

Fig. S1

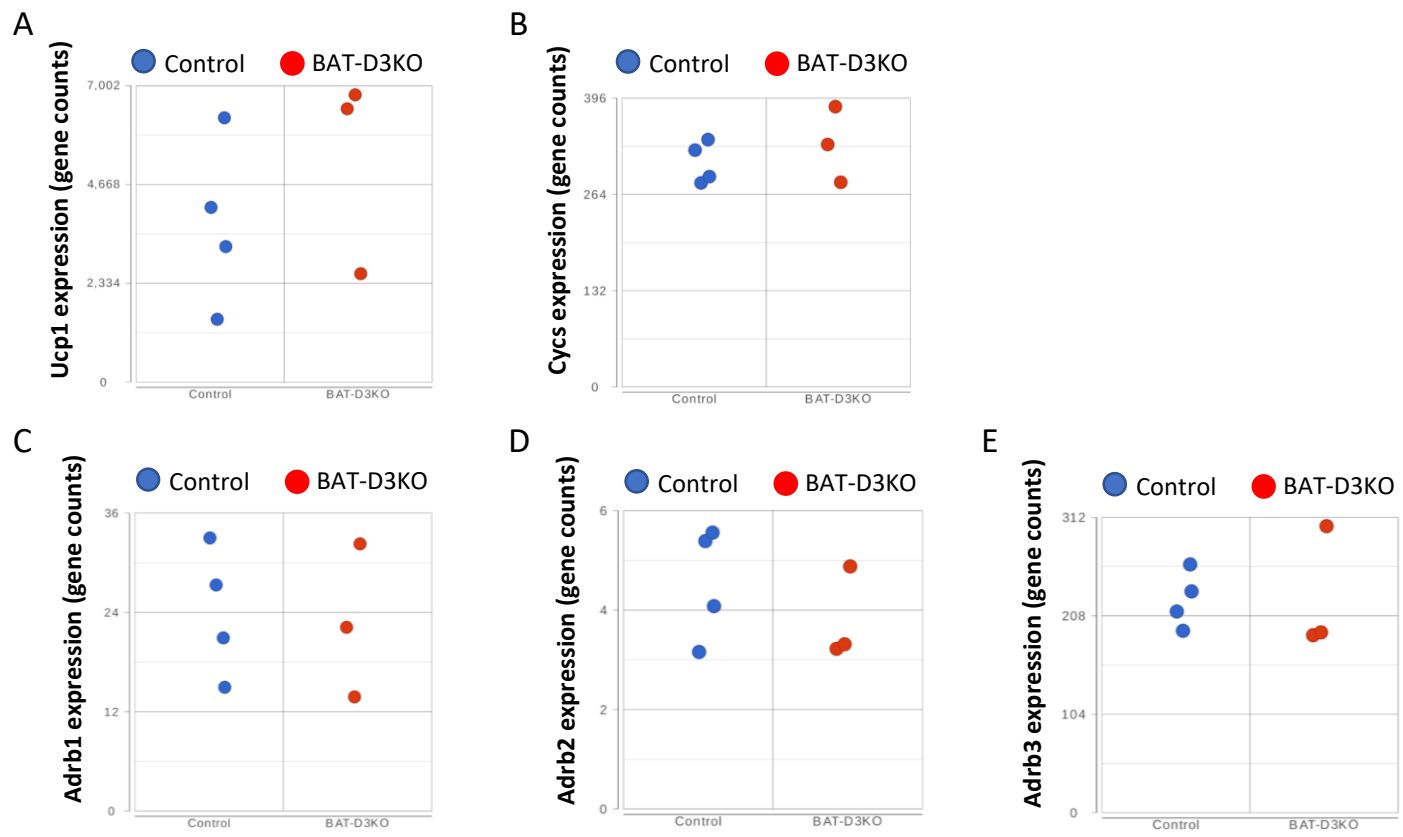
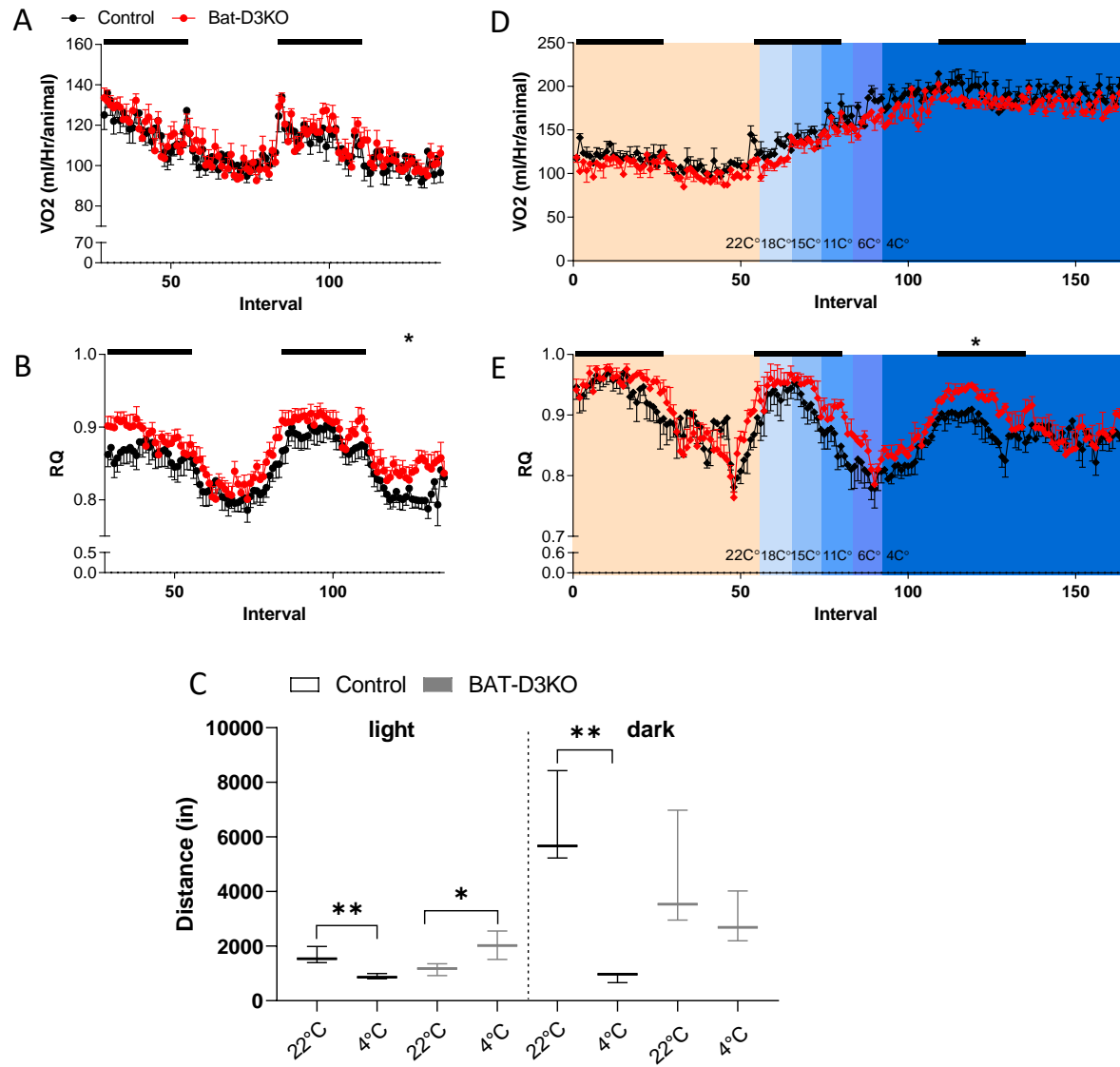


Fig. S2



Supplementary figure legend

Fig. S1 – BAT gene expression in the adult BAT-D3KO mice. (A) BAT Ucp1 expression using Rna-seq counts; (B) Same as A but Cyp11a1 is shown; (C) Same as A but Adrb1 is shown; (D) same as A but Adrb2 is shown; and (E) same as A but Adrb3 is shown. Values are mean \pm SEM; n=3-4/group.

Fig. S2 – C.L.A.M.S. metabolic profile and ambulatory movements of adult BAT-D3KO mice. (A) VO₂ in control and BAT-D3KO mice at room temperature; black bars indicate 12h of dark cycles; all animals were kept on chow diet; (B) Same as A, except that shown is the respiratory quotient (RQ); (C) Ambulatory movements of adult BAT-D3KO mice; distance traveled on the home cage on 12h period of light and dark cycle; (D) Same as A, except that the environment temperature was gradually decreased at each 4-hour interval until it reached 4°C; and (E) Same as D, except that shown is respiratory quotient (RQ). all values are shown as mean \pm SEM; n=4-9/group; * p \leq 0.05; and **p<0.01 vs control (Student's t-test).

Table S1- Distribution of genotypes

Percentage	Flox D3 allele			Cre allele	
	WT	FloxD3 Homozygous	FloxD3 Heterozygous	WT	CRE
Expected	25%	25%	50%	25%	75%
Obtained	29%	21%	50%	38%	62%

Note: percentage was calculated using 76 animals born from 9 different breeders. The average number of pups from each litter was 6.

Table S2- iBAT weight of BAT-D3KO and controls animals at different ages.

Age	Brow fat		<i>p</i> value
	control	BAT-D3KO	
E18.5	0.010±0.003	0.028±0.034	0.21
P1	0.008±0.001	0.007±0.0008	0.46

All tissues are expressing in g of wet tissue/body weight in g. The values are the mean ± SD of 4-9 independent samples. *p* value is Mann-Whitney test.

Table S3- Morphometric data of adult BAT-D3KO and control mice.

Tissue	control	BAT-D3KO	<i>p</i> value
brown fat	0.0054±0.002	0.0053±0.004	0.19
epididymal Fat	0.0373±0.016	0.0360±0.002	0.46
liver	0.0793±0.013	0.0650±0.018	0.13
brain	0.0247±0.001	0.0237±0.002	0.19
gastrocnemius	0.0075±0.001	0.0063±0.001	0.09
heart	0.0098±0.0083	0.0070±0.001	0.11
kidney	0.0100±0.002	0.0129±0.003	0.05
pancreas	0.0141±0.002	0.0117±0.001	0.06
Tibia length (mm)	18.1±0.144	18.3±0.239	0.13

All tissues are expressing in g of wet tissue/tibia length in millimeters. The values are the mean ± SD of 4-6 independent samples. *p* value is t-test.

Table S4– Oligonucleotide Primers

Gene		Sequence
peroxisome proliferator activated receptor alpha	PPARa Forward	AGAGCCCCATCTGCTCTCTC
	PPARa Reverse	ACTGGTAGTCTGCAAAACCAAA
18S rRNA	18S Forward	GTAACCCGTTGAACCCATT
	18S Reverse	CCATCCAATCGGTAGTAGCG
uncoupling protein 1	UCP1 Forward	AAGCTGTGCGATGTCCATGT
	UCP1 Reverse	AAGCCACAAACCTTTGAAAA
deiodinase, iodothyronine, type II	DIO2 Forward (Primer 1)	TCCTAGATGCCTACAAAACAGGTTA
	DIO2 Reverse (Primer 1)	GTCAGGTGGCTGAACCAAAG
deiodinase, iodothyronine, type II	DIO2 Forward (Primer 2)	GTCCGCAAATGACCCCTTT
	DIO2 Reverse (Primer 2)	CCCACCCACTCTCTGACTTTC
ELOVL family member 3, elongation of long chain fatty acids	Elovl3 Forward	GGACCTGATGCAACCTATGA
	Elovl3 Reverse	TCCGCGTTCTCATGTAGGTCT
Peroxisome Proliferator-Activated Receptor Gamma Coactivator 1-Alpha	PGC1a Forward	ATGTGTGCGCTTCTTGCTCT
	PGC1a Reverse	ATCTACTGCCTGGGGACCTT
Cell Death Inducing DFFA Like Effector A	Cidea Forward	TGACATTCATGGGATTGCAGAC
	Cidea Reverse	GGCCAGTTGTGATGACTAAGAC
PR domain containing 16	Prdm16 Forward	CCACCAGCGAGGACTTAC
	Prdm16 Reverse	GGAGGACTCTGGTAGCTCGAA
Peroxisome Proliferator-Activated Receptor Gamma, Coactivator 1 Beta	Pgc1 β Forward	TCCTGTAAAAGCCGGAGTAT
	Pgc1 β Reverse	GCTCTGGTAGGGGCAGTGA
Acyl-CoA Synthetase Long Chain Family Member 5	Acsl5 Forward	TCCTGACGTTTGAACGGC
	Acsl5 Reverse	CTCCCTCAATCCCCACAGAC
Cytochrome C Oxidase Subunit 8B	Cox8b Forward	TGTGGGGATCTCAGCCATAGT
	Cox8b Reverse	AGTGGGCTAAGACCCATCCTG
deiodinase, iodothyronine, type I	Dio1 Forward	GTGTGCGATACCTCCAGAAG
	Dio1 Reverse	GTTGTGTTGTCCGTCATATAG
Cyclophilin B	CycloB Forward	GGAGATGGCACAGGAGGAA
	CycloB Reverse	GCCCGTAGTGCTTCAGCTT

Table S5- Differentially expressed genes in adult BAT-D3KO iBAT.

Gene ID	Chromosome	Total counts	Maximum counts	P-value	FDR step up	Ratio	Log2(Ratio)	Fold change	LSMean (BAT-D3KO)	LSMean (Control)
Nr4a3	4	1.31E+02	6.86E+01	4.01E-03	3.13E-01	1.51E+01	3.91	15.07	4.01E+01	2.66E+00
Hspa1b	17	2.34E+02	1.15E+02	2.22E-02	3.52E-01	1.24E+01	3.63	12.40	7.05E+01	5.68E+00
Hspa1a	17	1.94E+02	9.76E+01	2.28E-02	3.52E-01	1.20E+01	3.59	12.00	5.81E+01	4.84E+00
Mmd2	5	1.85E+02	1.25E+02	3.34E-02	3.72E-01	9.14E+00	3.19	9.14	5.37E+01	5.88E+00
Dio2	12	1.76E+03	6.46E+02	8.53E-03	3.33E-01	7.25E+00	2.86	7.25	4.95E+02	6.83E+01
3930402G23Rik	8	2.15E+01	1.00E+01	1.79E-02	3.49E-01	6.80E+00	2.77	6.80	5.99E+00	8.80E-01
Nr4a1	15	8.70E+02	3.74E+02	1.96E-02	3.49E-01	6.71E+00	2.75	6.71	2.42E+02	3.60E+01
Irs2	8	4.74E+02	2.06E+02	2.52E-02	3.52E-01	4.77E+00	2.25	4.77	1.23E+02	2.59E+01
Hsph1	5	5.27E+02	2.21E+02	7.92E-03	3.33E-01	4.73E+00	2.24	4.73	1.37E+02	2.90E+01
Atf3	1	6.60E+01	2.98E+01	4.31E-02	3.92E-01	4.56E+00	2.19	4.56	1.70E+01	3.74E+00
Sdc4	2	6.70E+02	2.30E+02	2.28E-02	3.52E-01	3.83E+00	1.94	3.83	1.66E+02	4.32E+01
Nr4a2	2	1.89E+02	6.88E+01	1.52E-02	3.40E-01	3.80E+00	1.92	3.80	4.65E+01	1.23E+01
Noct	3	1.09E+03	3.79E+02	1.93E-02	3.49E-01	3.71E+00	1.89	3.71	2.67E+02	7.19E+01
Gm16062	11	2.84E+01	1.11E+01	4.09E-02	3.87E-01	3.63E+00	1.86	3.63	6.92E+00	1.91E+00
Nfil3	13	9.35E+01	3.65E+01	2.82E-02	3.54E-01	3.53E+00	1.82	3.53	2.26E+01	6.41E+00
Rgs2	1	5.23E+02	1.57E+02	1.39E-02	3.36E-01	3.43E+00	1.78	3.43	1.26E+02	3.66E+01
Mafb	2	1.30E+02	4.62E+01	4.69E-03	3.17E-01	3.40E+00	1.76	3.40	3.12E+01	9.19E+00
Gem	4	2.16E+01	8.73E+00	4.50E-02	3.95E-01	3.35E+00	1.75	3.35	5.16E+00	1.54E+00
P4ha1	10	2.30E+02	8.01E+01	3.77E-02	3.83E-01	3.13E+00	1.65	3.13	5.38E+01	1.72E+01
Ppargc1a	5	6.63E+02	2.19E+02	2.19E-02	3.52E-01	3.13E+00	1.65	3.13	1.55E+02	4.95E+01
Mreg	1	2.94E+01	9.40E+00	4.84E-02	4.02E-01	3.13E+00	1.65	3.13	6.87E+00	2.19E+00
Dnajb1	8	3.37E+02	1.15E+02	6.73E-03	3.33E-01	3.09E+00	1.63	3.09	7.84E+01	2.53E+01
Cldn1	16	1.94E+01	6.33E+00	1.37E-02	3.36E-01	2.94E+00	1.56	2.94	4.45E+00	1.51E+00
Lipg	18	5.44E+01	1.67E+01	4.78E-02	4.02E-01	2.80E+00	1.48	2.80	1.23E+01	4.39E+00
Siah2	3	3.99E+01	1.23E+01	3.05E-03	3.13E-01	2.73E+00	1.45	2.73	8.93E+00	3.27E+00
Col11a2	17	3.63E+01	9.49E+00	2.78E-02	3.53E-01	2.70E+00	1.43	2.70	8.11E+00	3.00E+00
Rel	11	7.18E+01	2.27E+01	6.33E-03	3.33E-01	2.70E+00	1.43	2.70	1.60E+01	5.94E+00
Gm7816	5	1.81E+02	4.95E+01	6.81E-03	3.33E-01	2.63E+00	1.40	2.63	4.00E+01	1.52E+01

Syt14	1	2.92E+01	1.00E+01	2.40E-02	3.52E-01	2.61E+00	1.38	2.61	6.44E+00	2.47E+00
Hsp25-ps1	13	1.47E+02	3.84E+01	1.77E-04	3.13E-01	2.56E+00	1.36	2.56	3.23E+01	1.26E+01
Gm15542	7	3.65E+02	9.99E+01	7.61E-03	3.33E-01	2.54E+00	1.35	2.54	7.97E+01	3.14E+01
Mc5r	18	1.40E+01	4.04E+00	5.67E-03	3.33E-01	2.54E+00	1.35	2.54	3.06E+00	1.20E+00
Klhl25	7	1.35E+02	3.42E+01	1.03E-02	3.33E-01	2.53E+00	1.34	2.53	2.96E+01	1.17E+01
Hlx	1	6.48E+01	2.04E+01	2.22E-02	3.52E-01	2.47E+00	1.30	2.47	1.40E+01	5.69E+00
Dnaja1	4	6.51E+02	1.78E+02	8.19E-03	3.33E-01	2.40E+00	1.26	2.40	1.39E+02	5.81E+01
G0s2	1	1.24E+03	3.07E+02	9.46E-03	3.33E-01	2.38E+00	1.25	2.38	2.64E+02	1.11E+02
Ifi211	1	1.17E+01	3.33E+00	1.86E-02	3.49E-01	2.32E+00	1.21	2.32	2.47E+00	1.07E+00
Cdkn1a	17	1.99E+02	4.47E+01	8.85E-03	3.33E-01	2.32E+00	1.21	2.32	4.22E+01	1.82E+01
Gpx3	11	6.94E+03	2.03E+03	3.24E-02	3.69E-01	2.31E+00	1.21	2.31	1.47E+03	6.34E+02
Gm44777	7	1.13E+01	3.38E+00	4.49E-02	3.95E-01	2.31E+00	1.21	2.31	2.39E+00	1.03E+00
Hspb1	5	1.93E+02	4.46E+01	4.29E-04	3.13E-01	2.25E+00	1.17	2.25	4.04E+01	1.79E+01
Bag3	7	3.88E+02	1.11E+02	5.98E-03	3.33E-01	2.25E+00	1.17	2.25	8.11E+01	3.61E+01
Gm43079	3	1.19E+01	3.68E+00	4.57E-02	3.96E-01	2.23E+00	1.16	2.23	2.49E+00	1.11E+00
Gm20427	17	3.29E+01	7.51E+00	4.27E-02	3.91E-01	2.22E+00	1.15	2.22	6.85E+00	3.09E+00
Gm16023	4	1.14E+01	3.13E+00	3.20E-02	3.66E-01	2.21E+00	1.14	2.21	2.37E+00	1.07E+00
mt-Rnr2	M	3.45E+04	1.05E+04	3.70E-02	3.82E-01	2.18E+00	1.12	2.18	7.13E+03	3.27E+03
Col12a1	9	1.01E+02	2.30E+01	6.32E-03	3.33E-01	2.16E+00	1.11	2.16	2.09E+01	9.63E+00
Fam222a	5	1.66E+01	3.97E+00	1.57E-02	3.41E-01	2.16E+00	1.11	2.16	3.42E+00	1.58E+00
Dedd2	7	1.40E+02	3.34E+01	1.24E-03	3.13E-01	2.13E+00	1.09	2.13	2.87E+01	1.35E+01
Gm12226	11	1.19E+01	3.22E+00	3.96E-02	3.86E-01	2.11E+00	1.08	2.11	2.44E+00	1.16E+00
Gm38394	1	2.06E+02	4.89E+01	2.52E-02	3.52E-01	2.08E+00	1.05	2.08	4.17E+01	2.01E+01
Chka	19	6.86E+01	1.74E+01	2.30E-02	3.52E-01	2.06E+00	1.05	2.06	1.39E+01	6.73E+00
Atl2	17	8.40E+02	2.19E+02	3.31E-02	3.72E-01	2.04E+00	1.03	2.04	1.69E+02	8.31E+01
Fam126b	1	7.80E+02	1.91E+02	1.73E-02	3.49E-01	2.01E+00	1.01	2.01	1.56E+02	7.76E+01
Pde4d	13	6.11E+02	1.60E+02	1.56E-02	3.40E-01	1.98E+00	0.99	1.98	1.22E+02	6.14E+01
Pbld1	10	3.69E+01	8.71E+00	1.29E-02	3.33E-01	1.98E+00	0.99	1.98	7.36E+00	3.71E+00
Apoe	7	1.88E+03	4.37E+02	6.67E-03	3.33E-01	1.97E+00	0.98	1.97	3.73E+02	1.89E+02
Slc38a2	15	6.74E+02	1.62E+02	2.07E-02	3.52E-01	1.97E+00	0.98	1.97	1.34E+02	6.80E+01
Dnaja4	9	1.28E+02	3.51E+01	1.59E-02	3.42E-01	1.97E+00	0.98	1.97	2.55E+01	1.30E+01

