosphorylation // inferred from electronic annotation // 0006915 // apoptotic process // not rec
NM_172505	/NM_00072999				0.0073	1.14	1.46	1.45	-1.69	<i>Hjurp</i>	Holliday junction recognition protein	0007049 // cell cycle // inferred from electronic annotation // 0007059 // chromosome segregation // not recorded //
NM_010474		0.0356842			0.03568	1.36	-1.38	1.15	-1.73	<i>Hs3t1</i>	heparan sulfate (glucosamine) 3-O-sulfotransferase 1	0008152 // metabolic process // inferred from electronic annotation
NM_011607	/NM_00087337	0.0063502			0.00635	1.30	1.57	1.11	-1.79	<i>Tnc</i>	tenascin C	0001649 // osteoblast differentiation // not recorded // 0007155 // cell adhesion // inferred from electronic annotatio
NM_011121		0.0320034			0.032	1.03	-1.04	1.04	-1.80	<i>Plk1</i>	polo-like kinase 1	0000070 // mitotic sister chromatid segregation // not recorded // 0000086 // G2/M transition of mitotic cell cycle // r
NM_010766		0.0334347			0.03343	1.21	-1.26	-1.04	-1.86	<i>Marco</i>	macrophage receptor with collagenous structure	0002376 // immune system process // inferred from electronic annotation // 0006897 // endocytosis // inferred from
NM_010104		0.01573			0.01573	-1.17	1.25	-1.14	-1.96	<i>Edn1</i>	endothelin 1	0000122 // negative regulation of transcription from RNA polymerase II promoter // not recorded // 0001501 // skelet
NM_010809		0.0118081	0.0270064		0.01181	-1.37	1.03	-1.19	-1.97	<i>Mmp3</i>	matrix metalloproteinase 3	0006508 // proteolysis // inferred from mutant phenotype // 0006508 // proteolysis // not recorded // 0010727 // nee
NM_009364	/NM_001012514	0.017611			0.01761	1.72	1.30	1.02	-2.02	<i>Tjp2</i>	tissue factor pathway inhibitor 2	0007596 // blood coagulation // inferred from electronic annotation // 0007599 // hemostasis // inferred from elect
NM_010295	/NM_006510812	0.0441905	0.0416133		0.04419	1.17	1.29	1.18	-2.38	<i>Cic</i>	glutamate-cysteine ligase, catalytic subunit	0006534 // cysteine metabolic process // not recorded // 0006536 // glutamate metabolic process // not recorded // K
NM_00117544	/NM_00228937				0.02289	1.48	1.32	-1.20	-2.42	<i>Hist1h2ao</i> // <i>Hist1h2ap</i>	histone cluster 1, H2ao // histone cluster 1, H2ap	0006325 // chromatin organization // not recorded // 0006342 // chromatin silencing // not recorded // 0008285 // m
NM_009264		0.0042823			0.00428	2.18	1.35	-1.13	-2.52	<i>Spr1a</i>	small proline-rich protein 1A	0018149 // peptide cross-linking // not recorded // 0003012 // keratinocyte differentiation // not recorded // 0003424
NM_025748	/NM_00136061	0.01361			0.01361	1.09	-1.05	-1.08	-2.63	<i>Adat1</i>	adenosine deaminase, tRNA-specific 2	0002100 // tRNA wobble adenosine to inosine editing // inferred from electronic annotation // 0006400 // tRNA modif
NM_001131054	/NM_013917	0.0144328	2.02E-04	0.01443	0.01443	-4.12	-3.09	-1.84	-2.81	<i>Pttg1</i>	pituitary tumor-transforming gene 1	0001558 // regulation of cell growth // not recorded // 000

**Table S8. Common genes altered by O3 in Tnfr-, Tlr4-, and Nfkb1-dependent manner.**

Venn Diagram analysis of Tnfr-dependent genes (n=2180, pooled from 24-72 hr O3), Tlr4-dependent genes (n=2320, pooled from 24- and 48-hr O3; Bauer et al. 2011 Env Health Perspect, GEO#GSE20715) and Nfkb1-dependent genes (n=2397, 48-hr O3).

Tlr4 mutant strain-C3H/HeJ (HeJ), Tlr4 normal strain-C3H/HeOJ (OJ).

Fold difference (FD); positive-higher in KO or HeJ-O3, negative-lower in KO or HeJ-O3, compared to corresponding WT or OJ-O3.