AW011738	4	4.47E+01	1.14E+01	1.78E-02	3.49E-01	1.96E+00	0.97	1.96	8.86E+00	4.52E+00
Per1	11	3.32E+02	8.75E+01	3.71E-02	3.82E-01	1.94E+00	0.95	1.94	6.56E+01	3.39E+01
Ccdc117	11	2.01E+02	5.23E+01	6.59E-03	3.33E-01	1.94E+00	0.95	1.94	3.98E+01	2.05E+01
Chordc1	9	3.26E+02	8.00E+01	2.63E-02	3.52E-01	1.93E+00	0.95	1.93	6.42E+01	3.33E+01
Gm43859	3	8.84E+00	2.19E+00	3.24E-02	3.69E-01	1.90E+00	0.93	1.90	1.73E+00	9.11E-01
Mxd1	6	7.19E+01	1.70E+01	2.24E-02	3.52E-01	1.89E+00	0.92	1.89	1.40E+01	7.44E+00
Dnajb4	3	3.57E+02	8.81E+01	3.27E-03	3.13E-01	1.88E+00	0.91	1.88	6.96E+01	3.71E+01
Shb	4	1.46E+02	3.44E+01	1.13E-02	3.33E-01	1.87E+00	0.91	1.87	2.84E+01	1.52E+01
Foxo1	3	5.21E+02	1.25E+02	5.96E-03	3.33E-01	1.87E+00	0.90	1.87	1.01E+02	5.42E+01
Resf1	6	2.67E+02	6.23E+01	4.94E-02	4.03E-01	1.86E+00	0.90	1.86	5.18E+01	2.78E+01
Hdc	2	3.47E+01	8.10E+00	2.45E-02	3.52E-01	1.86E+00	0.90	1.86	6.73E+00	3.62E+00
Pnrc1	4	3.32E+02	8.36E+01	3.62E-02	3.80E-01	1.86E+00	0.89	1.86	6.44E+01	3.47E+01
Cth	3	9.80E+00	2.55E+00	4.16E-02	3.90E-01	1.86E+00	0.89	1.86	1.90E+00	1.02E+00
Hsp90aa1	12	1.32E+03	3.48E+02	2.21E-02	3.52E-01	1.85E+00	0.89	1.85	2.56E+02	1.38E+02
Cebpb	2	4.46E+02	1.13E+02	2.74E-02	3.52E-01	1.85E+00	0.89	1.85	8.64E+01	4.67E+01
Zfp516	18	1.05E+02	2.51E+01	1.20E-02	3.33E-01	1.84E+00	0.88	1.84	2.04E+01	1.11E+01
Baz1a	12	1.22E+02	2.85E+01	1.08E-02	3.33E-01	1.84E+00	0.88	1.84	2.36E+01	1.28E+01
Hmgcr	13	9.83E+01	2.33E+01	2.33E-02	3.52E-01	1.84E+00	0.88	1.84	1.90E+01	1.03E+01
Myrip	9	2.77E+01	6.99E+00	1.43E-02	3.38E-01	1.83E+00	0.87	1.83	5.35E+00	2.92E+00
Chd1	17	2.55E+02	5.96E+01	2.23E-03	3.13E-01	1.83E+00	0.87	1.83	4.93E+01	2.69E+01
2610037D02Rik	15	1.27E+01	2.88E+00	2.87E-02	3.56E-01	1.82E+00	0.86	1.82	2.44E+00	1.34E+00
Osbp2	11	1.58E+01	3.85E+00	2.92E-02	3.58E-01	1.81E+00	0.86	1.81	3.03E+00	1.67E+00
Gm12346	11	6.50E+02	1.72E+02	2.78E-02	3.53E-01	1.81E+00	0.85	1.81	1.25E+02	6.90E+01
Gm16378	8	7.71E+00	1.70E+00	1.26E-02	3.33E-01	1.78E+00	0.83	1.78	1.47E+00	8.25E-01
Chchd2-ps	4	2.48E+01	6.18E+00	9.62E-03	3.33E-01	1.77E+00	0.82	1.77	4.71E+00	2.66E+00
Zswim5	4	3.36E+01	7.33E+00	2.78E-02	3.53E-01	1.75E+00	0.81	1.75	6.35E+00	3.62E+00
Kdm6a	X	1.41E+02	3.17E+01	2.46E-02	3.52E-01	1.75E+00	0.81	1.75	2.68E+01	1.53E+01
Dleu2	14	9.97E+01	2.21E+01	3.21E-02	3.66E-01	1.74E+00	0.80	1.74	1.88E+01	1.08E+01
Tes	6	1.26E+01	2.78E+00	1.24E-03	3.13E-01	1.73E+00	0.79	1.73	2.36E+00	1.37E+00
Stip1	19	3.12E+02	6.81E+01	9.60E-03	3.33E-01	1.73E+00	0.79	1.73	5.87E+01	3.40E+01
Gm37893	1	2.94E+01	6.23E+00	1.53E-02	3.40E-01	1.72E+00	0.78	1.72	5.53E+00	3.21E+00

Med26	8	3.56E+01	9.23E+00	5.00E-02	4.05E-01	1.71E+00	0.78	1.71	6.68E+00	3.90E+00
Mapkapk2	1	1.18E+03	2.73E+02	3.20E-02	3.66E-01	1.70E+00	0.77	1.70	2.20E+02	1.29E+02
Gm5844	3	8.52E+01	2.09E+01	4.34E-02	3.92E-01	1.69E+00	0.76	1.69	1.59E+01	9.38E+00
Gm16973	14	2.55E+01	5.99E+00	2.27E-02	3.52E-01	1.66E+00	0.73	1.66	4.71E+00	2.83E+00
Etfbkmt	6	1.79E+02	4.08E+01	3.58E-02	3.80E-01	1.66E+00	0.73	1.66	3.30E+01	1.99E+01
Vgll4	6	5.70E+02	1.31E+02	4.21E-02	3.90E-01	1.66E+00	0.73	1.66	1.05E+02	6.35E+01
Gm7600	8	1.35E+01	3.00E+00	9.17E-03	3.33E-01	1.66E+00	0.73	1.66	2.50E+00	1.51E+00
Skil	3	3.41E+02	6.83E+01	2.34E-03	3.13E-01	1.65E+00	0.73	1.65	6.30E+01	3.81E+01
Pcdhgc5	18	1.15E+01	2.77E+00	3.08E-02	3.62E-01	1.65E+00	0.72	1.65	2.11E+00	1.28E+00
Lpcat4	2	1.01E+01	2.04E+00	2.92E-03	3.13E-01	1.65E+00	0.72	1.65	1.86E+00	1.13E+00
Mat2a	6	1.16E+03	2.35E+02	2.92E-03	3.13E-01	1.64E+00	0.71	1.64	2.14E+02	1.30E+02
Naa16	14	6.37E+01	1.44E+01	1.24E-02	3.33E-01	1.64E+00	0.71	1.64	1.17E+01	7.14E+00
Rgcc	14	5.82E+02	1.45E+02	3.77E-02	3.83E-01	1.63E+00	0.70	1.63	1.07E+02	6.55E+01
Slc7a6	8	3.55E+02	7.36E+01	2.72E-03	3.13E-01	1.63E+00	0.70	1.63	6.50E+01	4.00E+01
Six4	12	1.54E+01	3.50E+00	4.14E-02	3.90E-01	1.62E+00	0.70	1.62	2.83E+00	1.74E+00
Tmc4	7	1.92E+01	4.17E+00	4.23E-02	3.90E-01	1.62E+00	0.70	1.62	3.52E+00	2.17E+00
Kdm6b	11	4.11E+02	9.13E+01	2.21E-02	3.52E-01	1.62E+00	0.70	1.62	7.51E+01	4.64E+01
Nop58	1	8.75E+01	1.74E+01	3.67E-03	3.13E-01	1.62E+00	0.69	1.62	1.60E+01	9.89E+00
Pfkfb3	2	4.89E+03	1.05E+03	2.82E-02	3.54E-01	1.61E+00	0.69	1.61	8.93E+02	5.53E+02
Sfpq	4	4.56E+02	8.48E+01	2.69E-03	3.13E-01	1.61E+00	0.69	1.61	8.31E+01	5.15E+01
Yrdc	4	7.78E+01	1.52E+01	1.06E-02	3.33E-01	1.61E+00	0.68	1.61	1.42E+01	8.82E+00
A930004J17Rik	4	2.18E+01	4.97E+00	4.89E-02	4.02E-01	1.60E+00	0.68	1.60	3.97E+00	2.47E+00
Car3	3	1.66E+04	3.40E+03	1.78E-02	3.49E-01	1.60E+00	0.68	1.60	3.03E+03	1.89E+03
Uspl1	5	2.03E+02	4.54E+01	1.67E-02	3.46E-01	1.60E+00	0.68	1.60	3.70E+01	2.31E+01
Dynll1	5	1.66E+02	3.20E+01	1.13E-02	3.33E-01	1.59E+00	0.67	1.59	3.01E+01	1.89E+01
Ahsa1	12	3.69E+02	8.15E+01	1.42E-02	3.38E-01	1.59E+00	0.67	1.59	6.70E+01	4.20E+01
Slc25a33	4	1.88E+02	3.99E+01	5.00E-02	4.05E-01	1.59E+00	0.67	1.59	3.41E+01	2.14E+01
Pigx	16	3.71E+01	8.52E+00	2.99E-02	3.58E-01	1.58E+00	0.66	1.58	6.72E+00	4.24E+00
Ddx3x	X	2.25E+03	4.88E+02	1.53E-02	3.40E-01	1.58E+00	0.66	1.58	4.07E+02	2.57E+02
Bdp1	13	1.55E+02	2.91E+01	3.89E-05	2.22E-01	1.58E+00	0.66	1.58	2.81E+01	1.78E+01
1500015A07Rik	18	1.56E+01	3.22E+00	3.91E-02	3.86E-01	1.58E+00	0.66	1.58	2.82E+00	1.78E+00

Tob2	15	1.56E+03	2.94E+02	1.08E-02	3.33E-01	1.58E+00	0.66	1.58	2.81E+02	1.78E+02
Zfp593	4	2.00E+01	4.28E+00	2.31E-02	3.52E-01	1.58E+00	0.66	1.58	3.62E+00	2.29E+00
Gm5763	X	6.50E+01	1.45E+01	4.51E-02	3.95E-01	1.58E+00	0.66	1.58	1.17E+01	7.44E+00
Gm26621	15	1.22E+01	2.41E+00	3.97E-02	3.86E-01	1.57E+00	0.65	1.57	2.21E+00	1.40E+00
Ptges3	10	3.52E+02	6.88E+01	4.07E-03	3.14E-01	1.57E+00	0.65	1.57	6.35E+01	4.04E+01
Trpv2	11	1.12E+01	2.18E+00	2.08E-02	3.52E-01	1.57E+00	0.65	1.57	2.01E+00	1.28E+00
Pprc1	19	8.44E+01	1.59E+01	5.85E-03	3.33E-01	1.57E+00	0.65	1.57	1.52E+01	9.71E+00
Mphosph10	7	7.60E+01	1.60E+01	5.31E-03	3.33E-01	1.56E+00	0.64	1.56	1.37E+01	8.75E+00
Hspa4l	3	3.30E+02	6.90E+01	8.05E-03	3.33E-01	1.56E+00	0.64	1.56	5.93E+01	3.80E+01
Dlc1	8	1.76E+03	3.96E+02	4.28E-02	3.92E-01	1.55E+00	0.64	1.55	3.16E+02	2.03E+02
Fubp1	3	3.42E+02	6.62E+01	3.92E-03	3.13E-01	1.55E+00	0.63	1.55	6.13E+01	3.95E+01
Rgs3	4	3.95E+02	8.28E+01	1.44E-02	3.38E-01	1.55E+00	0.63	1.55	7.08E+01	4.57E+01
Atoh8	6	2.26E+01	4.27E+00	2.00E-02	3.50E-01	1.55E+00	0.63	1.55	4.05E+00	2.62E+00
Ahsa2	11	2.73E+02	6.00E+01	3.71E-02	3.82E-01	1.54E+00	0.62	1.54	4.89E+01	3.17E+01
Alkbh1	12	5.60E+01	1.08E+01	8.26E-04	3.13E-01	1.54E+00	0.62	1.54	1.00E+01	6.50E+00
Jmjd6	11	1.74E+02	3.65E+01	1.27E-02	3.33E-01	1.54E+00	0.62	1.54	3.11E+01	2.02E+01
Slc35e2	4	2.50E+02	4.95E+01	3.18E-02	3.66E-01	1.54E+00	0.62	1.54	4.47E+01	2.91E+01
Mllt1	17	1.89E+02	3.91E+01	3.54E-02	3.79E-01	1.54E+00	0.62	1.54	3.37E+01	2.20E+01
Trir	8	1.05E+02	2.37E+01	1.98E-02	3.49E-01	1.54E+00	0.62	1.54	1.87E+01	1.22E+01
Gm44986	7	8.80E+00	1.95E+00	3.51E-02	3.78E-01	1.54E+00	0.62	1.54	1.57E+00	1.02E+00
Garem1	18	8.00E+00	1.67E+00	3.95E-02	3.86E-01	1.53E+00	0.62	1.53	1.43E+00	9.30E-01
Cdkn1c	7	1.31E+02	2.82E+01	1.38E-02	3.36E-01	1.53E+00	0.62	1.53	2.33E+01	1.52E+01
Snrpf	10	3.02E+01	6.60E+00	7.62E-03	3.33E-01	1.53E+00	0.62	1.53	5.38E+00	3.51E+00
Gm15832	1	7.80E+00	1.49E+00	3.49E-03	3.13E-01	1.53E+00	0.61	1.53	1.39E+00	9.08E-01
Bloc1s4	5	5.24E+01	1.02E+01	1.24E-02	3.33E-01	1.53E+00	0.61	1.53	9.33E+00	6.10E+00
Gm12905	4	9.50E+00	1.81E+00	3.91E-02	3.86E-01	1.52E+00	0.60	1.52	1.69E+00	1.11E+00
Zbtb21	16	1.06E+02	2.14E+01	3.27E-03	3.13E-01	1.52E+00	0.60	1.52	1.88E+01	1.24E+01
Tlnrd1	7	1.10E+02	2.36E+01	3.90E-02	3.86E-01	1.52E+00	0.60	1.52	1.95E+01	1.28E+01
1810055G02Rik	19	3.33E+01	6.42E+00	7.35E-03	3.33E-01	1.52E+00	0.60	1.52	5.90E+00	3.90E+00
Gm11847	4	4.78E+01	9.74E+00	1.12E-02	3.33E-01	1.51E+00	0.60	1.51	8.46E+00	5.59E+00
Ndel1	11	3.15E+02	6.62E+01	1.33E-02	3.36E-01	1.51E+00	0.59	1.51	5.58E+01	3.69E+01

Tjap1	17	6.65E+01	1.21E+01	2.98E-02	3.58E-01	1.51E+00	0.59	1.51	1.18E+01	7.80E+00
Rpl10a	17	6.90E+01	1.29E+01	1.23E-02	3.33E-01	1.51E+00	0.59	1.51	1.22E+01	8.09E+00
Swf1	1	7.93E+01	1.67E+01	2.59E-02	3.52E-01	1.51E+00	0.59	1.51	1.40E+01	9.30E+00
Zfp968	2	1.21E+01	2.44E+00	1.73E-02	3.49E-01	1.51E+00	0.59	1.51	2.14E+00	1.42E+00
Ncald	15	1.13E+01	2.28E+00	6.55E-03	3.33E-01	1.50E+00	0.59	1.50	2.00E+00	1.33E+00
Cdkn2c	4	4.19E+02	7.73E+01	9.86E-04	3.13E-01	1.50E+00	0.58	1.50	7.39E+01	4.93E+01
Akirin1	4	4.04E+02	7.62E+01	3.57E-03	3.13E-01	1.50E+00	0.58	1.50	7.12E+01	4.76E+01
2410004B18Rik	3	4.65E+01	8.30E+00	2.10E-03	3.13E-01	1.50E+00	0.58	1.50	8.19E+00	5.48E+00
Gm10335	10	1.46E+02	3.04E+01	3.97E-02	3.86E-01	1.49E+00	0.58	1.49	2.58E+01	1.73E+01
2810001G20Rik	11	1.73E+01	3.34E+00	3.76E-03	3.13E-01	1.49E+00	0.58	1.49	3.05E+00	2.04E+00
Fbxo4	15	5.99E+01	1.15E+01	2.18E-03	3.13E-01	1.49E+00	0.58	1.49	1.05E+01	7.06E+00
Psmg3	5	3.56E+01	7.05E+00	4.23E-02	3.90E-01	1.49E+00	0.58	1.49	6.27E+00	4.20E+00
Kti12	4	8.18E+01	1.45E+01	3.24E-04	3.13E-01	1.49E+00	0.58	1.49	1.44E+01	9.65E+00
Gm37254	1	1.64E+01	3.01E+00	1.83E-02	3.49E-01	1.49E+00	0.57	1.49	2.88E+00	1.93E+00
Gm9523	5	1.40E+01	2.77E+00	3.03E-02	3.59E-01	1.49E+00	0.57	1.49	2.46E+00	1.65E+00
Sde2	1	1.01E+02	2.07E+01	4.77E-02	4.02E-01	1.49E+00	0.57	1.49	1.77E+01	1.19E+01
Endog	2	1.40E+02	2.79E+01	3.30E-02	3.71E-01	1.48E+00	0.57	1.48	2.46E+01	1.66E+01
Spata1	3	9.55E+00	1.89E+00	3.60E-02	3.80E-01	1.48E+00	0.57	1.48	1.67E+00	1.13E+00
Rpl27	11	2.57E+01	4.70E+00	2.07E-03	3.13E-01	1.48E+00	0.56	1.48	4.50E+00	3.04E+00
Tbc1d10a	11	2.69E+01	5.06E+00	2.99E-02	3.58E-01	1.48E+00	0.56	1.48	4.71E+00	3.18E+00
Sphk2	7	1.41E+02	2.75E+01	4.03E-03	3.13E-01	1.48E+00	0.56	1.48	2.47E+01	1.68E+01
Emc6	11	4.16E+02	7.69E+01	1.75E-02	3.49E-01	1.48E+00	0.56	1.48	7.29E+01	4.94E+01
Hoxa5	6	1.12E+02	2.18E+01	1.24E-02	3.33E-01	1.47E+00	0.56	1.47	1.97E+01	1.33E+01
Ppp1r14b	19	1.49E+02	3.01E+01	4.07E-02	3.87E-01	1.47E+00	0.56	1.47	2.60E+01	1.77E+01
Gm42517	5	8.38E+00	1.82E+00	3.76E-02	3.83E-01	1.47E+00	0.56	1.47	1.47E+00	9.96E-01
Gpr162	6	7.54E+00	1.41E+00	1.58E-02	3.42E-01	1.47E+00	0.56	1.47	1.32E+00	8.96E-01
Saysd1	14	2.04E+01	3.72E+00	1.77E-02	3.49E-01	1.47E+00	0.56	1.47	3.57E+00	2.42E+00
Gm11478	11	7.59E+01	1.67E+01	4.94E-02	4.03E-01	1.47E+00	0.56	1.47	1.33E+01	9.02E+00
Gm11405	4	1.01E+01	1.88E+00	1.77E-02	3.49E-01	1.47E+00	0.56	1.47	1.77E+00	1.21E+00
Exosc3	4	4.24E+01	8.24E+00	1.86E-02	3.49E-01	1.47E+00	0.55	1.47	7.41E+00	5.05E+00
Gm17300	4	1.27E+01	2.68E+00	2.88E-02	3.57E-01	1.47E+00	0.55	1.47	2.22E+00	1.51E+00

Rpl23	11	8.16E+01	1.56E+01	7.21E-03	3.33E-01	1.47E+00	0.55	1.47	1.43E+01	9.72E+00
Gramd1b	9	1.17E+02	2.13E+01	3.08E-02	3.62E-01	1.47E+00	0.55	1.47	2.04E+01	1.39E+01
Tbx3	5	1.02E+02	1.89E+01	2.57E-02	3.52E-01	1.47E+00	0.55	1.47	1.78E+01	1.22E+01
Snrpg	6	1.06E+01	2.17E+00	4.48E-02	3.95E-01	1.46E+00	0.55	1.46	1.85E+00	1.27E+00
Klhl11	11	2.17E+01	4.39E+00	2.10E-02	3.52E-01	1.46E+00	0.55	1.46	3.79E+00	2.59E+00
Ripk1	13	1.19E+02	2.24E+01	2.41E-02	3.52E-01	1.46E+00	0.55	1.46	2.07E+01	1.41E+01
Zscan29	2	1.57E+02	3.31E+01	2.44E-02	3.52E-01	1.46E+00	0.54	1.46	2.73E+01	1.88E+01
Zbtb10	3	8.76E+01	1.69E+01	3.15E-02	3.66E-01	1.45E+00	0.54	1.45	1.52E+01	1.05E+01
Tm2d3	7	6.70E+01	1.35E+01	1.80E-02	3.49E-01	1.45E+00	0.54	1.45	1.16E+01	8.02E+00
Plekha8	6	1.05E+02	2.21E+01	2.16E-02	3.52E-01	1.45E+00	0.53	1.45	1.82E+01	1.26E+01
Homer1	13	1.23E+02	2.38E+01	3.76E-02	3.83E-01	1.45E+00	0.53	1.45	2.13E+01	1.47E+01
Gm43808	5	7.56E+00	1.44E+00	2.23E-02	3.52E-01	1.45E+00	0.53	1.45	1.31E+00	9.07E-01
Taf1d	9	1.94E+02	3.47E+01	1.50E-02	3.40E-01	1.45E+00	0.53	1.45	3.36E+01	2.32E+01
Cnm2	19	2.98E+02	5.71E+01	2.45E-02	3.52E-01	1.45E+00	0.53	1.45	5.17E+01	3.58E+01
Pard6g	18	2.87E+01	5.49E+00	1.92E-02	3.49E-01	1.45E+00	0.53	1.45	4.97E+00	3.44E+00
Smco4	9	3.61E+01	6.49E+00	1.99E-02	3.49E-01	1.44E+00	0.53	1.44	6.26E+00	4.33E+00
Gm10243	6	2.46E+01	5.30E+00	3.00E-02	3.59E-01	1.44E+00	0.53	1.44	4.26E+00	2.95E+00
Map11	5	5.28E+01	9.81E+00	4.65E-02	3.98E-01	1.44E+00	0.53	1.44	9.15E+00	6.34E+00
Alg11	8	7.85E+01	1.54E+01	4.88E-02	4.02E-01	1.44E+00	0.53	1.44	1.36E+01	9.43E+00
Elf2	13	3.45E+02	6.67E+01	4.20E-02	3.90E-01	1.44E+00	0.53	1.44	5.98E+01	4.15E+01
Rplp2	7	4.51E+02	8.37E+01	6.96E-03	3.33E-01	1.44E+00	0.53	1.44	7.81E+01	5.42E+01
Helz2	2	5.26E+02	1.01E+02	2.85E-02	3.55E-01	1.44E+00	0.53	1.44	9.10E+01	6.31E+01
Tmem33	5	3.65E+02	6.80E+01	1.29E-02	3.33E-01	1.44E+00	0.53	1.44	6.32E+01	4.39E+01
Sephs2	7	1.08E+03	2.00E+02	2.05E-02	3.52E-01	1.44E+00	0.52	1.44	1.87E+02	1.30E+02
Zbtb11	16	1.50E+02	2.86E+01	2.83E-03	3.13E-01	1.44E+00	0.52	1.44	2.59E+01	1.80E+01
Hnrnpu	1	1.59E+03	2.86E+02	9.57E-04	3.13E-01	1.44E+00	0.52	1.44	2.76E+02	1.92E+02
Zfc3h1	10	1.91E+02	3.45E+01	3.93E-03	3.13E-01	1.44E+00	0.52	1.44	3.31E+01	2.30E+01
Ret	6	1.11E+01	2.21E+00	3.17E-02	3.66E-01	1.44E+00	0.52	1.44	1.91E+00	1.33E+00
Scarb1	5	2.92E+02	5.46E+01	2.60E-02	3.52E-01	1.44E+00	0.52	1.44	5.05E+01	3.52E+01
Chchd10	10	2.27E+03	4.84E+02	2.95E-02	3.58E-01	1.44E+00	0.52	1.44	3.93E+02	2.74E+02
Zfp142	1	1.43E+02	2.81E+01	2.09E-02	3.52E-01	1.43E+00	0.52	1.43	2.48E+01	1.73E+01

Ube2j2	4	9.06E+01	1.65E+01	2.42E-03	3.13E-01	1.43E+00	0.52	1.43	1.56E+01	1.09E+01
Nob1	8	5.85E+01	1.22E+01	1.02E-02	3.33E-01	1.43E+00	0.52	1.43	1.01E+01	7.05E+00
Psmg4	13	1.91E+01	3.50E+00	5.04E-03	3.27E-01	1.43E+00	0.52	1.43	3.31E+00	2.31E+00
Slc25a38	9	7.79E+01	1.37E+01	6.94E-03	3.33E-01	1.43E+00	0.52	1.43	1.34E+01	9.38E+00
Mrps24	11	1.82E+02	4.13E+01	4.62E-02	3.97E-01	1.43E+00	0.52	1.43	3.14E+01	2.20E+01
Tsc22d2	3	1.65E+02	3.21E+01	5.37E-03	3.33E-01	1.43E+00	0.52	1.43	2.85E+01	1.99E+01
A630072M18Rik	5	2.49E+01	4.82E+00	1.56E-02	3.41E-01	1.43E+00	0.52	1.43	4.30E+00	3.01E+00
Gm12918	4	4.61E+02	8.53E+01	1.31E-03	3.13E-01	1.43E+00	0.52	1.43	7.96E+01	5.56E+01
Pthr1	2	8.31E+00	1.64E+00	1.34E-02	3.36E-01	1.43E+00	0.52	1.43	1.43E+00	1.00E+00
Tut1	19	8.51E+01	1.55E+01	4.61E-03	3.17E-01	1.43E+00	0.52	1.43	1.47E+01	1.03E+01
Tatdn2	6	2.19E+02	4.30E+01	4.44E-02	3.95E-01	1.43E+00	0.52	1.43	3.79E+01	2.65E+01
Gm10762	2	5.40E+01	9.73E+00	8.97E-03	3.33E-01	1.43E+00	0.51	1.43	9.31E+00	6.52E+00
Med21	6	8.31E+01	1.72E+01	3.47E-02	3.77E-01	1.43E+00	0.51	1.43	1.43E+01	1.00E+01
Rnmt	18	1.54E+02	3.09E+01	2.67E-02	3.52E-01	1.43E+00	0.51	1.43	2.65E+01	1.86E+01
Mier3	13	1.35E+02	2.43E+01	2.55E-02	3.52E-01	1.43E+00	0.51	1.43	2.32E+01	1.63E+01
Ssr2	3	2.84E+02	5.74E+01	2.18E-02	3.52E-01	1.43E+00	0.51	1.43	4.90E+01	3.44E+01
Ints8	4	8.13E+01	1.62E+01	2.70E-02	3.52E-01	1.42E+00	0.51	1.42	1.40E+01	9.83E+00
Gm8741	17	8.70E+00	1.67E+00	2.67E-03	3.13E-01	1.42E+00	0.51	1.42	1.50E+00	1.05E+00
Cenpv	11	7.19E+01	1.34E+01	5.10E-03	3.27E-01	1.42E+00	0.51	1.42	1.24E+01	8.69E+00
Gm13136	4	2.71E+01	4.81E+00	6.75E-03	3.33E-01	1.42E+00	0.51	1.42	4.67E+00	3.28E+00
Ppan	9	5.40E+01	1.03E+01	1.94E-02	3.49E-01	1.42E+00	0.51	1.42	9.30E+00	6.53E+00
Rbm14	19	1.29E+02	2.50E+01	2.10E-02	3.52E-01	1.42E+00	0.51	1.42	2.23E+01	1.56E+01
Qtrt2	16	9.78E+01	1.77E+01	2.93E-03	3.13E-01	1.42E+00	0.51	1.42	1.68E+01	1.18E+01
1110065P20Rik	4	7.97E+01	1.57E+01	1.95E-02	3.49E-01	1.42E+00	0.51	1.42	1.37E+01	9.64E+00
Gm34220	12	8.94E+00	1.76E+00	3.59E-02	3.80E-01	1.42E+00	0.51	1.42	1.54E+00	1.08E+00
Gm9899	5	4.57E+02	8.36E+01	7.07E-03	3.33E-01	1.42E+00	0.51	1.42	7.87E+01	5.54E+01
Taf7	18	4.07E+01	8.42E+00	4.83E-02	4.02E-01	1.42E+00	0.50	1.42	6.99E+00	4.93E+00
Gon7	12	2.41E+01	4.80E+00	3.41E-02	3.76E-01	1.42E+00	0.50	1.42	4.14E+00	2.92E+00
2300009A05Rik	9	7.07E+01	1.51E+01	2.55E-02	3.52E-01	1.42E+00	0.50	1.42	1.21E+01	8.58E+00
Traf4	11	4.31E+02	8.62E+01	3.60E-02	3.80E-01	1.41E+00	0.50	1.41	7.39E+01	5.23E+01
Chchd2	5	2.21E+03	3.92E+02	5.44E-03	3.33E-01	1.41E+00	0.50	1.41	3.79E+02	2.68E+02

Ppid	3	1.45E+02	2.69E+01	2.64E-02	3.52E-01	1.41E+00	0.50	1.41	2.49E+01	1.76E+01
Dcun1d5	9	1.45E+02	2.72E+01	1.39E-02	3.36E-01	1.41E+00	0.50	1.41	2.49E+01	1.76E+01
Uap1l1	2	1.45E+01	2.88E+00	2.16E-02	3.52E-01	1.41E+00	0.50	1.41	2.48E+00	1.76E+00
Rps26	10	1.33E+02	2.31E+01	4.32E-04	3.13E-01	1.41E+00	0.50	1.41	2.28E+01	1.62E+01
Pcf11	7	2.69E+02	5.04E+01	1.27E-02	3.33E-01	1.41E+00	0.50	1.41	4.61E+01	3.27E+01
Dhrs13	11	1.73E+01	3.31E+00	4.76E-03	3.17E-01	1.41E+00	0.49	1.41	2.96E+00	2.10E+00
H13	2	3.06E+02	6.07E+01	3.78E-02	3.83E-01	1.41E+00	0.49	1.41	5.23E+01	3.72E+01
Fxn	19	5.18E+01	1.03E+01	1.50E-02	3.40E-01	1.41E+00	0.49	1.41	8.87E+00	6.30E+00
Eif1-ps2	13	2.92E+01	5.47E+00	1.92E-02	3.49E-01	1.41E+00	0.49	1.41	4.99E+00	3.55E+00
Gm17029	4	1.48E+01	2.92E+00	1.55E-02	3.40E-01	1.41E+00	0.49	1.41	2.53E+00	1.80E+00
Rps17	7	7.83E+01	1.64E+01	1.84E-02	3.49E-01	1.40E+00	0.49	1.40	1.34E+01	9.54E+00
Ephb2	4	2.58E+01	5.06E+00	4.75E-02	4.02E-01	1.40E+00	0.49	1.40	4.42E+00	3.15E+00
Leng9	7	3.28E+01	6.44E+00	4.48E-02	3.95E-01	1.40E+00	0.49	1.40	5.60E+00	3.99E+00
Pdik1l	4	6.92E+01	1.22E+01	3.59E-03	3.13E-01	1.40E+00	0.49	1.40	1.18E+01	8.43E+00
Snx16	3	2.70E+01	5.20E+00	1.15E-02	3.33E-01	1.40E+00	0.49	1.40	4.61E+00	3.29E+00
Gm43737	3	2.46E+01	4.38E+00	1.84E-02	3.49E-01	1.40E+00	0.49	1.40	4.20E+00	2.99E+00
Ccnt1	15	2.71E+02	5.19E+01	8.19E-03	3.33E-01	1.40E+00	0.49	1.40	4.63E+01	3.30E+01
Zfp954	7	3.17E+01	6.48E+00	4.15E-02	3.90E-01	1.40E+00	0.49	1.40	5.42E+00	3.87E+00
Igf2	7	8.12E+01	1.55E+01	1.63E-02	3.45E-01	1.40E+00	0.49	1.40	1.39E+01	9.91E+00
Mir17hg	14	1.75E+01	3.58E+00	1.89E-02	3.49E-01	1.40E+00	0.48	1.40	3.00E+00	2.14E+00
Tysnd1	10	4.12E+02	8.01E+01	1.06E-02	3.33E-01	1.40E+00	0.48	1.40	7.03E+01	5.03E+01
Actr5	2	2.62E+01	5.30E+00	2.52E-02	3.52E-01	1.40E+00	0.48	1.40	4.47E+00	3.20E+00
Rbm4	19	6.14E+01	1.22E+01	2.17E-02	3.52E-01	1.40E+00	0.48	1.40	1.05E+01	7.49E+00
Rps15a-ps4	4	2.89E+01	5.24E+00	2.72E-02	3.52E-01	1.39E+00	0.48	1.39	4.93E+00	3.53E+00
Polr2k	15	2.07E+01	4.01E+00	2.49E-02	3.52E-01	1.39E+00	0.48	1.39	3.53E+00	2.53E+00
Mtcp1	X	2.32E+01	4.52E+00	4.79E-02	4.02E-01	1.39E+00	0.48	1.39	3.96E+00	2.84E+00
Rpl35	2	7.26E+01	1.52E+01	1.97E-02	3.49E-01	1.39E+00	0.48	1.39	1.24E+01	8.87E+00
Chpf	1	5.91E+01	1.12E+01	8.99E-03	3.33E-01	1.39E+00	0.48	1.39	1.01E+01	7.22E+00
Mak16	8	7.07E+01	1.25E+01	1.23E-02	3.33E-01	1.39E+00	0.48	1.39	1.20E+01	8.64E+00
Tmem251	12	5.18E+01	1.03E+01	3.15E-02	3.66E-01	1.39E+00	0.48	1.39	8.83E+00	6.34E+00
Rpl9-ps7	2	5.98E+01	1.23E+01	3.95E-02	3.86E-01	1.39E+00	0.48	1.39	1.02E+01	7.31E+00

Gm7536	3	5.12E+02	9.83E+01	2.85E-02	3.55E-01	1.39E+00	0.48	1.39	8.73E+01	6.27E+01
Wdr82	9	2.23E+02	3.99E+01	2.23E-03	3.13E-01	1.39E+00	0.48	1.39	3.80E+01	2.73E+01
Gm12940	4	5.43E+01	1.12E+01	4.54E-02	3.95E-01	1.39E+00	0.48	1.39	9.24E+00	6.64E+00
Atp5d	10	1.98E+03	4.10E+02	2.26E-02	3.52E-01	1.39E+00	0.48	1.39	3.37E+02	2.43E+02
Gm50431	19	6.38E+01	1.25E+01	3.60E-02	3.80E-01	1.39E+00	0.48	1.39	1.09E+01	7.81E+00
Ninj1	13	2.13E+02	3.95E+01	1.35E-02	3.36E-01	1.39E+00	0.47	1.39	3.63E+01	2.61E+01
Ccnl1	3	4.67E+02	9.18E+01	2.46E-02	3.52E-01	1.39E+00	0.47	1.39	7.95E+01	5.72E+01
Rpl13	8	6.03E+01	1.17E+01	3.29E-03	3.13E-01	1.39E+00	0.47	1.39	1.02E+01	7.38E+00
Mapk1ip1l	14	2.57E+02	4.54E+01	1.08E-02	3.33E-01	1.39E+00	0.47	1.39	4.36E+01	3.15E+01
2310057M21Rik	7	4.89E+01	1.01E+01	3.80E-02	3.83E-01	1.39E+00	0.47	1.39	8.31E+00	5.99E+00
Zbed4	15	7.13E+01	1.39E+01	4.56E-02	3.96E-01	1.39E+00	0.47	1.39	1.21E+01	8.74E+00
Rcor1	12	1.86E+02	3.67E+01	2.41E-02	3.52E-01	1.38E+00	0.47	1.38	3.16E+01	2.28E+01
Pcbd2	13	4.83E+01	9.09E+00	3.31E-03	3.13E-01	1.38E+00	0.47	1.38	8.20E+00	5.92E+00
Zfp619	7	1.30E+01	2.33E+00	3.74E-02	3.83E-01	1.38E+00	0.47	1.38	2.20E+00	1.60E+00
Gm14399	2	2.27E+01	4.00E+00	3.82E-02	3.83E-01	1.38E+00	0.47	1.38	3.86E+00	2.79E+00
Cacybp	1	2.89E+02	5.39E+01	2.71E-02	3.52E-01	1.38E+00	0.46	1.38	4.89E+01	3.55E+01
Gm6472	X	4.27E+02	8.30E+01	8.20E-03	3.33E-01	1.38E+00	0.46	1.38	7.24E+01	5.25E+01
Cacnb3	15	8.17E+00	1.57E+00	4.90E-02	4.02E-01	1.38E+00	0.46	1.38	1.38E+00	1.00E+00
Yeats4	10	6.50E+01	1.20E+01	4.00E-03	3.13E-01	1.38E+00	0.46	1.38	1.10E+01	7.99E+00
Mtf1	4	1.41E+02	2.82E+01	2.61E-02	3.52E-01	1.38E+00	0.46	1.38	2.39E+01	1.74E+01
Ndufb2	6	4.35E+02	7.57E+01	1.05E-03	3.13E-01	1.38E+00	0.46	1.38	7.36E+01	5.35E+01
Rps26-ps1	8	1.77E+02	3.45E+01	1.25E-02	3.33E-01	1.38E+00	0.46	1.38	3.00E+01	2.18E+01
Lsm1	8	7.92E+01	1.35E+01	2.32E-03	3.13E-01	1.38E+00	0.46	1.38	1.34E+01	9.74E+00
Uba5	9	1.77E+02	3.30E+01	2.29E-02	3.52E-01	1.37E+00	0.46	1.37	2.99E+01	2.18E+01
Peli1	11	8.84E+01	1.60E+01	1.10E-02	3.33E-01	1.37E+00	0.46	1.37	1.49E+01	1.09E+01
Lrp3	7	1.58E+02	2.69E+01	1.78E-02	3.49E-01	1.37E+00	0.46	1.37	2.67E+01	1.94E+01
Rbm8a	3	1.25E+02	2.38E+01	1.51E-02	3.40E-01	1.37E+00	0.46	1.37	2.12E+01	1.54E+01
Med20	17	2.44E+02	4.23E+01	4.35E-03	3.17E-01	1.37E+00	0.46	1.37	4.13E+01	3.01E+01
Rps6	4	9.50E+01	1.76E+01	3.36E-03	3.13E-01	1.37E+00	0.46	1.37	1.61E+01	1.17E+01
Ogfr	2	1.54E+02	2.87E+01	3.62E-03	3.13E-01	1.37E+00	0.46	1.37	2.60E+01	1.90E+01
Card19	13	1.03E+02	1.98E+01	4.13E-02	3.90E-01	1.37E+00	0.45	1.37	1.74E+01	1.27E+01