RefSeq Transcript ID	Tnfr FD 24 hr	Tnfr FD 48 hr	Tnfr FD 72 hr	Tlr4 FD 24 hr	Tlr4 FD 48 hr	Nfkb1 FD 48 hr	Gene Symbol	Gene Title	Gene Ontology Biological Process
NM_001252332//NM_001212	1.02	1.18	1.16	-1.05	-1.02	-1.07	<i>Sept8</i>	septin 8	0000166 // nucleotide binding // inferred from electronic annotation//0005515 // protein bin
NM_001177945//NM_00111	-1.10	-1.01	1.02	-1.12	-1.01	1.19	<i>Aamdc</i>	adipogenesis associated Mth938 domain containing	0043066 // negative regulation of apoptotic process // inferred from mutant phenotype//004
NM_001038587//NM_00114	1.31	1.19	1.09	1.06	-1.24	1.12	<i>Adar</i>	adenosine deaminase, RNA-specific	0001649 // osteoblast differentiation // inferred from mutant phenotype//0001701 // in uter
NM_025748//XM_0112432C	1.09	-1.05	-1.08	1.08	1.12	-2.63	<i>Adat2</i>	adenosine deaminase, tRNA-specific 2	0002100 // tRNA wobble adenosine to inosine editing // inferred from electronic annotation//
NM_007440//XM_01124867	-1.04	-1.25	-1.01	1.43	1.00	1.42	<i>Alox12</i>	arachidonate 12-lipoxygenase	0006629 // lipid metabolic process // inferred from electronic annotation//0006631 // fatty a
NM_001286040//NM_00121	-1.15	-1.11	1.00	1.04	-1.03	-1.11	<i>Anks1</i>	ankyrin repeat and SAM domain containing 1	0006929 // substrate-dependent cell migration // inferred from direct assay//0016322 // neu
NM_018829//XM_0065192E	1.08	1.22	1.15	-1.04	1.03	-1.15	<i>Ap3m1</i>	adaptor-related protein complex 3, mu 1 subunit	0006810 // transport // inferred from electronic annotation//0006886 // intracellular protein
NM_001314013//NM_05301	1.06	1.10	1.15	-1.05	1.13	1.07	<i>Atg5</i>	autophagy related 5	0000045 // autophagosome assembly // inferred from mutant phenotype//0000422 // mitop
NM_007591	-1.11	1.25	1.22	-1.38	1.05	-1.11	<i>Calr</i>	calreticulin	0000122 // negative regulation of transcription from RNA polymerase II promoter // not recor
NM_001080126//NM_00121	1.24	1.15	1.17	1.06	1.15	-1.13	<i>Casp8</i>	caspase 8	0001525 // angiogenesis // inferred from mutant phenotype//0001841 // neural tube formati
NM_001159738//NM_01691	-1.33	-1.18	-1.22	-1.04	1.53	1.56	<i>Ccl20</i>	chemokine (C-C motif) ligand 20	002548 // monocyte chemotaxis // --//0006935 // chemotaxis // not recorded//0006954 //
NM_001111099//NM_00761	-1.83	-1.03	-1.41	2.20	1.26	1.78	<i>Cdkn1a</i>	cyclin-dependent kinase inhibitor 1A (P21)	0000079 // regulation of cyclin-dependent protein serine/threonine kinase activity // inferred
NM_016675//XM_0065284E	1.14	1.00	-1.01	1.04	1.16	1.25	<i>Cldn2</i>	claudin 2	0016338 // calcium-independent cell-cell adhesion via plasma membrane cell-adhesion molec
NM_001252479//NM_13391	1.19	-1.03	-1.19	1.05	1.20	1.24	<i>Cmtm7</i>	CKLF-like MARVEL transmembrane domain containing 7	0002337 // B-1a B cell differentiation // inferred from mutant phenotype//0006935 // chemo
NM_001037859//NM_00771	1.03	-1.12	-1.02	-1.10	-1.10	1.22	<i>Csf1r</i>	colony stimulating factor 1 receptor	0001934 // positive regulation of protein phosphorylation // not recorded//0002376 // immu
NM_001136086//NM_00121	-1.07	1.16	1.10	1.04	1.23	-1.31	<i>Dpysl3</i>	dihydropyrimidinase-like 3	0007399 // nervous system development // inferred from direct assay//0008152 // metaboli
NM_010104	-1.17	1.25	-1.14	1.62	1.18	-1.96	<i>Edn1</i>	endothelin 1	0000122 // negative regulation of transcription from RNA polymerase II promoter // not recor
NM_010485//XM_0065086E	-1.02	1.20	1.15	-1.11	-1.03	-1.10	<i>Elavl1</i>	ELAV (embryonic lethal, abnormal vision)-like 1 (Hu antigen R)	0006417 // regulation of translation // not recorded//0045727 // positive regulation of transla