Wdr89	12	3.31E+02	6.15E+01	9.84E-03	3.33E-01	1.37E+00	0.45	1.37	5.59E+01	4.08E+01
Mars2	1	8.64E+01	1.66E+01	1.72E-02	3.49E-01	1.37E+00	0.45	1.37	1.46E+01	1.07E+01
Rps8	4	1.92E+02	3.57E+01	7.90E-03	3.33E-01	1.37E+00	0.45	1.37	3.24E+01	2.37E+01
Gm4895	10	1.14E+02	2.13E+01	3.77E-02	3.83E-01	1.37E+00	0.45	1.37	1.92E+01	1.41E+01
Clk1	1	5.74E+02	1.08E+02	1.39E-02	3.36E-01	1.37E+00	0.45	1.37	9.68E+01	7.08E+01
Zbtb6	2	1.13E+02	1.98E+01	6.99E-04	3.13E-01	1.37E+00	0.45	1.37	1.90E+01	1.39E+01
Snhg6	1	2.41E+01	4.17E+00	1.38E-02	3.36E-01	1.37E+00	0.45	1.37	4.07E+00	2.98E+00
Mrpl34	8	3.75E+02	7.05E+01	2.88E-02	3.56E-01	1.37E+00	0.45	1.37	6.32E+01	4.63E+01
Tpt1	14	8.72E+02	1.67E+02	2.60E-02	3.52E-01	1.36E+00	0.45	1.36	1.47E+02	1.08E+02
Fbxo30	10	1.45E+02	2.58E+01	1.22E-02	3.33E-01	1.36E+00	0.45	1.36	2.44E+01	1.79E+01
Trim65	11	7.98E+01	1.45E+01	3.15E-02	3.66E-01	1.36E+00	0.45	1.36	1.34E+01	9.86E+00
Sprtn	8	2.87E+02	4.97E+01	1.27E-03	3.13E-01	1.36E+00	0.45	1.36	4.83E+01	3.55E+01
Nkrf	X	1.92E+01	3.62E+00	2.18E-02	3.52E-01	1.36E+00	0.44	1.36	3.24E+00	2.38E+00
Slc19a2	1	5.53E+01	9.73E+00	4.53E-02	3.95E-01	1.36E+00	0.44	1.36	9.31E+00	6.85E+00
Syvn1	19	2.33E+02	4.15E+01	1.67E-02	3.46E-01	1.36E+00	0.44	1.36	3.91E+01	2.88E+01
Ikzf2	1	7.32E+01	1.36E+01	1.50E-02	3.40E-01	1.36E+00	0.44	1.36	1.23E+01	9.06E+00
Csrp2	10	1.43E+02	2.63E+01	1.98E-02	3.49E-01	1.36E+00	0.44	1.36	2.40E+01	1.77E+01
Mydgf	17	1.15E+02	2.09E+01	1.57E-02	3.41E-01	1.36E+00	0.44	1.36	1.93E+01	1.42E+01
Ahctf1	1	2.65E+02	4.92E+01	2.79E-02	3.53E-01	1.36E+00	0.44	1.36	4.45E+01	3.28E+01
Rps5	7	5.29E+02	1.05E+02	3.33E-02	3.72E-01	1.36E+00	0.44	1.36	8.89E+01	6.56E+01
Sema4b	7	2.69E+02	4.94E+01	4.86E-02	4.02E-01	1.35E+00	0.44	1.35	4.51E+01	3.33E+01
Ptpn18	1	1.97E+01	3.49E+00	2.80E-02	3.53E-01	1.35E+00	0.44	1.35	3.31E+00	2.45E+00
Sf3b6	12	1.15E+02	2.22E+01	3.30E-02	3.71E-01	1.35E+00	0.44	1.35	1.93E+01	1.43E+01
Brms1	19	5.15E+01	9.05E+00	6.01E-03	3.33E-01	1.35E+00	0.44	1.35	8.64E+00	6.39E+00
Tmem185b	1	6.07E+01	1.09E+01	8.61E-04	3.13E-01	1.35E+00	0.43	1.35	1.02E+01	7.53E+00
Pdia5	16	3.27E+01	5.73E+00	7.78E-03	3.33E-01	1.35E+00	0.43	1.35	5.48E+00	4.05E+00
Gm11837	4	2.24E+01	4.15E+00	2.43E-02	3.52E-01	1.35E+00	0.43	1.35	3.75E+00	2.78E+00
Zfp948	17	4.73E+01	8.12E+00	4.82E-03	3.19E-01	1.35E+00	0.43	1.35	7.93E+00	5.87E+00
Rpl34-ps1	6	7.38E+01	1.43E+01	2.53E-02	3.52E-01	1.35E+00	0.43	1.35	1.24E+01	9.17E+00
Gm5805	15	3.20E+01	6.18E+00	9.91E-03	3.33E-01	1.35E+00	0.43	1.35	5.37E+00	3.98E+00
Serpinh1	7	1.26E+03	2.19E+02	5.77E-03	3.33E-01	1.35E+00	0.43	1.35	2.11E+02	1.56E+02

Rps10-ps2	16	1.91E+02	3.65E+01	2.13E-02	3.52E-01	1.35E+00	0.43	1.35	3.20E+01	2.37E+01
Hsp90ab1	17	5.43E+03	1.07E+03	3.90E-02	3.86E-01	1.35E+00	0.43	1.35	9.09E+02	6.75E+02
Gm7859	15	1.02E+01	1.78E+00	2.67E-02	3.52E-01	1.35E+00	0.43	1.35	1.70E+00	1.26E+00
Fam13b	18	6.00E+01	1.12E+01	1.72E-02	3.49E-01	1.35E+00	0.43	1.35	1.00E+01	7.46E+00
Ctdp1	18	5.92E+01	1.07E+01	6.14E-04	3.13E-01	1.34E+00	0.43	1.34	9.91E+00	7.37E+00
Morf4l2	X	3.73E+02	6.41E+01	2.65E-02	3.52E-01	1.34E+00	0.43	1.34	6.23E+01	4.64E+01
Apba3	10	2.94E+02	5.37E+01	2.97E-02	3.58E-01	1.34E+00	0.43	1.34	4.91E+01	3.66E+01
Cox14	15	3.08E+02	5.88E+01	1.17E-02	3.33E-01	1.34E+00	0.43	1.34	5.15E+01	3.83E+01
Nt5dc3	10	7.45E+01	1.41E+01	2.39E-02	3.52E-01	1.34E+00	0.43	1.34	1.25E+01	9.28E+00
Chchd7	4	1.11E+02	1.92E+01	8.28E-03	3.33E-01	1.34E+00	0.43	1.34	1.86E+01	1.38E+01
Srsf7	17	1.94E+02	3.32E+01	1.08E-02	3.33E-01	1.34E+00	0.42	1.34	3.25E+01	2.42E+01
Ciao2b	8	5.84E+01	1.00E+01	2.88E-03	3.13E-01	1.34E+00	0.42	1.34	9.77E+00	7.28E+00
Ppp4r3a	12	2.84E+02	5.07E+01	2.18E-02	3.52E-01	1.34E+00	0.42	1.34	4.75E+01	3.54E+01
Rybp	6	8.26E+01	1.53E+01	3.98E-02	3.86E-01	1.34E+00	0.42	1.34	1.38E+01	1.03E+01
6720427107Rik	13	2.56E+01	4.75E+00	4.52E-02	3.95E-01	1.34E+00	0.42	1.34	4.28E+00	3.19E+00
Rps7	12	9.61E+01	1.74E+01	8.63E-03	3.33E-01	1.34E+00	0.42	1.34	1.61E+01	1.20E+01
Dohh	10	1.43E+02	2.63E+01	1.05E-02	3.33E-01	1.34E+00	0.42	1.34	2.38E+01	1.78E+01
Gm45902	2	1.62E+01	2.99E+00	4.38E-02	3.93E-01	1.34E+00	0.42	1.34	2.71E+00	2.03E+00
Gm50107	17	1.43E+01	2.74E+00	9.13E-03	3.33E-01	1.34E+00	0.42	1.34	2.39E+00	1.78E+00
Zfp704	3	1.24E+02	2.33E+01	9.64E-03	3.33E-01	1.34E+00	0.42	1.34	2.08E+01	1.55E+01
Srf	17	9.10E+01	1.73E+01	1.43E-02	3.38E-01	1.34E+00	0.42	1.34	1.52E+01	1.14E+01
Rbm7	9	3.20E+02	5.96E+01	2.03E-02	3.51E-01	1.34E+00	0.42	1.34	5.34E+01	4.00E+01
Nolc1	19	2.09E+02	3.64E+01	4.41E-02	3.94E-01	1.34E+00	0.42	1.34	3.48E+01	2.61E+01
Gm15501	7	5.21E+02	9.48E+01	2.46E-03	3.13E-01	1.34E+00	0.42	1.34	8.68E+01	6.50E+01
Tmem170b	13	1.59E+02	2.96E+01	3.20E-02	3.66E-01	1.34E+00	0.42	1.34	2.65E+01	1.98E+01
Rpl36-ps12	6	1.28E+02	2.34E+01	1.75E-02	3.49E-01	1.33E+00	0.42	1.33	2.13E+01	1.60E+01
Pias4	10	8.03E+01	1.58E+01	3.62E-02	3.80E-01	1.33E+00	0.42	1.33	1.34E+01	1.00E+01
Btg3	16	5.42E+01	1.04E+01	8.24E-03	3.33E-01	1.33E+00	0.42	1.33	9.03E+00	6.77E+00
Wipi2	5	9.96E+02	1.84E+02	2.76E-02	3.53E-01	1.33E+00	0.41	1.33	1.66E+02	1.25E+02
Lypla2	4	1.97E+02	3.48E+01	3.83E-03	3.13E-01	1.33E+00	0.41	1.33	3.28E+01	2.46E+01
Josd2	7	8.07E+01	1.51E+01	2.49E-02	3.52E-01	1.33E+00	0.41	1.33	1.34E+01	1.01E+01

Arl5b	2	1.42E+02	2.49E+01	7.19E-03	3.33E-01	1.33E+00	0.41	1.33	2.36E+01	1.78E+01
Gm2991	15	1.09E+01	2.08E+00	4.46E-02	3.95E-01	1.33E+00	0.41	1.33	1.81E+00	1.36E+00
Rpl37	15	2.33E+01	4.30E+00	3.39E-02	3.75E-01	1.33E+00	0.41	1.33	3.88E+00	2.92E+00
Lzic	4	1.85E+02	3.27E+01	4.39E-03	3.17E-01	1.33E+00	0.41	1.33	3.08E+01	2.31E+01
Arl6ip6	2	9.75E+01	1.66E+01	4.33E-02	3.92E-01	1.33E+00	0.41	1.33	1.62E+01	1.22E+01
Akt1s1	7	2.30E+02	4.29E+01	1.72E-02	3.49E-01	1.33E+00	0.41	1.33	3.82E+01	2.87E+01
Rbm5	9	5.07E+02	9.33E+01	4.25E-02	3.91E-01	1.33E+00	0.41	1.33	8.44E+01	6.34E+01
Safb2	17	3.52E+02	6.22E+01	8.27E-03	3.33E-01	1.33E+00	0.41	1.33	5.85E+01	4.40E+01
Luc7l3	11	3.30E+02	5.98E+01	9.00E-03	3.33E-01	1.33E+00	0.41	1.33	5.50E+01	4.14E+01
Slc22a23	13	3.03E+02	5.83E+01	1.44E-02	3.38E-01	1.33E+00	0.41	1.33	5.04E+01	3.80E+01
Hnrnpab	11	5.56E+02	9.96E+01	4.42E-03	3.17E-01	1.33E+00	0.41	1.33	9.24E+01	6.96E+01
Dgat1	15	1.14E+03	2.11E+02	2.54E-02	3.52E-01	1.33E+00	0.41	1.33	1.89E+02	1.43E+02
2310009B15Rik	1	2.45E+01	4.73E+00	3.17E-02	3.66E-01	1.33E+00	0.41	1.33	4.07E+00	3.07E+00
Rbm15b	9	1.34E+02	2.43E+01	9.36E-03	3.33E-01	1.33E+00	0.41	1.33	2.23E+01	1.68E+01
Tdg	10	1.01E+02	1.82E+01	3.16E-02	3.66E-01	1.33E+00	0.41	1.33	1.68E+01	1.26E+01
Zfp35	18	1.01E+02	1.88E+01	2.43E-02	3.52E-01	1.33E+00	0.41	1.33	1.68E+01	1.27E+01
Lonrf1	8	5.41E+01	1.07E+01	3.78E-02	3.83E-01	1.33E+00	0.41	1.33	9.00E+00	6.78E+00
Mogs	6	8.37E+01	1.48E+01	2.94E-02	3.58E-01	1.33E+00	0.41	1.33	1.39E+01	1.05E+01
Setd1b	5	1.92E+02	3.47E+01	3.37E-03	3.13E-01	1.33E+00	0.41	1.33	3.19E+01	2.41E+01
2700097O09Rik	12	9.19E+01	1.62E+01	1.34E-02	3.36E-01	1.33E+00	0.41	1.33	1.53E+01	1.15E+01
Ago3	4	1.87E+02	3.37E+01	3.24E-02	3.69E-01	1.33E+00	0.41	1.33	3.10E+01	2.34E+01
Rps2	17	1.06E+03	1.94E+02	1.62E-02	3.44E-01	1.32E+00	0.41	1.32	1.76E+02	1.33E+02
Capn15	17	1.29E+02	2.42E+01	3.87E-02	3.86E-01	1.32E+00	0.41	1.32	2.13E+01	1.61E+01
Jade1	3	3.46E+02	6.31E+01	2.35E-02	3.52E-01	1.32E+00	0.40	1.32	5.75E+01	4.34E+01
Fgd6	10	4.10E+01	7.36E+00	1.91E-02	3.49E-01	1.32E+00	0.40	1.32	6.81E+00	5.15E+00
Sub1	15	2.30E+02	4.28E+01	1.34E-02	3.36E-01	1.32E+00	0.40	1.32	3.82E+01	2.89E+01
Cbll1	12	5.87E+01	1.03E+01	8.91E-03	3.33E-01	1.32E+00	0.40	1.32	9.74E+00	7.37E+00
Fkrp	7	8.39E+01	1.50E+01	7.97E-03	3.33E-01	1.32E+00	0.40	1.32	1.39E+01	1.05E+01
Atf2	2	6.17E+02	1.10E+02	2.48E-02	3.52E-01	1.32E+00	0.40	1.32	1.02E+02	7.75E+01
Gm2000	1	2.92E+02	5.19E+01	1.47E-03	3.13E-01	1.32E+00	0.40	1.32	4.84E+01	3.67E+01
1700123O20Rik	14	1.39E+02	2.52E+01	1.01E-02	3.33E-01	1.32E+00	0.40	1.32	2.30E+01	1.74E+01

Elovl5	9	9.23E+02	1.69E+02	1.18E-02	3.33E-01	1.32E+00	0.40	1.32	1.53E+02	1.16E+02
Rlim	X	2.80E+02	4.90E+01	1.61E-03	3.13E-01	1.32E+00	0.40	1.32	4.65E+01	3.52E+01
Tpst2	5	1.22E+02	2.16E+01	1.14E-02	3.33E-01	1.32E+00	0.40	1.32	2.02E+01	1.53E+01
Ubald1	16	1.00E+02	1.91E+01	1.95E-02	3.49E-01	1.32E+00	0.40	1.32	1.66E+01	1.26E+01
Gm9843	16	2.52E+02	4.67E+01	2.68E-02	3.52E-01	1.32E+00	0.40	1.32	4.18E+01	3.17E+01
Rps2-ps10	18	7.17E+02	1.29E+02	2.75E-02	3.52E-01	1.32E+00	0.40	1.32	1.19E+02	9.01E+01
Ccdc84	9	9.04E+01	1.59E+01	2.56E-02	3.52E-01	1.32E+00	0.40	1.32	1.50E+01	1.14E+01
Pura	18	1.51E+02	2.55E+01	5.52E-03	3.33E-01	1.32E+00	0.40	1.32	2.50E+01	1.90E+01
Rpl27-ps3	18	1.60E+02	3.14E+01	4.62E-02	3.97E-01	1.32E+00	0.40	1.32	2.64E+01	2.01E+01
Amd1	10	1.99E+02	3.53E+01	3.27E-03	3.13E-01	1.32E+00	0.40	1.32	3.29E+01	2.50E+01
Lclat1	17	2.43E+02	4.39E+01	4.87E-02	4.02E-01	1.32E+00	0.40	1.32	4.03E+01	3.06E+01
Eef1e1	13	5.06E+01	9.14E+00	3.47E-02	3.77E-01	1.32E+00	0.40	1.32	8.37E+00	6.36E+00
Rbm47	5	2.96E+02	5.53E+01	4.81E-02	4.02E-01	1.32E+00	0.40	1.32	4.90E+01	3.72E+01
Lysmd3	13	1.66E+02	3.02E+01	3.06E-03	3.13E-01	1.32E+00	0.40	1.32	2.75E+01	2.09E+01
Atg12	18	3.52E+02	6.55E+01	3.45E-02	3.77E-01	1.32E+00	0.40	1.32	5.82E+01	4.43E+01
Rpl36a	X	2.10E+01	3.81E+00	4.37E-02	3.93E-01	1.32E+00	0.40	1.32	3.48E+00	2.65E+00
Zfp592	7	2.80E+02	5.29E+01	1.27E-02	3.33E-01	1.31E+00	0.39	1.31	4.63E+01	3.52E+01
Ccdc107	4	5.28E+01	9.54E+00	1.10E-02	3.33E-01	1.31E+00	0.39	1.31	8.74E+00	6.65E+00
Ftsj3	11	1.56E+02	2.84E+01	2.70E-02	3.52E-01	1.31E+00	0.39	1.31	2.58E+01	1.96E+01
Med9	11	1.11E+02	2.03E+01	1.55E-02	3.40E-01	1.31E+00	0.39	1.31	1.83E+01	1.39E+01
Srsf9	5	1.30E+02	2.29E+01	3.85E-03	3.13E-01	1.31E+00	0.39	1.31	2.16E+01	1.64E+01
Zcchc9	13	7.24E+01	1.40E+01	3.78E-02	3.83E-01	1.31E+00	0.39	1.31	1.20E+01	9.12E+00
Snip1	4	6.10E+01	1.04E+01	1.13E-03	3.13E-01	1.31E+00	0.39	1.31	1.01E+01	7.68E+00
Mfsd14a	3	2.62E+02	4.66E+01	1.58E-02	3.41E-01	1.31E+00	0.39	1.31	4.34E+01	3.30E+01
Gm7334	17	5.79E+01	1.02E+01	1.42E-02	3.37E-01	1.31E+00	0.39	1.31	9.57E+00	7.29E+00
Rpl18	7	2.14E+02	4.07E+01	3.78E-02	3.83E-01	1.31E+00	0.39	1.31	3.54E+01	2.70E+01
Samd4b	7	2.79E+02	4.94E+01	4.93E-02	4.03E-01	1.31E+00	0.39	1.31	4.61E+01	3.51E+01
Mesd	7	2.25E+02	4.03E+01	4.05E-02	3.87E-01	1.31E+00	0.39	1.31	3.72E+01	2.84E+01
E2f5	3	4.80E+01	8.48E+00	1.94E-02	3.49E-01	1.31E+00	0.39	1.31	7.93E+00	6.05E+00
B4galt3	1	7.27E+01	1.27E+01	3.98E-02	3.86E-01	1.31E+00	0.39	1.31	1.20E+01	9.16E+00
Mboat7	7	2.45E+02	4.11E+01	8.34E-03	3.33E-01	1.31E+00	0.39	1.31	4.05E+01	3.09E+01

Nol8	13	1.06E+02	2.05E+01	1.63E-02	3.45E-01	1.31E+00	0.39	1.31	1.75E+01	1.34E+01
Smim11	16	9.26E+01	1.73E+01	2.74E-02	3.52E-01	1.31E+00	0.39	1.31	1.53E+01	1.17E+01
Fkbp4	6	4.96E+02	8.34E+01	3.40E-04	3.13E-01	1.31E+00	0.39	1.31	8.19E+01	6.25E+01
Lin7c	2	2.69E+02	4.86E+01	1.19E-02	3.33E-01	1.31E+00	0.39	1.31	4.44E+01	3.39E+01
Gm3362	15	4.86E+01	8.99E+00	4.83E-02	4.02E-01	1.31E+00	0.39	1.31	8.03E+00	6.14E+00
Slc30a5	13	2.13E+02	3.84E+01	1.76E-02	3.49E-01	1.31E+00	0.39	1.31	3.51E+01	2.68E+01
Rps19	7	3.32E+02	6.12E+01	1.02E-02	3.33E-01	1.31E+00	0.39	1.31	5.48E+01	4.19E+01
Hmgn1	16	2.60E+02	4.97E+01	2.10E-02	3.52E-01	1.31E+00	0.39	1.31	4.29E+01	3.28E+01
Rpl28-ps1	1	3.14E+02	5.98E+01	1.88E-02	3.49E-01	1.31E+00	0.39	1.31	5.19E+01	3.97E+01
Zbtb43	2	2.37E+02	4.49E+01	3.71E-02	3.82E-01	1.31E+00	0.39	1.31	3.91E+01	2.99E+01
E130309D02Rik	5	8.14E+01	1.41E+01	6.90E-03	3.33E-01	1.31E+00	0.39	1.31	1.34E+01	1.03E+01
Desi2	1	1.79E+02	3.10E+01	4.65E-03	3.17E-01	1.31E+00	0.39	1.31	2.95E+01	2.26E+01
Cdv3-ps	14	3.93E+01	7.03E+00	4.70E-03	3.17E-01	1.31E+00	0.39	1.31	6.48E+00	4.96E+00
Rce1	19	5.98E+01	1.07E+01	1.49E-02	3.40E-01	1.31E+00	0.39	1.31	9.87E+00	7.55E+00
Trabd	15	2.47E+02	4.19E+01	1.05E-02	3.33E-01	1.31E+00	0.39	1.31	4.08E+01	3.12E+01
Rpl17-ps8	X	1.42E+02	2.72E+01	1.39E-02	3.36E-01	1.31E+00	0.38	1.31	2.35E+01	1.80E+01
Top1	2	3.57E+02	6.09E+01	2.14E-02	3.52E-01	1.31E+00	0.38	1.31	5.88E+01	4.51E+01
Tle1	4	7.88E+01	1.34E+01	2.36E-04	3.13E-01	1.31E+00	0.38	1.31	1.30E+01	9.96E+00
Saraf	8	6.14E+02	1.11E+02	2.87E-02	3.56E-01	1.30E+00	0.38	1.30	1.01E+02	7.76E+01
Spen	4	3.96E+02	6.81E+01	1.11E-02	3.33E-01	1.30E+00	0.38	1.30	6.53E+01	5.01E+01
Met	6	3.08E+02	5.59E+01	5.43E-03	3.33E-01	1.30E+00	0.38	1.30	5.08E+01	3.90E+01
Sreb2	15	2.88E+02	5.21E+01	3.66E-02	3.82E-01	1.30E+00	0.38	1.30	4.74E+01	3.64E+01
Slc35d1	4	5.40E+01	9.34E+00	4.29E-03	3.17E-01	1.30E+00	0.38	1.30	8.90E+00	6.83E+00
Rps20	4	1.81E+02	3.24E+01	1.41E-02	3.37E-01	1.30E+00	0.38	1.30	2.99E+01	2.29E+01
Nrf1	6	5.38E+01	9.81E+00	3.49E-02	3.77E-01	1.30E+00	0.38	1.30	8.87E+00	6.80E+00
Tnfrsf1a	6	4.85E+02	8.74E+01	4.67E-02	3.98E-01	1.30E+00	0.38	1.30	7.98E+01	6.13E+01
Ccdc86	19	4.29E+01	7.93E+00	4.96E-02	4.03E-01	1.30E+00	0.38	1.30	7.07E+00	5.43E+00
Col13a1	10	1.07E+01	1.85E+00	3.32E-02	3.72E-01	1.30E+00	0.38	1.30	1.76E+00	1.35E+00
Mcf2	17	4.35E+02	7.82E+01	3.81E-02	3.83E-01	1.30E+00	0.38	1.30	7.17E+01	5.50E+01
Ubfd1	7	1.97E+02	3.39E+01	2.82E-02	3.54E-01	1.30E+00	0.38	1.30	3.24E+01	2.49E+01
Zfx	X	1.66E+02	3.03E+01	8.82E-03	3.33E-01	1.30E+00	0.38	1.30	2.73E+01	2.10E+01

Tmem68	4	6.74E+01	1.22E+01	3.05E-03	3.13E-01	1.30E+00	0.38	1.30	1.11E+01	8.53E+00
Cactin	10	8.65E+01	1.48E+01	2.80E-03	3.13E-01	1.30E+00	0.38	1.30	1.42E+01	1.09E+01
Tgfbr3	5	5.55E+02	9.69E+01	2.60E-02	3.52E-01	1.30E+00	0.38	1.30	9.14E+01	7.03E+01
Bmpr1a	14	3.09E+02	5.76E+01	2.98E-02	3.58E-01	1.30E+00	0.38	1.30	5.09E+01	3.91E+01
Heatr1	13	9.33E+01	1.70E+01	4.30E-02	3.92E-01	1.30E+00	0.38	1.30	1.54E+01	1.18E+01
Pop5	5	1.30E+02	2.35E+01	1.85E-02	3.49E-01	1.30E+00	0.38	1.30	2.13E+01	1.64E+01
Med13	11	4.15E+02	7.37E+01	4.42E-02	3.94E-01	1.30E+00	0.38	1.30	6.83E+01	5.25E+01
Golph3	15	6.27E+02	1.08E+02	3.75E-02	3.83E-01	1.30E+00	0.38	1.30	1.03E+02	7.94E+01
Rpl8	15	8.35E+02	1.49E+02	3.19E-03	3.13E-01	1.30E+00	0.38	1.30	1.37E+02	1.06E+02
Atp13a1	8	1.65E+02	2.94E+01	2.78E-02	3.53E-01	1.30E+00	0.38	1.30	2.71E+01	2.09E+01
Ranbp2	10	6.90E+02	1.19E+02	3.66E-03	3.13E-01	1.30E+00	0.38	1.30	1.13E+02	8.74E+01
Tmem128	5	1.49E+02	2.74E+01	2.33E-02	3.52E-01	1.30E+00	0.38	1.30	2.45E+01	1.89E+01
Cpsf6	10	2.70E+02	4.68E+01	2.99E-03	3.13E-01	1.30E+00	0.38	1.30	4.44E+01	3.42E+01
Atp7a	X	3.35E+01	6.14E+00	3.42E-02	3.77E-01	1.30E+00	0.38	1.30	5.51E+00	4.25E+00
Timm10b	7	1.55E+02	2.78E+01	9.63E-03	3.33E-01	1.30E+00	0.37	1.30	2.55E+01	1.96E+01
Rwdd4a	8	1.49E+02	2.50E+01	8.37E-03	3.33E-01	1.30E+00	0.37	1.30	2.44E+01	1.89E+01
Gng5	3	2.60E+02	4.81E+01	3.36E-02	3.74E-01	1.30E+00	0.37	1.30	4.27E+01	3.30E+01
Oaz2	9	4.18E+02	7.39E+01	1.66E-02	3.46E-01	1.30E+00	0.37	1.30	6.87E+01	5.30E+01
Ostc	3	4.27E+01	7.37E+00	7.04E-03	3.33E-01	1.30E+00	0.37	1.30	7.02E+00	5.42E+00
Pgm3	9	1.66E+01	2.79E+00	2.43E-04	3.13E-01	1.30E+00	0.37	1.30	2.73E+00	2.11E+00
Ube2v2	16	9.15E+01	1.63E+01	1.68E-02	3.47E-01	1.29E+00	0.37	1.29	1.50E+01	1.16E+01
Rpl18-ps2	6	1.14E+02	2.12E+01	1.18E-02	3.33E-01	1.29E+00	0.37	1.29	1.88E+01	1.45E+01
Ankrd54	15	5.17E+01	8.74E+00	3.41E-02	3.76E-01	1.29E+00	0.37	1.29	8.49E+00	6.56E+00
Crkl	16	2.60E+02	4.42E+01	3.48E-03	3.13E-01	1.29E+00	0.37	1.29	4.26E+01	3.30E+01
Cdc37l1	19	4.12E+02	7.13E+01	8.99E-03	3.33E-01	1.29E+00	0.37	1.29	6.76E+01	5.22E+01
Gm12696	4	5.24E+01	9.75E+00	4.76E-02	4.02E-01	1.29E+00	0.37	1.29	8.60E+00	6.65E+00
Gm10073	8	1.26E+02	2.28E+01	7.92E-03	3.33E-01	1.29E+00	0.37	1.29	2.07E+01	1.60E+01
Etv3	3	3.45E+02	6.27E+01	3.90E-02	3.86E-01	1.29E+00	0.37	1.29	5.66E+01	4.38E+01
Polr1c	17	8.44E+01	1.49E+01	4.91E-02	4.03E-01	1.29E+00	0.37	1.29	1.38E+01	1.07E+01
Rbm17	2	1.55E+02	2.63E+01	2.89E-02	3.57E-01	1.29E+00	0.37	1.29	2.54E+01	1.96E+01
Ccdc137	11	6.56E+01	1.19E+01	9.73E-03	3.33E-01	1.29E+00	0.37	1.29	1.08E+01	8.33E+00

Ticam1	17	1.13E+02	2.05E+01	3.68E-02	3.82E-01	1.29E+00	0.37	1.29	1.85E+01	1.43E+01
Snx3	10	4.92E+02	8.56E+01	8.87E-03	3.33E-01	1.29E+00	0.37	1.29	8.05E+01	6.25E+01
Rps12	10	4.07E+01	7.03E+00	1.06E-02	3.33E-01	1.29E+00	0.37	1.29	6.67E+00	5.18E+00
Rpl31	1	3.71E+01	6.78E+00	1.11E-02	3.33E-01	1.29E+00	0.37	1.29	6.08E+00	4.71E+00
Donson	16	2.18E+01	3.75E+00	4.77E-02	4.02E-01	1.29E+00	0.37	1.29	3.57E+00	2.77E+00
Fbxo34	14	8.33E+01	1.56E+01	1.31E-02	3.34E-01	1.29E+00	0.37	1.29	1.37E+01	1.06E+01
Klhl18	9	1.08E+02	1.82E+01	3.19E-03	3.13E-01	1.29E+00	0.37	1.29	1.77E+01	1.37E+01
Zfp397	18	2.25E+02	3.79E+01	1.39E-03	3.13E-01	1.29E+00	0.37	1.29	3.68E+01	2.86E+01
Safb	17	4.00E+02	6.64E+01	2.47E-03	3.13E-01	1.29E+00	0.36	1.29	6.55E+01	5.09E+01
Rpl21	5	1.75E+02	3.40E+01	4.64E-02	3.98E-01	1.29E+00	0.36	1.29	2.86E+01	2.23E+01
Atg9a	1	2.36E+02	3.95E+01	2.32E-02	3.52E-01	1.29E+00	0.36	1.29	3.86E+01	3.00E+01
Fau	19	6.51E+01	1.13E+01	8.38E-04	3.13E-01	1.28E+00	0.36	1.28	1.07E+01	8.29E+00
Maml1	11	1.07E+02	1.76E+01	2.53E-02	3.52E-01	1.28E+00	0.36	1.28	1.74E+01	1.36E+01
Rab11fip1	8	1.93E+01	3.28E+00	1.68E-03	3.13E-01	1.28E+00	0.36	1.28	3.15E+00	2.45E+00
Polr2d	18	4.70E+01	8.04E+00	1.46E-03	3.13E-01	1.28E+00	0.36	1.28	7.69E+00	5.99E+00
Thoc1	18	1.04E+02	1.86E+01	1.14E-02	3.33E-01	1.28E+00	0.36	1.28	1.70E+01	1.33E+01
Ppm1g	5	2.80E+02	4.78E+01	9.88E-03	3.33E-01	1.28E+00	0.36	1.28	4.57E+01	3.57E+01
Smg8	11	7.44E+01	1.33E+01	1.39E-02	3.36E-01	1.28E+00	0.36	1.28	1.22E+01	9.48E+00
Snrpd1	18	4.42E+01	8.20E+00	1.59E-02	3.42E-01	1.28E+00	0.36	1.28	7.23E+00	5.64E+00
Sft2d1	17	3.87E+01	7.24E+00	4.05E-02	3.87E-01	1.28E+00	0.36	1.28	6.33E+00	4.94E+00
Rpl6	5	2.62E+02	4.76E+01	1.30E-02	3.33E-01	1.28E+00	0.36	1.28	4.27E+01	3.34E+01
Zfand2b	1	6.88E+01	1.18E+01	1.96E-02	3.49E-01	1.28E+00	0.36	1.28	1.12E+01	8.78E+00
Ssh1	5	1.71E+02	3.06E+01	2.25E-02	3.52E-01	1.28E+00	0.36	1.28	2.80E+01	2.19E+01
Mrpl52	14	6.86E+01	1.17E+01	1.62E-02	3.44E-01	1.28E+00	0.35	1.28	1.12E+01	8.75E+00
Slc39a10	1	7.51E+01	1.26E+01	1.92E-02	3.49E-01	1.28E+00	0.35	1.28	1.22E+01	9.58E+00
Fbxo28	1	1.48E+02	2.69E+01	2.75E-02	3.52E-01	1.28E+00	0.35	1.28	2.41E+01	1.88E+01
Uqcrq	11	2.31E+03	3.91E+02	2.61E-02	3.52E-01	1.28E+00	0.35	1.28	3.77E+02	2.95E+02
Zfhx3	8	1.11E+02	1.90E+01	6.36E-03	3.33E-01	1.28E+00	0.35	1.28	1.81E+01	1.42E+01
Magoh	4	6.85E+01	1.18E+01	1.55E-02	3.40E-01	1.28E+00	0.35	1.28	1.12E+01	8.75E+00
Zmynd19	2	4.97E+01	8.58E+00	7.98E-03	3.33E-01	1.28E+00	0.35	1.28	8.11E+00	6.36E+00
Ilkap	1	1.61E+02	2.87E+01	3.89E-02	3.86E-01	1.28E+00	0.35	1.28	2.62E+01	2.06E+01

Dusp11	6	4.30E+02	7.41E+01	1.54E-02	3.40E-01	1.27E+00	0.35	1.27	7.01E+01	5.50E+01
Pigyl	9	7.17E+01	1.19E+01	3.04E-02	3.59E-01	1.27E+00	0.35	1.27	1.17E+01	9.16E+00
N4bp2	5	7.50E+01	1.29E+01	3.02E-02	3.59E-01	1.27E+00	0.35	1.27	1.22E+01	9.59E+00
N4bp2l2	5	1.94E+02	3.39E+01	1.62E-02	3.44E-01	1.27E+00	0.35	1.27	3.16E+01	2.48E+01
Prmt6	3	4.84E+01	9.38E+00	4.25E-02	3.91E-01	1.27E+00	0.35	1.27	7.89E+00	6.19E+00
Arf6	12	1.59E+02	2.93E+01	1.74E-02	3.49E-01	1.27E+00	0.35	1.27	2.58E+01	2.03E+01
Edf1	2	5.46E+02	9.22E+01	2.03E-02	3.51E-01	1.27E+00	0.35	1.27	8.89E+01	6.99E+01
Rps19bp1	15	4.67E+01	8.24E+00	5.98E-03	3.33E-01	1.27E+00	0.35	1.27	7.60E+00	5.97E+00
Uba52	8	1.73E+02	3.01E+01	7.01E-03	3.33E-01	1.27E+00	0.35	1.27	2.82E+01	2.22E+01
Gm20342	1	3.09E+01	5.46E+00	8.67E-03	3.33E-01	1.27E+00	0.35	1.27	5.03E+00	3.96E+00
Prcc	3	1.65E+02	3.00E+01	4.63E-02	3.98E-01	1.27E+00	0.35	1.27	2.68E+01	2.11E+01
Ankra2	13	5.07E+01	8.39E+00	8.02E-03	3.33E-01	1.27E+00	0.35	1.27	8.25E+00	6.49E+00
Rpl36	17	1.84E+02	3.37E+01	4.79E-02	4.02E-01	1.27E+00	0.35	1.27	2.99E+01	2.35E+01
Atp5j	16	6.21E+02	1.16E+02	1.48E-02	3.40E-01	1.27E+00	0.35	1.27	1.01E+02	7.95E+01
C9orf72	4	1.40E+02	2.41E+01	1.46E-02	3.39E-01	1.27E+00	0.35	1.27	2.28E+01	1.80E+01
Stt3b	9	7.75E+02	1.33E+02	4.65E-03	3.17E-01	1.27E+00	0.35	1.27	1.26E+02	9.92E+01
Ncoa5	2	9.62E+01	1.69E+01	4.54E-02	3.95E-01	1.27E+00	0.35	1.27	1.56E+01	1.23E+01
Rpl29	9	3.23E+02	6.08E+01	2.14E-02	3.52E-01	1.27E+00	0.34	1.27	5.25E+01	4.13E+01
Kbtbd2	6	2.00E+02	3.33E+01	4.16E-02	3.90E-01	1.27E+00	0.34	1.27	3.25E+01	2.56E+01
Cic	7	3.79E+02	6.52E+01	7.36E-03	3.33E-01	1.27E+00	0.34	1.27	6.16E+01	4.86E+01
Gm49336	14	1.67E+02	2.89E+01	8.45E-04	3.13E-01	1.27E+00	0.34	1.27	2.72E+01	2.14E+01
Nup153	13	2.17E+02	3.76E+01	5.61E-03	3.33E-01	1.27E+00	0.34	1.27	3.53E+01	2.78E+01
Foxk2	11	2.90E+02	4.75E+01	3.55E-02	3.79E-01	1.27E+00	0.34	1.27	4.72E+01	3.72E+01
Gm10275	10	4.62E+02	8.88E+01	4.84E-02	4.02E-01	1.27E+00	0.34	1.27	7.51E+01	5.92E+01
Nectin2	7	4.47E+02	8.06E+01	4.78E-02	4.02E-01	1.27E+00	0.34	1.27	7.27E+01	5.73E+01
Irf2bp1	7	9.36E+01	1.75E+01	3.38E-02	3.75E-01	1.27E+00	0.34	1.27	1.52E+01	1.20E+01
Zbtb20	16	9.83E+02	1.62E+02	2.31E-02	3.52E-01	1.27E+00	0.34	1.27	1.60E+02	1.26E+02
Zfp746	6	8.84E+01	1.60E+01	2.03E-02	3.51E-01	1.27E+00	0.34	1.27	1.44E+01	1.13E+01
Zfp654	16	1.44E+02	2.57E+01	8.38E-03	3.33E-01	1.27E+00	0.34	1.27	2.33E+01	1.84E+01
Rps13-ps1	8	2.62E+02	4.84E+01	3.50E-02	3.77E-01	1.27E+00	0.34	1.27	4.25E+01	3.36E+01
Fam49b	15	1.16E+02	2.20E+01	3.77E-02	3.83E-01	1.27E+00	0.34	1.27	1.89E+01	1.49E+01