NM_001136077//NM_00121	-1.06	-1.00	1.04	1.05	-1.16	1.10	<i>Enpp2</i>	ectonucleotide pyrophosphatase/phosphodiesterase 2	0001953 // negative regulation of cell-matrix adhesion // not recorded//0006629 // lipid met
NM_001081225//NM_17261	-1.40	-1.08	1.12	-1.24	-1.20	-1.15	<i>Fam178a</i>	family with sequence similarity 178, member A	0006281 // DNA repair // inferred from electronic annotation//0006974 // cellular response t
NM_025912//XM_0065000E	1.02	-1.01	-1.09	1.08	1.17	1.10	<i>Fam210b</i>	family with sequence similarity 210, member B	0016020 // membrane // inferred from electronic annotation//0016021 // integral componen
NM_008086	-1.00	-1.12	-1.06	-1.17	-1.04	1.10	<i>Gas1</i>	growth arrest specific 1	0002053 // positive regulation of mesenchymal cell proliferation // inferred from mutant phen
NM_001039129//NM_00111	1.53	1.18	1.20	1.10	-1.18	-1.25	<i>Hnnpa1</i>	heterogeneous nuclear ribonucleoprotein A1 pseudogene//predicted gene 5803//heterogeneous nuclea	0000380 // alternative mRNA splicing, via spliceosome // inferred from direct assay//0006391
XM_011238903//XM_01123	2.61	3.75	3.71	1.18	-1.42	1.12	<i>Gm37416//Gm39743//Gm3</i>	predicted gene, 37416//predicted gene, 39743//predicted gene, 40611//predicted gene, 40814//predi	0006278 // RNA-dependent DNA replication // inferred from electronic annotation//0008152
NM_001080707//NM_00111	-1.21	-1.10	1.62	-1.30	-1.49	1.14	<i>Gpr155</i>	G protein-coupled receptor 155	0035556 // intracellular signal transduction // inferred from electronic annotation//0050890 ,
NM_153071//XM_0112431E	-1.10	-1.02	-1.07	-1.14	-1.43	1.33	<i>Gprc6a</i>	G protein-coupled receptor, family C, group 6, member A	0007165 // signal transduction // inferred from electronic annotation//0007186 // G-protein i
NM_010344	1.29	1.07	1.10	1.07	1.15	1.16	<i>Gsr</i>	glutathione reductase	0006749 // glutathione metabolic process // inferred by curator//0006749 // glutathione met
NM_026113//XM_00651282	1.14	1.30	1.08	-1.08	1.27	-1.02	<i>Gtf3c6</i>	general transcription factor IIIC, polypeptide 6, alpha	0006351 // transcription, DNA-templated // not recorded//0006383 // transcription from RN
NM_022331//XM_0065312E	-1.56	1.12	-1.09	-1.22	-1.48	1.21	<i>Herpud1</i>	homocysteine-inducible, endoplasmic reticulum stress-inducible, ubiquitin-like domain member 1	0006511 // ubiquitin-dependent protein catabolic process // inferred from direct assay//0006
NM_019447//XM_0065040E	-1.17	-1.16	1.03	1.09	-1.20	-1.07	<i>Hgfac</i>	hepatocyte growth factor activator	0006508 // proteolysis // inferred from electronic annotation
NM_010474	1.36	-1.38	1.15	1.36	1.39	-1.73	<i>Hs3st1</i>	heparan sulfate (glucosamine) 3-O-sulfotransferase 1	0008152 // metabolic process // inferred from electronic annotation
NM_172015//XM_00651682	-1.05	1.08	1.02	-1.12	1.06	-1.10	<i>Iars</i>	isoleucine-tRNA synthetase	0001649 // osteoblast differentiation // not recorded//0006412 // translation // inferred fr
NM_010501//XM_0112471E	1.29	-1.08	1.28	-1.13	1.07	1.41	<i>Ifit3</i>	interferon-induced protein with tetratricopeptide repeats 3	0002376 // immune system process // inferred from electronic annotation//0008285 // negat
NM_001308535//NM_01351	1.20	1.12	1.15	-1.06	1.02	-1.49	<i>Il2rg</i>	interleukin 2 receptor, gamma chain	0010468 // regulation of gene expression // inferred from mutant phenotype//0010628 // po
NM_008403//XM_0065149E	1.14	1.08	-1.02	1.11	1.14	-1.01	<i>Irgb1bp1</i>	integrin beta 1 binding protein 1	0001525 // angiogenesis // inferred from electronic annotation//0002043 // blood vessel end
NM_001159299//NM_00121	1.45	1.53	1.02	-1.19	1.14	-1.59	<i>Ithi4</i>	inter alpha-trypsin inhibitor, heavy chain 4	0006953 // acute-phase response // inferred from electronic annotation//0010466 // negativ
NM_008409	1.13	1.11	1.12	1.04	-1.03	-1.03	<i>Itm2a</i>	integral membrane protein 2A	0005515 // protein binding // inferred from electronic annotation
NM_031248	1.06	1.12	1.09	-1.03	1.14	1.05	<i>Lamtor2</i>	late endosomal/lysosomal adaptor, MAPK and MTOR activator 2	0000186 // activation of MAPKK activity // inferred from direct assay//0016049 // cell growth
NM_008491	1.67	1.43	1.37	-1.10	1.54	-1.20	<i>Lcn2</i>	lipocalin 2	0002376 // immune system process // inferred from electronic annotation//0006810 // trans
NM_025828	-1.02	1.16	1.09	-1.06	-1.13	-1.06	<i>Lman2</i>	lectin, mannose-binding 2	0006810 // transport // inferred from electronic annotation//0006890 // retrograde vesicle-tr
NM_001164885//NM_02281	-1.24	-1.06	1.16	1.02	-1.18	1.27	<i>Lpin2</i>	lipin 2	0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 //
NM_010766	1.21	-1.26	-1.04	2.27	4.07	-1.86	<i>Marco</i>	macrophage receptor with collagenous structure	0002376 // immune system process // inferred from electronic annotation//0006897 // endo
NM_001081392//NM_13381	-1.03	1.02	-1.05	-1.08	1.10	-1.05	<i>Mdn1</i>	midasin homolog (yeast)	0000027 // ribosomal large subunit assembly // inferred from electronic annotation//000815
NM_025578	-1.02	1.12	1.00	-1.04	1.12	-1.08	<i>Mrs25</i>	mitochondrial ribosomal protein S25	0032543 // mitochondrial translation // inferred by curator
NM_001008542//NM_00101	1.04	-1.11	1.07	1.09	-1.13	-1.07	<i>Mxi1</i>	MAX interactor 1, dimerization protein	0000122 // negative regulation of transcription from RNA polymerase II promoter // inferred f
NM_026526//XM_0065194E	1.06	1.11	-1.02	-1.05	1.07	-1.02	<i>N6amt2</i>	N-6 adenine-specific DNA methyltransferase 2 (putative)	0032259 // methylation // inferred from electronic annotation
NM_026554	-1.01	1.26	1.16	-1.22	1.10	-1.12	<i>Ncbp2</i>	nuclear cap binding protein subunit 2	0000184 // nuclear-transcribed mRNA catabolic process, nonsense-mediated decay // not rec
NM_001286037//NM_01081	1.45	1.09	-1.14	-1.06	-1.38	1.19	<i>Ncf1</i>	neutrophil cytosolic factor 1	0001878 // response to yeast // inferred from mutant phenotype//0001909 // leukocyte med
NM_010880//XM_0065292E	1.44	1.29	1.45	1.02	1.04	-1.19	<i>Ncl</i>	nucleolin	0001525 // angiogenesis // not recorded//0006897 // endocytosis // not recorded//0007283
NM_134010//XM_00651301	1.09	1.12	1.08	1.06	1.10	-1.10	<i>Nup107</i>	nucleoporin 107	0000973 // posttranscriptional tethering of RNA polymerase II gene DNA at nuclear periphery
NM_011119	1.08	1.01	1.17	-1.02	1.12	-1.12	<i>Pa2g4</i>	proliferation-associated 2G4	0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 //
NM_172924//XM_0065111E	1.09	1.19	-1.05	1.02	-1.15	-1.37	<i>Peak1</i>	pseudopodium-enriched atypical kinase 1	0006468 // protein phosphorylation // not recorded//0016310 // phosphorylation // inferre
NM_011072	1.26	1.05	-1.13	-1.17	1.17	-1.07	<i>Pfn1</i>	profilin 1	0001843 // neural tube closure // inferred from genetic interaction//0006357 // regulation of
NM_133942//XM_00650714	-1.14	1.11	1.07	-1.02	1.20	-1.11	<i>Plekha1</i>	pleckstrin homology domain containing, family A (phosphoinositide binding specific) member 1	0001553 // luteinization // inferred from genetic interaction//0007283 // spermatogenesis //