Rnf26	9	9.66E+01	1.65E+01	3.01E-02	3.59E-01	1.27E+00	0.34	1.27	1.57E+01	1.24E+01
Spata2	2	1.82E+02	3.14E+01	2.30E-02	3.52E-01	1.27E+00	0.34	1.27	2.96E+01	2.34E+01
Slc10a3	X	5.10E+01	8.67E+00	4.95E-02	4.03E-01	1.27E+00	0.34	1.27	8.28E+00	6.54E+00
Epc1	18	1.15E+02	1.89E+01	1.35E-02	3.36E-01	1.27E+00	0.34	1.27	1.87E+01	1.48E+01
Prr14	7	1.47E+02	2.48E+01	2.29E-02	3.52E-01	1.27E+00	0.34	1.27	2.39E+01	1.89E+01
Rbmx	X	1.75E+02	3.16E+01	2.46E-02	3.52E-01	1.26E+00	0.34	1.26	2.85E+01	2.25E+01
Dcaf12	4	2.07E+02	3.51E+01	1.81E-03	3.13E-01	1.26E+00	0.34	1.26	3.36E+01	2.66E+01
Fam104a	11	1.23E+02	2.35E+01	4.14E-02	3.90E-01	1.26E+00	0.34	1.26	2.00E+01	1.58E+01
Gm8730	8	1.01E+02	1.82E+01	1.07E-02	3.33E-01	1.26E+00	0.34	1.26	1.64E+01	1.30E+01
Fcor	8	1.08E+02	1.78E+01	1.07E-02	3.33E-01	1.26E+00	0.34	1.26	1.76E+01	1.39E+01
Jagn1	6	1.42E+02	2.54E+01	5.17E-03	3.28E-01	1.26E+00	0.34	1.26	2.30E+01	1.82E+01
Gm9493	19	7.96E+01	1.49E+01	4.27E-02	3.91E-01	1.26E+00	0.34	1.26	1.29E+01	1.02E+01
lsg20l2	3	8.25E+01	1.38E+01	4.88E-02	4.02E-01	1.26E+00	0.34	1.26	1.34E+01	1.06E+01
Hsf1	15	1.19E+02	2.02E+01	1.81E-03	3.13E-01	1.26E+00	0.34	1.26	1.93E+01	1.53E+01
Nhp2	11	7.77E+01	1.42E+01	2.18E-02	3.52E-01	1.26E+00	0.34	1.26	1.26E+01	9.98E+00
Brd4	17	2.69E+02	4.71E+01	2.97E-02	3.58E-01	1.26E+00	0.34	1.26	4.36E+01	3.45E+01
Mif4gd	11	4.12E+02	6.88E+01	4.45E-03	3.17E-01	1.26E+00	0.34	1.26	6.67E+01	5.29E+01
Serpini1	3	9.91E+00	1.70E+00	4.22E-02	3.90E-01	1.26E+00	0.34	1.26	1.61E+00	1.27E+00
Tbc1d25	X	3.57E+01	6.13E+00	2.08E-02	3.52E-01	1.26E+00	0.34	1.26	5.79E+00	4.59E+00
Phrf1	7	2.63E+02	4.36E+01	1.30E-02	3.33E-01	1.26E+00	0.33	1.26	4.25E+01	3.37E+01
Opa3	7	2.88E+02	5.03E+01	4.32E-02	3.92E-01	1.26E+00	0.33	1.26	4.66E+01	3.70E+01
Cdk2ap1	5	1.02E+02	1.81E+01	3.95E-02	3.86E-01	1.26E+00	0.33	1.26	1.65E+01	1.31E+01
Sh3gl1	17	8.36E+01	1.47E+01	4.80E-02	4.02E-01	1.26E+00	0.33	1.26	1.35E+01	1.07E+01
Zswim7	11	5.18E+01	9.37E+00	1.54E-02	3.40E-01	1.26E+00	0.33	1.26	8.39E+00	6.66E+00
Ppp4c	7	2.03E+02	3.41E+01	3.56E-03	3.13E-01	1.26E+00	0.33	1.26	3.29E+01	2.61E+01
Supt6	11	5.07E+02	9.42E+01	2.94E-02	3.58E-01	1.26E+00	0.33	1.26	8.21E+01	6.52E+01
Gbp1	13	3.31E+02	6.01E+01	4.42E-02	3.94E-01	1.26E+00	0.33	1.26	5.36E+01	4.25E+01
Gm20604	12	4.26E+01	7.42E+00	3.67E-02	3.82E-01	1.26E+00	0.33	1.26	6.90E+00	5.48E+00
Ptbp1	10	3.66E+02	6.26E+01	3.94E-02	3.86E-01	1.26E+00	0.33	1.26	5.93E+01	4.71E+01
Rabggtb	3	2.55E+02	4.50E+01	2.75E-02	3.52E-01	1.26E+00	0.33	1.26	4.13E+01	3.29E+01
Rplp0	5	1.17E+03	2.17E+02	3.19E-02	3.66E-01	1.26E+00	0.33	1.26	1.89E+02	1.51E+02

Rpl7a-ps11	X	4.27E+02	7.87E+01	3.47E-02	3.77E-01	1.26E+00	0.33	1.26	6.91E+01	5.49E+01
Nfya	17	1.09E+02	1.80E+01	2.42E-02	3.52E-01	1.26E+00	0.33	1.26	1.77E+01	1.41E+01
Hinfo	9	1.25E+02	2.09E+01	1.46E-02	3.40E-01	1.26E+00	0.33	1.26	2.02E+01	1.61E+01
Ythdc1	5	2.97E+02	5.08E+01	2.40E-02	3.52E-01	1.26E+00	0.33	1.26	4.81E+01	3.83E+01
Snrpc	17	1.11E+02	1.89E+01	1.90E-02	3.49E-01	1.26E+00	0.33	1.26	1.79E+01	1.42E+01
Irf3	7	1.90E+02	3.38E+01	1.03E-02	3.33E-01	1.26E+00	0.33	1.26	3.07E+01	2.45E+01
Dhx15	5	4.18E+02	7.07E+01	1.14E-02	3.33E-01	1.26E+00	0.33	1.26	6.76E+01	5.38E+01
Fnbp4	2	1.97E+02	3.23E+01	4.60E-02	3.97E-01	1.26E+00	0.33	1.26	3.18E+01	2.53E+01
Gm10076	14	3.26E+02	5.47E+01	6.62E-03	3.33E-01	1.26E+00	0.33	1.26	5.26E+01	4.19E+01
Pcbp1	6	6.60E+02	1.18E+02	2.18E-02	3.52E-01	1.26E+00	0.33	1.26	1.07E+02	8.50E+01
Azi2	9	4.36E+02	7.44E+01	4.04E-02	3.87E-01	1.25E+00	0.33	1.25	7.05E+01	5.62E+01
Srsf2	11	8.96E+02	1.53E+02	1.17E-02	3.33E-01	1.25E+00	0.33	1.25	1.45E+02	1.15E+02
Prdm2	4	1.94E+02	3.27E+01	1.81E-02	3.49E-01	1.25E+00	0.33	1.25	3.14E+01	2.50E+01
Ss18l2	9	1.14E+02	2.00E+01	2.68E-02	3.52E-01	1.25E+00	0.33	1.25	1.84E+01	1.47E+01
Rpl7l1	17	3.36E+02	5.88E+01	4.08E-02	3.87E-01	1.25E+00	0.32	1.25	5.42E+01	4.33E+01
Rexo4	2	7.92E+01	1.35E+01	8.69E-03	3.33E-01	1.25E+00	0.32	1.25	1.28E+01	1.02E+01
Dgka	10	5.91E+01	1.01E+01	4.37E-02	3.93E-01	1.25E+00	0.32	1.25	9.54E+00	7.62E+00
Cox5b	1	1.38E+03	2.32E+02	1.17E-02	3.33E-01	1.25E+00	0.32	1.25	2.23E+02	1.78E+02
Phb2	6	9.47E+02	1.65E+02	3.57E-02	3.80E-01	1.25E+00	0.32	1.25	1.53E+02	1.22E+02
Prkrip1	5	4.79E+01	8.61E+00	1.22E-02	3.33E-01	1.25E+00	0.32	1.25	7.73E+00	6.18E+00
Lemd2	17	1.13E+02	2.13E+01	4.14E-02	3.90E-01	1.25E+00	0.32	1.25	1.83E+01	1.46E+01
Ssr4	X	2.00E+02	3.56E+01	1.10E-02	3.33E-01	1.25E+00	0.32	1.25	3.22E+01	2.58E+01
Rnpc3	3	9.27E+01	1.50E+01	5.80E-05	2.22E-01	1.25E+00	0.32	1.25	1.50E+01	1.20E+01
Rnf2	1	1.14E+02	1.87E+01	1.95E-02	3.49E-01	1.25E+00	0.32	1.25	1.84E+01	1.47E+01
Pdcd11	19	1.64E+02	2.86E+01	4.21E-03	3.14E-01	1.25E+00	0.32	1.25	2.65E+01	2.12E+01
Mex3c	18	1.96E+02	3.34E+01	2.62E-02	3.52E-01	1.25E+00	0.32	1.25	3.17E+01	2.54E+01
Aup1	6	3.33E+02	5.63E+01	1.37E-02	3.36E-01	1.25E+00	0.32	1.25	5.37E+01	4.30E+01
Eed	7	9.43E+01	1.56E+01	4.07E-04	3.13E-01	1.25E+00	0.32	1.25	1.52E+01	1.22E+01
Sirt1	10	1.31E+02	2.18E+01	1.29E-02	3.33E-01	1.25E+00	0.32	1.25	2.11E+01	1.69E+01
Tra2b	16	2.90E+02	5.13E+01	4.34E-02	3.92E-01	1.25E+00	0.32	1.25	4.68E+01	3.75E+01
Hnrnpa2b1	6	2.31E+03	3.95E+02	9.18E-03	3.33E-01	1.25E+00	0.32	1.25	3.73E+02	2.99E+02

Gad1l	9	2.68E+01	4.71E+00	2.24E-02	3.52E-01	1.25E+00	0.32	1.25	4.31E+00	3.46E+00
Sh3rf1	8	6.66E+01	1.14E+01	7.70E-03	3.33E-01	1.25E+00	0.32	1.25	1.07E+01	8.60E+00
Prpf4b	13	6.40E+02	1.10E+02	9.13E-03	3.33E-01	1.25E+00	0.32	1.25	1.03E+02	8.27E+01
Nelfa	5	6.28E+01	1.08E+01	3.29E-03	3.13E-01	1.25E+00	0.32	1.25	1.01E+01	8.11E+00
Gm8226	9	5.08E+02	9.27E+01	3.12E-02	3.64E-01	1.25E+00	0.32	1.25	8.18E+01	6.56E+01
Rpl28	7	4.08E+01	6.98E+00	8.53E-03	3.33E-01	1.25E+00	0.32	1.25	6.57E+00	5.27E+00
Atxn7l3b	10	3.70E+02	6.21E+01	2.74E-02	3.52E-01	1.25E+00	0.32	1.25	5.95E+01	4.77E+01
Rps9	7	7.67E+02	1.31E+02	4.69E-03	3.17E-01	1.25E+00	0.32	1.25	1.23E+02	9.91E+01
Slc35e1	8	3.44E+02	5.74E+01	1.34E-02	3.36E-01	1.25E+00	0.32	1.25	5.55E+01	4.45E+01
Slc7a6os	8	7.22E+01	1.29E+01	4.22E-02	3.90E-01	1.25E+00	0.32	1.25	1.16E+01	9.33E+00
3110056K07Rik	12	3.43E+01	6.05E+00	1.53E-02	3.40E-01	1.25E+00	0.32	1.25	5.53E+00	4.44E+00
Cpsf4	5	6.00E+01	1.10E+01	3.07E-02	3.61E-01	1.25E+00	0.32	1.25	9.66E+00	7.76E+00
Ptpn4	1	7.32E+02	1.24E+02	2.34E-02	3.52E-01	1.25E+00	0.32	1.25	1.18E+02	9.47E+01
Erp29	5	1.55E+02	2.73E+01	2.99E-02	3.58E-01	1.25E+00	0.32	1.25	2.50E+01	2.01E+01
Sowahc	10	3.96E+02	6.65E+01	9.50E-03	3.33E-01	1.25E+00	0.32	1.25	6.37E+01	5.12E+01
Unc45a	7	2.44E+02	4.20E+01	1.75E-02	3.49E-01	1.25E+00	0.32	1.25	3.94E+01	3.16E+01
Heatr3	8	1.53E+02	2.50E+01	2.02E-02	3.51E-01	1.25E+00	0.32	1.25	2.47E+01	1.98E+01
Ndufc2	7	8.70E+02	1.44E+02	1.75E-02	3.49E-01	1.24E+00	0.32	1.24	1.40E+02	1.13E+02
Rpl14	9	1.49E+02	2.77E+01	4.03E-02	3.87E-01	1.24E+00	0.32	1.24	2.41E+01	1.93E+01
Gm12263	11	4.36E+01	7.99E+00	3.72E-02	3.82E-01	1.24E+00	0.32	1.24	7.01E+00	5.63E+00
Clk4	11	3.29E+02	5.95E+01	3.84E-02	3.84E-01	1.24E+00	0.31	1.24	5.29E+01	4.25E+01
Rpl12	2	2.91E+01	4.93E+00	4.37E-02	3.93E-01	1.24E+00	0.31	1.24	4.67E+00	3.76E+00
Mamld1	X	9.32E+01	1.74E+01	4.62E-02	3.97E-01	1.24E+00	0.31	1.24	1.50E+01	1.21E+01
Gm9625	13	9.59E+01	1.64E+01	5.51E-03	3.33E-01	1.24E+00	0.31	1.24	1.54E+01	1.24E+01
Arf5	6	1.74E+02	3.00E+01	9.22E-03	3.33E-01	1.24E+00	0.31	1.24	2.81E+01	2.26E+01
Rpl32	6	3.50E+02	6.40E+01	3.59E-02	3.80E-01	1.24E+00	0.31	1.24	5.62E+01	4.52E+01
Tm2d1	4	8.16E+01	1.33E+01	1.70E-03	3.13E-01	1.24E+00	0.31	1.24	1.31E+01	1.06E+01
Hnrnph1	11	1.02E+03	1.69E+02	6.86E-03	3.33E-01	1.24E+00	0.31	1.24	1.63E+02	1.32E+02
Anp32e	3	3.44E+02	6.14E+01	4.23E-02	3.90E-01	1.24E+00	0.31	1.24	5.53E+01	4.45E+01
Zfp628	7	5.14E+01	8.46E+00	4.02E-02	3.87E-01	1.24E+00	0.31	1.24	8.27E+00	6.65E+00
Gm5525	1	1.53E+01	2.66E+00	1.61E-02	3.44E-01	1.24E+00	0.31	1.24	2.46E+00	1.98E+00

Washc4	10	1.12E+02	1.88E+01	1.06E-02	3.33E-01	1.24E+00	0.31	1.24	1.80E+01	1.45E+01
Txnrd1	10	5.75E+02	1.00E+02	2.28E-02	3.52E-01	1.24E+00	0.31	1.24	9.25E+01	7.45E+01
Cox8a	19	3.03E+03	5.45E+02	2.16E-02	3.52E-01	1.24E+00	0.31	1.24	4.87E+02	3.92E+02
Gm5801	14	2.62E+01	4.53E+00	4.23E-02	3.90E-01	1.24E+00	0.31	1.24	4.22E+00	3.40E+00
Ssu72	4	2.09E+02	3.52E+01	7.57E-03	3.33E-01	1.24E+00	0.31	1.24	3.35E+01	2.70E+01
Brpf1	6	2.39E+02	3.94E+01	7.63E-04	3.13E-01	1.24E+00	0.31	1.24	3.83E+01	3.09E+01
Gm9385	9	3.48E+02	6.00E+01	6.06E-03	3.33E-01	1.24E+00	0.31	1.24	5.59E+01	4.50E+01
Sh2b2	5	8.95E+02	1.54E+02	4.37E-02	3.93E-01	1.24E+00	0.31	1.24	1.44E+02	1.16E+02
Upf1	8	2.69E+02	4.69E+01	1.06E-02	3.33E-01	1.24E+00	0.31	1.24	4.33E+01	3.49E+01
Rbm27	18	1.48E+02	2.62E+01	2.15E-02	3.52E-01	1.24E+00	0.31	1.24	2.38E+01	1.92E+01
Nhlrc2	19	2.77E+02	4.67E+01	3.07E-03	3.13E-01	1.24E+00	0.31	1.24	4.45E+01	3.59E+01
Rpl34	3	1.21E+02	2.08E+01	3.77E-02	3.83E-01	1.24E+00	0.31	1.24	1.94E+01	1.56E+01
Supt5	7	3.28E+02	5.55E+01	4.23E-02	3.90E-01	1.24E+00	0.31	1.24	5.26E+01	4.25E+01
Gm11273	13	7.23E+02	1.23E+02	8.39E-03	3.33E-01	1.24E+00	0.31	1.24	1.16E+02	9.37E+01
Clta	4	2.08E+02	3.76E+01	1.26E-02	3.33E-01	1.24E+00	0.31	1.24	3.34E+01	2.70E+01
Tbp	17	8.11E+01	1.36E+01	3.02E-02	3.59E-01	1.24E+00	0.31	1.24	1.30E+01	1.05E+01
Tasor2	13	1.29E+02	2.23E+01	3.19E-02	3.66E-01	1.24E+00	0.31	1.24	2.07E+01	1.67E+01
Ilf3	9	1.82E+02	3.13E+01	1.60E-02	3.44E-01	1.24E+00	0.31	1.24	2.91E+01	2.35E+01
Tomm40	7	3.65E+02	6.25E+01	4.25E-02	3.91E-01	1.24E+00	0.31	1.24	5.86E+01	4.74E+01
Zfp131	13	2.18E+02	3.63E+01	3.01E-02	3.59E-01	1.24E+00	0.31	1.24	3.49E+01	2.82E+01
Alkbh6	7	8.35E+01	1.45E+01	1.98E-02	3.49E-01	1.24E+00	0.31	1.24	1.34E+01	1.08E+01
Rcc1l	5	1.18E+02	2.05E+01	2.67E-02	3.52E-01	1.24E+00	0.31	1.24	1.89E+01	1.53E+01
Chic2	5	8.04E+01	1.34E+01	3.70E-02	3.82E-01	1.24E+00	0.31	1.24	1.29E+01	1.04E+01
Brd1	15	2.17E+02	3.70E+01	3.54E-03	3.13E-01	1.24E+00	0.31	1.24	3.48E+01	2.82E+01
Stk16	1	2.80E+02	4.68E+01	3.88E-02	3.86E-01	1.24E+00	0.30	1.24	4.49E+01	3.63E+01
Mettl1	10	3.45E+01	6.09E+00	4.86E-02	4.02E-01	1.24E+00	0.30	1.24	5.53E+00	4.48E+00
Ewsr1	11	4.67E+02	8.05E+01	3.38E-02	3.75E-01	1.23E+00	0.30	1.23	7.49E+01	6.07E+01
Gm26631	9	4.36E+01	7.14E+00	2.85E-02	3.55E-01	1.23E+00	0.30	1.23	6.98E+00	5.66E+00
Appbp2	11	3.07E+02	5.11E+01	7.03E-03	3.33E-01	1.23E+00	0.30	1.23	4.92E+01	3.98E+01
Tmed2	5	1.17E+03	2.02E+02	2.03E-02	3.52E-01	1.23E+00	0.30	1.23	1.87E+02	1.52E+02
Dedd	1	1.16E+02	1.98E+01	9.74E-03	3.33E-01	1.23E+00	0.30	1.23	1.85E+01	1.50E+01

Unc50	1	1.38E+02	2.54E+01	4.97E-02	4.04E-01	1.23E+00	0.30	1.23	2.21E+01	1.79E+01
Man1a2	3	1.66E+02	2.86E+01	2.13E-02	3.52E-01	1.23E+00	0.30	1.23	2.66E+01	2.16E+01
Atg101	15	1.61E+02	2.75E+01	1.21E-02	3.33E-01	1.23E+00	0.30	1.23	2.58E+01	2.10E+01
Zfp318	17	1.69E+02	2.97E+01	4.83E-02	4.02E-01	1.23E+00	0.30	1.23	2.71E+01	2.20E+01
Sin3b	8	2.51E+02	4.18E+01	2.91E-02	3.57E-01	1.23E+00	0.30	1.23	4.02E+01	3.27E+01
Rbbp6	7	3.48E+02	5.70E+01	2.30E-02	3.52E-01	1.23E+00	0.30	1.23	5.57E+01	4.52E+01
Mtrf1l	10	3.23E+01	5.83E+00	2.44E-02	3.52E-01	1.23E+00	0.30	1.23	5.17E+00	4.20E+00
Ythdf1	2	2.00E+02	3.48E+01	3.97E-02	3.86E-01	1.23E+00	0.30	1.23	3.20E+01	2.60E+01
Esco1	18	9.22E+01	1.61E+01	2.01E-02	3.50E-01	1.23E+00	0.30	1.23	1.47E+01	1.20E+01
Zdhhc16	19	5.56E+01	9.91E+00	3.50E-02	3.78E-01	1.23E+00	0.30	1.23	8.90E+00	7.24E+00
Tor1b	2	1.81E+02	3.18E+01	2.27E-02	3.52E-01	1.23E+00	0.30	1.23	2.89E+01	2.35E+01
Polr3e	7	9.61E+01	1.66E+01	9.32E-03	3.33E-01	1.23E+00	0.30	1.23	1.54E+01	1.25E+01
Fbrs	7	2.43E+02	4.09E+01	2.71E-02	3.52E-01	1.23E+00	0.30	1.23	3.88E+01	3.16E+01
Klhl7	5	1.58E+02	2.72E+01	4.99E-02	4.05E-01	1.23E+00	0.30	1.23	2.53E+01	2.06E+01
H3f3b	11	5.55E+02	9.71E+01	4.36E-02	3.93E-01	1.23E+00	0.30	1.23	8.88E+01	7.23E+01
Nom1	5	1.20E+02	2.05E+01	2.35E-02	3.52E-01	1.23E+00	0.30	1.23	1.91E+01	1.56E+01
Zcchc8	5	1.23E+02	2.09E+01	2.39E-02	3.52E-01	1.23E+00	0.30	1.23	1.97E+01	1.60E+01
Csnk1a1	18	9.64E+02	1.57E+02	1.86E-03	3.13E-01	1.23E+00	0.30	1.23	1.54E+02	1.26E+02
Aff4	11	6.68E+02	1.17E+02	3.52E-02	3.79E-01	1.23E+00	0.30	1.23	1.07E+02	8.69E+01
Rpl9-ps6	19	7.95E+02	1.39E+02	3.29E-02	3.71E-01	1.23E+00	0.29	1.23	1.27E+02	1.04E+02
Stk11	10	6.04E+02	1.02E+02	1.70E-02	3.49E-01	1.23E+00	0.29	1.23	9.65E+01	7.87E+01
Tent4b	8	2.36E+02	3.87E+01	2.93E-02	3.58E-01	1.23E+00	0.29	1.23	3.77E+01	3.07E+01
Ddx5	11	3.78E+03	6.41E+02	3.52E-02	3.78E-01	1.23E+00	0.29	1.23	6.04E+02	4.93E+02
Arfp2	7	2.52E+02	4.19E+01	1.82E-02	3.49E-01	1.22E+00	0.29	1.22	4.03E+01	3.29E+01
Rps27l	9	2.30E+02	3.77E+01	8.41E-03	3.33E-01	1.22E+00	0.29	1.22	3.66E+01	2.99E+01
Sf3b4	3	6.81E+01	1.15E+01	5.54E-03	3.33E-01	1.22E+00	0.29	1.22	1.09E+01	8.88E+00
Vezf1	11	2.76E+02	4.95E+01	2.53E-02	3.52E-01	1.22E+00	0.29	1.22	4.41E+01	3.60E+01
Med17	9	8.55E+01	1.42E+01	1.20E-02	3.33E-01	1.22E+00	0.29	1.22	1.36E+01	1.11E+01
Hypk	2	1.54E+02	2.57E+01	2.83E-02	3.55E-01	1.22E+00	0.29	1.22	2.45E+01	2.00E+01
Farsa	8	1.05E+02	1.76E+01	1.01E-03	3.13E-01	1.22E+00	0.29	1.22	1.67E+01	1.37E+01
Tra2a	6	2.47E+02	4.17E+01	4.08E-02	3.87E-01	1.22E+00	0.29	1.22	3.94E+01	3.22E+01

Kctd5	17	4.84E+01	8.46E+00	3.73E-02	3.83E-01	1.22E+00	0.29	1.22	7.73E+00	6.32E+00
Dctpp1	7	5.70E+01	9.30E+00	1.06E-03	3.13E-01	1.22E+00	0.29	1.22	9.08E+00	7.43E+00
Rc3h2	2	2.22E+02	3.66E+01	1.75E-03	3.13E-01	1.22E+00	0.29	1.22	3.54E+01	2.89E+01
Gtpbp4	13	2.12E+02	3.67E+01	9.72E-03	3.33E-01	1.22E+00	0.29	1.22	3.37E+01	2.76E+01
Mrps12	7	1.51E+02	2.54E+01	2.94E-02	3.58E-01	1.22E+00	0.29	1.22	2.41E+01	1.97E+01
Kdelr1	7	3.76E+02	6.23E+01	1.55E-02	3.40E-01	1.22E+00	0.29	1.22	5.99E+01	4.90E+01
Tmem199	11	8.84E+01	1.53E+01	3.73E-02	3.83E-01	1.22E+00	0.29	1.22	1.41E+01	1.15E+01
Cnot3	7	1.39E+02	2.25E+01	1.95E-02	3.49E-01	1.22E+00	0.29	1.22	2.21E+01	1.81E+01
Surf6	2	6.73E+01	1.09E+01	1.94E-02	3.49E-01	1.22E+00	0.29	1.22	1.07E+01	8.78E+00
Gata2	6	6.51E+01	1.14E+01	9.79E-03	3.33E-01	1.22E+00	0.29	1.22	1.04E+01	8.50E+00
Stx5a	19	2.27E+02	3.99E+01	4.87E-02	4.02E-01	1.22E+00	0.29	1.22	3.61E+01	2.96E+01
Ergic2	6	2.24E+02	3.91E+01	3.19E-02	3.66E-01	1.22E+00	0.29	1.22	3.56E+01	2.92E+01
Imp3	9	9.96E+01	1.71E+01	1.88E-02	3.49E-01	1.22E+00	0.29	1.22	1.59E+01	1.30E+01
Uck2	1	1.37E+02	2.26E+01	2.54E-02	3.52E-01	1.22E+00	0.29	1.22	2.19E+01	1.80E+01
Stard10	7	7.35E+01	1.21E+01	2.08E-02	3.52E-01	1.22E+00	0.29	1.22	1.17E+01	9.60E+00
AC163616.1	3	4.15E+01	7.20E+00	4.54E-02	3.95E-01	1.22E+00	0.29	1.22	6.60E+00	5.42E+00
Gm19680	1	1.14E+02	1.97E+01	1.98E-02	3.49E-01	1.22E+00	0.28	1.22	1.81E+01	1.49E+01
Uqcc3	19	1.89E+02	3.25E+01	4.08E-02	3.87E-01	1.22E+00	0.28	1.22	3.01E+01	2.47E+01
Dpf2	19	2.33E+02	3.84E+01	1.27E-03	3.13E-01	1.22E+00	0.28	1.22	3.70E+01	3.04E+01
Ndufa7	17	6.06E+02	1.05E+02	1.48E-02	3.40E-01	1.22E+00	0.28	1.22	9.64E+01	7.91E+01
Spryd4	10	4.14E+01	6.81E+00	4.52E-03	3.17E-01	1.22E+00	0.28	1.22	6.60E+00	5.42E+00
Map2k2	10	3.85E+02	6.71E+01	2.67E-02	3.52E-01	1.22E+00	0.28	1.22	6.13E+01	5.03E+01
Khdc4	3	3.31E+02	5.49E+01	4.17E-02	3.90E-01	1.22E+00	0.28	1.22	5.27E+01	4.33E+01
Dnajb11	16	1.44E+02	2.37E+01	8.40E-03	3.33E-01	1.22E+00	0.28	1.22	2.29E+01	1.88E+01
Pom121	5	1.87E+02	3.11E+01	3.03E-03	3.13E-01	1.22E+00	0.28	1.22	2.97E+01	2.44E+01
Sec61a2	2	8.28E+01	1.38E+01	3.91E-02	3.86E-01	1.22E+00	0.28	1.22	1.32E+01	1.08E+01
Pagr1a	7	1.89E+01	3.12E+00	3.71E-02	3.82E-01	1.22E+00	0.28	1.22	3.00E+00	2.47E+00
Srsf6	2	5.74E+02	9.80E+01	1.20E-02	3.33E-01	1.22E+00	0.28	1.22	9.12E+01	7.50E+01
Pnn	12	2.78E+02	4.65E+01	9.88E-03	3.33E-01	1.22E+00	0.28	1.22	4.42E+01	3.63E+01
Ric1	19	4.24E+02	7.41E+01	2.43E-02	3.52E-01	1.22E+00	0.28	1.22	6.73E+01	5.54E+01
Mtf2	5	7.90E+01	1.30E+01	2.32E-02	3.52E-01	1.21E+00	0.28	1.21	1.26E+01	1.03E+01

BC005537	13	1.11E+03	1.84E+02	3.76E-02	3.83E-01	1.21E+00	0.28	1.21	1.76E+02	1.45E+02
Usp16	16	3.18E+02	5.10E+01	3.40E-03	3.13E-01	1.21E+00	0.28	1.21	5.05E+01	4.16E+01
Gm6136	1	4.15E+02	7.15E+01	7.14E-03	3.33E-01	1.21E+00	0.28	1.21	6.59E+01	5.43E+01
Urb2	8	5.90E+01	1.02E+01	2.71E-02	3.52E-01	1.21E+00	0.28	1.21	9.37E+00	7.73E+00
Mrps7	11	3.96E+02	6.88E+01	1.14E-02	3.33E-01	1.21E+00	0.28	1.21	6.29E+01	5.19E+01
Oser1	2	1.06E+02	1.81E+01	4.80E-02	4.02E-01	1.21E+00	0.28	1.21	1.68E+01	1.39E+01
Txndc15	13	2.28E+02	3.74E+01	8.60E-03	3.33E-01	1.21E+00	0.28	1.21	3.62E+01	2.99E+01
Tomm20	8	4.14E+02	6.79E+01	6.92E-03	3.33E-01	1.21E+00	0.28	1.21	6.58E+01	5.42E+01
Hic1	11	6.31E+01	1.05E+01	3.61E-02	3.80E-01	1.21E+00	0.28	1.21	1.00E+01	8.26E+00
Ptpn1	2	1.71E+02	2.86E+01	1.82E-02	3.49E-01	1.21E+00	0.28	1.21	2.72E+01	2.24E+01
Ubac2	14	1.29E+02	2.14E+01	1.53E-02	3.40E-01	1.21E+00	0.28	1.21	2.04E+01	1.69E+01
Nipa2	7	2.03E+02	3.40E+01	1.49E-02	3.40E-01	1.21E+00	0.28	1.21	3.23E+01	2.66E+01
Rheb	5	3.21E+02	5.34E+01	1.01E-02	3.33E-01	1.21E+00	0.28	1.21	5.09E+01	4.20E+01
Mrfap1	5	9.89E+02	1.60E+02	4.01E-03	3.13E-01	1.21E+00	0.28	1.21	1.57E+02	1.30E+02
Camkk2	5	1.57E+02	2.59E+01	4.16E-02	3.90E-01	1.21E+00	0.28	1.21	2.48E+01	2.05E+01
Eif5a	11	1.30E+03	2.24E+02	2.76E-02	3.53E-01	1.21E+00	0.28	1.21	2.06E+02	1.70E+02
Mrps17	5	2.98E+02	5.04E+01	2.51E-02	3.52E-01	1.21E+00	0.28	1.21	4.73E+01	3.91E+01
Elavl1	8	2.90E+02	5.08E+01	3.81E-02	3.83E-01	1.21E+00	0.28	1.21	4.59E+01	3.79E+01
B3galnt2	13	9.68E+01	1.65E+01	2.06E-02	3.52E-01	1.21E+00	0.28	1.21	1.53E+01	1.27E+01
Dus1l	11	1.54E+02	2.65E+01	4.88E-02	4.02E-01	1.21E+00	0.28	1.21	2.43E+01	2.01E+01
Cox6a1	5	4.38E+03	7.87E+02	4.48E-02	3.95E-01	1.21E+00	0.27	1.21	6.95E+02	5.74E+02
Surf4	2	6.86E+02	1.10E+02	2.47E-02	3.52E-01	1.21E+00	0.27	1.21	1.09E+02	8.99E+01
Abhd12	2	2.42E+02	4.07E+01	9.85E-03	3.33E-01	1.21E+00	0.27	1.21	3.83E+01	3.17E+01
Lrrc41	4	2.55E+02	4.37E+01	1.13E-02	3.33E-01	1.21E+00	0.27	1.21	4.04E+01	3.34E+01
9930021J03Rik	19	1.50E+02	2.48E+01	2.58E-03	3.13E-01	1.21E+00	0.27	1.21	2.38E+01	1.97E+01
Ep300	15	3.94E+02	6.42E+01	3.63E-03	3.13E-01	1.21E+00	0.27	1.21	6.25E+01	5.17E+01
Eps8l2	7	2.22E+01	3.70E+00	1.89E-02	3.49E-01	1.21E+00	0.27	1.21	3.52E+00	2.91E+00
Yipf3	17	1.97E+02	3.24E+01	1.79E-02	3.49E-01	1.21E+00	0.27	1.21	3.12E+01	2.58E+01
Ubxn6	17	2.59E+02	4.18E+01	2.20E-02	3.52E-01	1.21E+00	0.27	1.21	4.10E+01	3.39E+01
Brd2	17	8.88E+02	1.52E+02	2.22E-02	3.52E-01	1.21E+00	0.27	1.21	1.41E+02	1.16E+02
Emsy	7	1.53E+02	2.52E+01	1.82E-03	3.13E-01	1.21E+00	0.27	1.21	2.43E+01	2.01E+01

2310061I04Rik	17	3.90E+02	6.79E+01	4.76E-02	4.02E-01	1.21E+00	0.27	1.21	6.18E+01	5.12E+01
Uhrf2	19	1.19E+02	1.95E+01	2.40E-02	3.52E-01	1.21E+00	0.27	1.21	1.89E+01	1.57E+01
Mfap1b	2	1.77E+02	2.91E+01	9.25E-03	3.33E-01	1.21E+00	0.27	1.21	2.81E+01	2.33E+01
Ccm2	11	1.50E+02	2.43E+01	1.45E-02	3.38E-01	1.21E+00	0.27	1.21	2.37E+01	1.97E+01
Gmeb2	2	9.79E+01	1.65E+01	2.51E-02	3.52E-01	1.20E+00	0.27	1.20	1.55E+01	1.29E+01
Sec61a1	6	4.15E+02	6.84E+01	2.34E-02	3.52E-01	1.20E+00	0.27	1.20	6.57E+01	5.45E+01
Fem1b	9	1.66E+02	2.70E+01	2.49E-03	3.13E-01	1.20E+00	0.27	1.20	2.63E+01	2.18E+01
Tmx1	12	2.34E+02	3.99E+01	4.87E-02	4.02E-01	1.20E+00	0.27	1.20	3.70E+01	3.07E+01
H3f3a	1	7.20E+02	1.26E+02	2.49E-02	3.52E-01	1.20E+00	0.27	1.20	1.14E+02	9.46E+01
Ddx21	10	3.14E+02	5.31E+01	3.43E-02	3.77E-01	1.20E+00	0.27	1.20	4.96E+01	4.12E+01
D230025D16Rik	8	1.75E+02	2.88E+01	2.67E-02	3.52E-01	1.20E+00	0.27	1.20	2.77E+01	2.30E+01
Srsf4	4	1.52E+02	2.46E+01	3.53E-02	3.79E-01	1.20E+00	0.27	1.20	2.40E+01	2.00E+01
Otulin	15	7.41E+01	1.28E+01	4.35E-02	3.92E-01	1.20E+00	0.27	1.20	1.17E+01	9.73E+00
Nol7	13	1.48E+02	2.56E+01	1.94E-02	3.49E-01	1.20E+00	0.27	1.20	2.35E+01	1.95E+01
Mrps26	2	1.26E+02	2.16E+01	1.19E-02	3.33E-01	1.20E+00	0.27	1.20	1.99E+01	1.66E+01
Spcs2	7	1.65E+02	2.85E+01	2.59E-02	3.52E-01	1.20E+00	0.27	1.20	2.60E+01	2.17E+01
Elob	17	2.71E+02	4.65E+01	1.27E-02	3.33E-01	1.20E+00	0.27	1.20	4.28E+01	3.56E+01
Hnrnpc	14	4.41E+02	7.53E+01	1.27E-02	3.33E-01	1.20E+00	0.27	1.20	6.97E+01	5.80E+01
Ppme1	7	2.03E+02	3.36E+01	4.23E-02	3.90E-01	1.20E+00	0.27	1.20	3.20E+01	2.66E+01
Ocel1	8	1.24E+02	2.04E+01	3.47E-02	3.77E-01	1.20E+00	0.27	1.20	1.96E+01	1.63E+01
Mrpl55	11	1.85E+02	3.07E+01	8.05E-03	3.33E-01	1.20E+00	0.27	1.20	2.92E+01	2.43E+01
1810026B05Rik	7	1.02E+02	1.70E+01	2.12E-02	3.52E-01	1.20E+00	0.26	1.20	1.62E+01	1.35E+01
Senp2	16	2.81E+02	4.71E+01	1.76E-02	3.49E-01	1.20E+00	0.26	1.20	4.44E+01	3.69E+01
Gm5148	3	2.05E+02	3.36E+01	1.39E-02	3.36E-01	1.20E+00	0.26	1.20	3.23E+01	2.69E+01
Rsrc2	5	2.74E+02	4.46E+01	1.40E-02	3.36E-01	1.20E+00	0.26	1.20	4.32E+01	3.60E+01
Max	12	1.86E+02	3.17E+01	2.44E-02	3.52E-01	1.20E+00	0.26	1.20	2.95E+01	2.45E+01
Neu1	17	1.33E+02	2.16E+01	3.49E-02	3.77E-01	1.20E+00	0.26	1.20	2.10E+01	1.75E+01
Ppil4	10	1.51E+02	2.56E+01	2.26E-03	3.13E-01	1.20E+00	0.26	1.20	2.38E+01	1.99E+01
Tsr1	11	8.52E+01	1.47E+01	1.85E-02	3.49E-01	1.20E+00	0.26	1.20	1.35E+01	1.12E+01
Gm43096	5	9.20E+00	1.64E+00	2.59E-02	3.52E-01	1.20E+00	0.26	1.20	1.45E+00	1.21E+00
Tmem248	5	2.21E+02	3.55E+01	1.37E-02	3.36E-01	1.20E+00	0.26	1.20	3.48E+01	2.91E+01

Tmem39b	4	1.82E+01	2.98E+00	3.64E-02	3.81E-01	1.20E+00	0.26	1.20	2.88E+00	2.40E+00
Tmed9	13	2.43E+02	4.06E+01	2.89E-02	3.57E-01	1.20E+00	0.26	1.20	3.83E+01	3.20E+01
Fbxl16	17	8.50E+00	1.47E+00	3.90E-02	3.86E-01	1.20E+00	0.26	1.20	1.34E+00	1.12E+00
Trappc5	8	1.38E+02	2.27E+01	2.44E-02	3.52E-01	1.20E+00	0.26	1.20	2.18E+01	1.82E+01
Eme2	17	1.64E+02	2.71E+01	4.84E-02	4.02E-01	1.20E+00	0.26	1.20	2.59E+01	2.16E+01
Lcor	19	5.95E+01	9.88E+00	2.72E-02	3.52E-01	1.20E+00	0.26	1.20	9.38E+00	7.84E+00
Gm10157	9	1.31E+02	2.15E+01	4.25E-02	3.91E-01	1.20E+00	0.26	1.20	2.06E+01	1.72E+01
Hnrnpa3	2	5.61E+02	9.17E+01	1.19E-02	3.33E-01	1.20E+00	0.26	1.20	8.85E+01	7.40E+01
Ndufs6	13	6.62E+02	1.11E+02	4.67E-02	3.98E-01	1.20E+00	0.26	1.20	1.04E+02	8.72E+01
Ppig	2	2.58E+02	4.12E+01	1.92E-02	3.49E-01	1.20E+00	0.26	1.20	4.06E+01	3.40E+01
Nab1	1	3.99E+02	6.35E+01	4.63E-03	3.17E-01	1.20E+00	0.26	1.20	6.29E+01	5.26E+01
Tbpl1	10	7.37E+01	1.19E+01	3.03E-02	3.59E-01	1.20E+00	0.26	1.20	1.16E+01	9.71E+00
Hnrnmp	17	4.73E+02	7.85E+01	4.34E-02	3.92E-01	1.20E+00	0.26	1.20	7.46E+01	6.23E+01
Ap2s1	7	1.75E+02	2.85E+01	9.93E-03	3.33E-01	1.20E+00	0.26	1.20	2.76E+01	2.31E+01
Snu13	15	2.15E+02	3.52E+01	3.28E-03	3.13E-01	1.20E+00	0.26	1.20	3.38E+01	2.83E+01
Pabpn1	14	3.07E+02	5.16E+01	2.69E-03	3.13E-01	1.20E+00	0.26	1.20	4.84E+01	4.05E+01
Ttc9c	19	2.20E+02	3.56E+01	3.69E-02	3.82E-01	1.20E+00	0.26	1.20	3.46E+01	2.90E+01
Lats1	10	2.87E+02	4.86E+01	1.51E-02	3.40E-01	1.19E+00	0.26	1.19	4.52E+01	3.79E+01
Cox7c	13	9.44E+02	1.62E+02	4.31E-02	3.92E-01	1.19E+00	0.26	1.19	1.49E+02	1.25E+02
Chml	1	5.33E+01	9.11E+00	2.49E-02	3.52E-01	1.19E+00	0.26	1.19	8.40E+00	7.03E+00
Dpm2	2	8.20E+01	1.33E+01	4.37E-04	3.13E-01	1.19E+00	0.26	1.19	1.29E+01	1.08E+01
Nol9	4	8.75E+01	1.44E+01	1.76E-02	3.49E-01	1.19E+00	0.26	1.19	1.38E+01	1.15E+01
Rps10	17	9.29E+01	1.57E+01	2.29E-02	3.52E-01	1.19E+00	0.26	1.19	1.46E+01	1.22E+01
Map3k2	18	1.96E+02	3.44E+01	2.35E-02	3.52E-01	1.19E+00	0.26	1.19	3.08E+01	2.58E+01
Mfsd5	15	1.11E+02	1.79E+01	3.66E-02	3.82E-01	1.19E+00	0.26	1.19	1.75E+01	1.47E+01
Fbxo42	4	1.29E+02	2.10E+01	3.74E-03	3.13E-01	1.19E+00	0.26	1.19	2.03E+01	1.70E+01
Tm2d2	8	1.86E+02	3.05E+01	2.26E-02	3.52E-01	1.19E+00	0.25	1.19	2.93E+01	2.45E+01
Cerk	15	6.58E+01	1.16E+01	3.29E-02	3.71E-01	1.19E+00	0.25	1.19	1.04E+01	8.68E+00
Acvr2a	2	1.37E+02	2.22E+01	1.04E-02	3.33E-01	1.19E+00	0.25	1.19	2.15E+01	1.80E+01
Rps15	10	6.45E+02	1.15E+02	2.51E-02	3.52E-01	1.19E+00	0.25	1.19	1.02E+02	8.52E+01
Mecp2	X	2.50E+02	4.03E+01	1.41E-02	3.36E-01	1.19E+00	0.25	1.19	3.93E+01	3.29E+01