NM_008947	1.11	1.36	1.42	1.02	1.32	-1.05	<i>Psmc1</i>	protease (prosome, macropain) 26S subunit, ATPase 1	0030163 // protein catabolic process // inferred from electronic annotation//0030433 // ER-a
NM_011189	1.22	1.05	1.31	-1.06	1.17	1.22	<i>Psme1</i>	proteasome (prosome, macropain) activator subunit 1 (PA28 alpha)	0002479 // antigen processing and presentation of exogenous peptide antigen via MHC class I
NM_001085492//XM_00651	-1.03	1.03	1.34	-1.24	-1.40	-1.15	<i>Rere</i>	arginine glutamic acid dipeptidase (RE) repeats	0000122 // negative regulation of transcription from RNA polymerase II promoter // inferred f
NM_133933	-1.06	1.18	-1.12	-1.05	1.27	-1.10	<i>Rpn1</i>	ribophorin 1	0006486 // protein glycosylation // inferred from electronic annotation//0018279 // protein t
NM_001166506//NM_00111	-1.18	-1.02	1.06	-1.01	-1.07	-1.03	<i>Sec14l1</i>	SEC14-like lipid binding 1	0006810 // transport // inferred from electronic annotation
NM_001164059//NM_01134	1.72	-1.04	-1.05	1.10	-1.18	1.91	<i>Sell</i>	selectin, lymphocyte	0007155 // cell adhesion // inferred from electronic annotation//0033198 // response to ATP
NM_009151//XM_00653022	1.21	-1.01	-1.06	1.23	-1.02	1.35	<i>Selplg</i>	selectin, platelet (p-selectin) ligand	0007155 // cell adhesion // inferred from electronic annotation//0050901 // leukocyte tether
NM_145156//XM_0065270E	1.12	-1.09	-1.11	1.17	1.05	1.10	<i>Slc25a28</i>	solute carrier family 25, member 28	0006810 // transport // inferred from electronic annotation//0006811 // ion transport // infer
NM_021535	1.22	1.24	1.15	1.03	1.12	-1.06	<i>Smu1</i>	smu-1 suppressor of mec-8 and unc-52 homolog (C. elegans)	0005634 // nucleus // inferred from electronic annotation//0005737 // cytoplasm // inferred
NM_144918	1.14	1.10	-1.00	-1.06	1.13	-1.10	<i>Smyd5</i>	SET and MYND domain containing 5	0032259 // methylation // inferred from electronic annotation
NM_001110310//NM_00111	1.03	1.08	1.06	-1.08	1.07	-1.07	<i>Snx12</i>	sorting nexin 12	0006810 // transport // inferred from electronic annotation//0006897 // endocytosis // not r
NM_009264	2.18	1.35	-1.13	1.87	2.22	-2.52	<i>Sprr1a</i>	small proline-rich protein 1A	0018149 // peptide cross-linking // not recorded//0030216 // keratinocyte differentiation // r
NM_011512//XM_00649782	1.10	1.05	1.18	1.00	1.12	1.03	<i>Surf4</i>	surfeit gene 4	0007030 // Golgi organization // not recorded//0010638 // positive regulation of organelle or
NM_001311156//NM_13391	1.10	-1.02	1.05	1.09	1.15	1.16	<i>Tcta</i>	T cell leukemia translocation altered gene	0016020 // membrane // inferred from electronic annotation//0016021 // integral componen
NM_017376//NM_153484//	1.11	1.11	1.74	-1.43	-1.66	-1.12	<i>Tef</i>	thyrotroph embryonic factor	0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 //
NM_009364//XM_00650504	1.72	1.30	1.02	-1.03	1.20	-2.02	<i>Tfpi2</i>	tissue factor pathway inhibitor 2	0007596 // blood coagulation // inferred from electronic annotation//0007599 // hemostasis
NM_011607//XM_00653777	1.30	1.57	1.11	-1.35	1.70	-1.79	<i>Tnc</i>	tenascin C	0001649 // osteoblast differentiation // not recorded//0007155 // cell adhesion // inferred fr
NM_009396//XM_0065157E	1.09	-1.20	1.02	1.10	1.32	1.40	<i>Tnfrsf25</i>	tumor necrosis factor, alpha-induced protein 2	0001525 // angiogenesis // inferred from electronic annotation//0006887 // exocytosis // not
NM_011653	-1.00	1.09	-1.01	1.03	1.24	-1.06	<i>Tuba1a</i>	tubulin, alpha 1A	0007017 // microtubule-based process // inferred from electronic annotation//0008152 // mi