Tgs1	4	1.02E+02	1.68E+01	2.53E-02	3.52E-01	1.19E+00	0.25	1.19	1.61E+01	1.35E+01
Tmem9b	7	2.04E+02	3.33E+01	2.28E-02	3.52E-01	1.19E+00	0.25	1.19	3.21E+01	2.69E+01
Rpp21	17	3.42E+01	5.42E+00	3.61E-02	3.80E-01	1.19E+00	0.25	1.19	5.38E+00	4.52E+00
Hmgxb3	18	1.51E+02	2.48E+01	2.76E-02	3.53E-01	1.19E+00	0.25	1.19	2.37E+01	1.99E+01
Egln2	7	2.59E+02	4.23E+01	1.87E-02	3.49E-01	1.19E+00	0.25	1.19	4.06E+01	3.42E+01
Tgfbr1	4	1.52E+02	2.50E+01	4.40E-02	3.93E-01	1.19E+00	0.25	1.19	2.39E+01	2.01E+01
Sf1	19	4.97E+02	8.03E+01	3.14E-02	3.66E-01	1.19E+00	0.25	1.19	7.81E+01	6.57E+01
Matr3	18	5.24E+02	8.60E+01	2.62E-02	3.52E-01	1.19E+00	0.25	1.19	8.24E+01	6.93E+01
Btf3	13	2.19E+02	3.69E+01	2.09E-02	3.52E-01	1.19E+00	0.25	1.19	3.44E+01	2.89E+01
Dgcr2	16	3.37E+02	5.54E+01	4.23E-02	3.90E-01	1.19E+00	0.25	1.19	5.30E+01	4.46E+01
Tmem47	X	3.81E+01	6.56E+00	3.59E-02	3.80E-01	1.19E+00	0.25	1.19	5.98E+00	5.03E+00
Ubxn7	16	2.06E+02	3.42E+01	2.59E-02	3.52E-01	1.19E+00	0.25	1.19	3.24E+01	2.72E+01
Cct6a	5	4.58E+02	7.49E+01	2.06E-02	3.52E-01	1.19E+00	0.25	1.19	7.19E+01	6.05E+01
Selenoi	5	1.49E+02	2.44E+01	6.86E-03	3.33E-01	1.19E+00	0.25	1.19	2.34E+01	1.97E+01
Ube2e3	2	1.60E+02	2.55E+01	2.61E-03	3.13E-01	1.19E+00	0.25	1.19	2.51E+01	2.11E+01
Dazap1	10	1.89E+02	3.12E+01	2.90E-02	3.57E-01	1.19E+00	0.25	1.19	2.97E+01	2.50E+01
Commd2	3	5.65E+01	9.31E+00	3.84E-02	3.84E-01	1.19E+00	0.25	1.19	8.88E+00	7.47E+00
Ncbp2	16	2.07E+02	3.34E+01	2.67E-02	3.52E-01	1.19E+00	0.25	1.19	3.25E+01	2.74E+01
Ubxn1	19	4.84E+02	7.83E+01	4.20E-02	3.90E-01	1.19E+00	0.25	1.19	7.60E+01	6.40E+01
Minpp1	19	8.18E+01	1.32E+01	9.29E-03	3.33E-01	1.19E+00	0.25	1.19	1.28E+01	1.08E+01
Pcbp2	15	9.80E+02	1.63E+02	3.79E-02	3.83E-01	1.19E+00	0.25	1.19	1.54E+02	1.30E+02
Polr2i	7	5.77E+01	9.37E+00	3.43E-02	3.77E-01	1.18E+00	0.24	1.18	9.04E+00	7.63E+00
Rbmxl1	8	8.66E+01	1.42E+01	4.39E-02	3.93E-01	1.18E+00	0.24	1.18	1.36E+01	1.15E+01
Erp44	4	1.70E+02	2.75E+01	3.45E-02	3.77E-01	1.18E+00	0.24	1.18	2.67E+01	2.25E+01
Ccdc124	8	1.26E+02	2.09E+01	6.23E-03	3.33E-01	1.18E+00	0.24	1.18	1.97E+01	1.66E+01
Tor1aip2	1	7.98E+02	1.29E+02	4.68E-02	3.99E-01	1.18E+00	0.24	1.18	1.25E+02	1.06E+02
U2af1	17	4.25E+01	6.95E+00	3.79E-02	3.83E-01	1.18E+00	0.24	1.18	6.67E+00	5.64E+00
Mrpl3	9	3.58E+02	5.93E+01	4.05E-02	3.87E-01	1.18E+00	0.24	1.18	5.60E+01	4.74E+01
Mbtd1	11	1.77E+02	2.92E+01	4.30E-02	3.92E-01	1.18E+00	0.24	1.18	2.78E+01	2.35E+01
Ndufa6	15	1.07E+03	1.73E+02	1.89E-02	3.49E-01	1.18E+00	0.24	1.18	1.67E+02	1.41E+02
Ndufb11	X	1.33E+03	2.23E+02	4.86E-02	4.02E-01	1.18E+00	0.24	1.18	2.08E+02	1.76E+02

Larp1b	3	1.83E+02	3.03E+01	2.36E-02	3.52E-01	1.18E+00	0.24	1.18	2.86E+01	2.42E+01
Msl1	11	3.87E+02	6.47E+01	1.18E-02	3.33E-01	1.18E+00	0.24	1.18	6.06E+01	5.13E+01
Mtmr10	7	1.90E+02	3.02E+01	2.30E-02	3.52E-01	1.18E+00	0.24	1.18	2.97E+01	2.52E+01
Hint2	4	2.37E+02	3.84E+01	7.33E-03	3.33E-01	1.18E+00	0.24	1.18	3.71E+01	3.15E+01
Nrg4	9	6.54E+02	1.07E+02	3.01E-02	3.59E-01	1.18E+00	0.24	1.18	1.02E+02	8.67E+01
Snrnp27	6	1.05E+02	1.84E+01	2.99E-02	3.58E-01	1.18E+00	0.24	1.18	1.64E+01	1.39E+01
Cdk13	13	2.82E+02	4.61E+01	1.64E-02	3.45E-01	1.18E+00	0.24	1.18	4.41E+01	3.74E+01
Ptpn2	18	8.48E+01	1.38E+01	2.83E-02	3.55E-01	1.18E+00	0.24	1.18	1.33E+01	1.12E+01
Sun2	15	8.99E+02	1.50E+02	2.65E-02	3.52E-01	1.18E+00	0.24	1.18	1.41E+02	1.19E+02
Ubn2	6	2.32E+02	3.88E+01	1.56E-02	3.40E-01	1.18E+00	0.24	1.18	3.63E+01	3.08E+01
Nfat5	8	3.37E+02	5.43E+01	5.16E-03	3.28E-01	1.18E+00	0.24	1.18	5.27E+01	4.47E+01
Gtf2a2	9	1.36E+02	2.19E+01	9.14E-03	3.33E-01	1.18E+00	0.24	1.18	2.13E+01	1.81E+01
Zfp868	8	4.82E+01	7.98E+00	2.65E-02	3.52E-01	1.18E+00	0.24	1.18	7.54E+00	6.40E+00
Setd2	9	3.02E+02	4.88E+01	1.09E-02	3.33E-01	1.18E+00	0.23	1.18	4.73E+01	4.02E+01
Gm12183	11	3.94E+02	6.58E+01	4.09E-02	3.88E-01	1.18E+00	0.23	1.18	6.16E+01	5.23E+01
Yipf4	17	3.56E+02	5.72E+01	1.85E-02	3.49E-01	1.18E+00	0.23	1.18	5.57E+01	4.74E+01
Mrpl18	17	3.81E+02	6.46E+01	2.30E-02	3.52E-01	1.18E+00	0.23	1.18	5.95E+01	5.06E+01
Tmed7	18	5.00E+02	8.29E+01	4.48E-02	3.95E-01	1.18E+00	0.23	1.18	7.81E+01	6.64E+01
Bag5	12	1.39E+02	2.22E+01	3.02E-02	3.59E-01	1.18E+00	0.23	1.18	2.17E+01	1.84E+01
Rictor	15	1.57E+02	2.58E+01	1.06E-02	3.33E-01	1.17E+00	0.23	1.17	2.44E+01	2.08E+01
Rsl1d1	16	2.23E+02	3.62E+01	2.29E-02	3.52E-01	1.17E+00	0.23	1.17	3.48E+01	2.97E+01
Krit1	5	1.84E+02	2.92E+01	2.35E-02	3.52E-01	1.17E+00	0.23	1.17	2.87E+01	2.44E+01
Ssna1	2	7.90E+01	1.26E+01	1.13E-02	3.33E-01	1.17E+00	0.23	1.17	1.23E+01	1.05E+01
Zfp146	7	1.55E+02	2.50E+01	3.12E-02	3.64E-01	1.17E+00	0.23	1.17	2.41E+01	2.06E+01
Vps36	8	1.85E+02	3.03E+01	1.30E-02	3.33E-01	1.17E+00	0.23	1.17	2.88E+01	2.46E+01
Vmp1	11	2.40E+02	4.07E+01	3.03E-02	3.59E-01	1.17E+00	0.23	1.17	3.74E+01	3.19E+01
Cox7b	X	2.91E+03	4.84E+02	3.02E-02	3.59E-01	1.17E+00	0.23	1.17	4.54E+02	3.88E+02
Otud4	8	3.92E+02	6.31E+01	8.43E-03	3.33E-01	1.17E+00	0.23	1.17	6.11E+01	5.22E+01
Golga7	8	2.34E+02	3.90E+01	7.90E-03	3.33E-01	1.17E+00	0.23	1.17	3.65E+01	3.11E+01
Tor1a	2	7.85E+01	1.38E+01	4.86E-02	4.02E-01	1.17E+00	0.23	1.17	1.22E+01	1.05E+01
Sf3a2	10	6.42E+01	1.07E+01	2.56E-02	3.52E-01	1.17E+00	0.23	1.17	1.00E+01	8.55E+00

Mlxip	5	3.40E+02	5.50E+01	2.59E-02	3.52E-01	1.17E+00	0.23	1.17	5.30E+01	4.53E+01
Aak1	6	3.48E+02	5.84E+01	2.67E-02	3.52E-01	1.17E+00	0.23	1.17	5.42E+01	4.63E+01
Polr1d	5	4.36E+02	7.10E+01	3.29E-02	3.71E-01	1.17E+00	0.23	1.17	6.78E+01	5.80E+01
Dram2	3	5.07E+02	8.59E+01	3.10E-02	3.63E-01	1.17E+00	0.23	1.17	7.90E+01	6.75E+01
Gm43980	6	3.15E+01	5.36E+00	4.65E-02	3.98E-01	1.17E+00	0.23	1.17	4.91E+00	4.20E+00
Npm3	19	3.35E+01	5.56E+00	4.64E-02	3.98E-01	1.17E+00	0.23	1.17	5.22E+00	4.47E+00
Ube2m	7	4.54E+02	7.70E+01	1.60E-02	3.44E-01	1.17E+00	0.23	1.17	7.06E+01	6.04E+01
Czib	4	1.33E+02	2.11E+01	6.62E-03	3.33E-01	1.17E+00	0.22	1.17	2.07E+01	1.77E+01
Mrpl38	11	4.33E+02	6.97E+01	1.87E-02	3.49E-01	1.17E+00	0.22	1.17	6.75E+01	5.78E+01
Ttl4	1	9.95E+01	1.57E+01	3.94E-02	3.86E-01	1.17E+00	0.22	1.17	1.55E+01	1.33E+01
Srp19	18	1.33E+02	2.15E+01	2.62E-02	3.52E-01	1.17E+00	0.22	1.17	2.08E+01	1.78E+01
Rundc1	11	9.64E+01	1.58E+01	2.72E-03	3.13E-01	1.17E+00	0.22	1.17	1.50E+01	1.28E+01
Mrpl17	7	3.53E+02	5.55E+01	2.69E-02	3.52E-01	1.17E+00	0.22	1.17	5.50E+01	4.71E+01
Mier1	4	2.50E+02	4.06E+01	3.30E-02	3.71E-01	1.17E+00	0.22	1.17	3.89E+01	3.33E+01
Eif1b	9	9.14E+01	1.50E+01	5.38E-03	3.33E-01	1.17E+00	0.22	1.17	1.42E+01	1.22E+01
Chchd1	14	1.68E+02	2.69E+01	1.86E-02	3.49E-01	1.17E+00	0.22	1.17	2.61E+01	2.24E+01
Srsf1	11	8.29E+02	1.33E+02	8.66E-03	3.33E-01	1.17E+00	0.22	1.17	1.29E+02	1.10E+02
Psmb4	3	4.62E+02	7.81E+01	3.84E-02	3.84E-01	1.17E+00	0.22	1.17	7.18E+01	6.16E+01
Trmt13	3	2.62E+01	4.34E+00	1.50E-02	3.40E-01	1.17E+00	0.22	1.17	4.08E+00	3.50E+00
Mrps21	3	2.78E+02	4.64E+01	3.96E-02	3.86E-01	1.17E+00	0.22	1.17	4.32E+01	3.71E+01
Rnf103	6	1.70E+02	2.87E+01	1.24E-02	3.33E-01	1.16E+00	0.22	1.16	2.65E+01	2.27E+01
Xpo4	14	1.28E+02	2.09E+01	2.95E-02	3.58E-01	1.16E+00	0.22	1.16	1.99E+01	1.71E+01
Casc3	11	1.79E+02	2.86E+01	1.23E-02	3.33E-01	1.16E+00	0.22	1.16	2.78E+01	2.39E+01
Dgcr6	16	2.64E+02	4.50E+01	1.67E-02	3.46E-01	1.16E+00	0.22	1.16	4.10E+01	3.52E+01
Rnf40	7	2.45E+02	3.91E+01	2.68E-02	3.52E-01	1.16E+00	0.22	1.16	3.81E+01	3.27E+01
Zfp871	17	3.11E+02	4.89E+01	4.67E-02	3.98E-01	1.16E+00	0.22	1.16	4.84E+01	4.15E+01
Tardbp	4	6.39E+02	1.04E+02	4.30E-02	3.92E-01	1.16E+00	0.22	1.16	9.93E+01	8.53E+01
Pycrl	15	1.30E+02	2.06E+01	5.89E-03	3.33E-01	1.16E+00	0.22	1.16	2.01E+01	1.73E+01
Pgam5	5	1.56E+02	2.52E+01	6.25E-03	3.33E-01	1.16E+00	0.22	1.16	2.42E+01	2.08E+01
Csnk2b	17	2.57E+02	4.24E+01	2.77E-02	3.53E-01	1.16E+00	0.22	1.16	3.99E+01	3.43E+01
Cstb	10	1.60E+02	2.58E+01	2.57E-03	3.13E-01	1.16E+00	0.22	1.16	2.49E+01	2.14E+01

Mapkapk5	5	1.35E+02	2.20E+01	1.74E-02	3.49E-01	1.16E+00	0.22	1.16	2.09E+01	1.80E+01
Ndufs7	10	1.02E+03	1.67E+02	1.78E-02	3.49E-01	1.16E+00	0.22	1.16	1.58E+02	1.36E+02
Papolg	11	4.52E+01	7.51E+00	3.94E-02	3.86E-01	1.16E+00	0.22	1.16	7.02E+00	6.04E+00
Ubr5	15	9.26E+02	1.55E+02	2.90E-02	3.57E-01	1.16E+00	0.22	1.16	1.44E+02	1.24E+02
Cdc26	4	1.30E+02	2.08E+01	2.03E-03	3.13E-01	1.16E+00	0.22	1.16	2.01E+01	1.73E+01
Pitpna	11	3.33E+02	5.37E+01	6.30E-03	3.33E-01	1.16E+00	0.21	1.16	5.17E+01	4.46E+01
Furin	7	6.82E+02	1.11E+02	4.78E-02	4.02E-01	1.16E+00	0.21	1.16	1.06E+02	9.11E+01
Serp1	3	9.34E+02	1.53E+02	3.40E-02	3.76E-01	1.16E+00	0.21	1.16	1.45E+02	1.25E+02
Ccdc32	2	6.97E+01	1.19E+01	4.39E-02	3.93E-01	1.16E+00	0.21	1.16	1.08E+01	9.32E+00
Nr1h2	7	2.96E+02	5.04E+01	3.45E-02	3.77E-01	1.16E+00	0.21	1.16	4.59E+01	3.96E+01
Mrm2	5	6.05E+01	9.78E+00	3.34E-02	3.72E-01	1.16E+00	0.21	1.16	9.38E+00	8.09E+00
Atf1	15	1.59E+02	2.59E+01	2.60E-02	3.52E-01	1.16E+00	0.21	1.16	2.46E+01	2.12E+01
Car4	11	1.39E+02	2.20E+01	4.58E-03	3.17E-01	1.16E+00	0.21	1.16	2.15E+01	1.86E+01
Smug1	15	9.74E+01	1.53E+01	3.20E-03	3.13E-01	1.16E+00	0.21	1.16	1.51E+01	1.30E+01
Gm4596	3	6.65E+01	1.10E+01	2.05E-02	3.52E-01	1.16E+00	0.21	1.16	1.03E+01	8.90E+00
Abce1	8	4.06E+02	6.46E+01	1.36E-02	3.36E-01	1.16E+00	0.21	1.16	6.29E+01	5.43E+01
Snrnp70	7	6.44E+02	1.06E+02	4.31E-02	3.92E-01	1.16E+00	0.21	1.16	9.97E+01	8.61E+01
Prxl2c	13	3.62E+02	5.68E+01	4.96E-02	4.03E-01	1.16E+00	0.21	1.16	5.60E+01	4.84E+01
Rnf111	9	1.61E+02	2.54E+01	1.95E-02	3.49E-01	1.16E+00	0.21	1.16	2.49E+01	2.16E+01
Zfp84	7	6.73E+01	1.06E+01	1.13E-03	3.13E-01	1.16E+00	0.21	1.16	1.04E+01	9.00E+00
Ovca2	11	1.04E+02	1.68E+01	4.66E-02	3.98E-01	1.16E+00	0.21	1.16	1.61E+01	1.39E+01
Ddx51	5	6.02E+01	1.02E+01	4.15E-02	3.90E-01	1.16E+00	0.21	1.16	9.32E+00	8.06E+00
Nipbl	15	3.33E+02	5.21E+01	4.23E-02	3.90E-01	1.16E+00	0.21	1.16	5.16E+01	4.46E+01
Osgep	14	1.38E+02	2.24E+01	2.96E-02	3.58E-01	1.16E+00	0.21	1.16	2.14E+01	1.85E+01
Strn4	7	2.58E+02	4.02E+01	2.21E-02	3.52E-01	1.16E+00	0.21	1.16	3.99E+01	3.45E+01
Ints13	6	1.68E+02	2.71E+01	1.70E-02	3.49E-01	1.16E+00	0.21	1.16	2.60E+01	2.25E+01
Rsbn1	3	1.24E+02	2.09E+01	4.65E-02	3.98E-01	1.15E+00	0.21	1.15	1.91E+01	1.66E+01
Rfx3	19	2.62E+01	4.26E+00	3.87E-02	3.86E-01	1.15E+00	0.21	1.15	4.06E+00	3.51E+00
Wapl	14	4.95E+02	8.12E+01	2.34E-02	3.52E-01	1.15E+00	0.21	1.15	7.65E+01	6.63E+01
Psmb3	11	3.38E+02	5.69E+01	4.60E-02	3.97E-01	1.15E+00	0.21	1.15	5.23E+01	4.53E+01
Zmiz2	11	3.09E+02	4.90E+01	4.53E-02	3.95E-01	1.15E+00	0.21	1.15	4.79E+01	4.15E+01

Ppp3r1	11	4.43E+02	7.16E+01	2.42E-02	3.52E-01	1.15E+00	0.21	1.15	6.85E+01	5.93E+01
Ythdf2	4	1.77E+02	2.81E+01	4.78E-02	4.02E-01	1.15E+00	0.21	1.15	2.74E+01	2.38E+01
Senp3	11	2.65E+02	4.41E+01	2.31E-02	3.52E-01	1.15E+00	0.21	1.15	4.10E+01	3.55E+01
Dr1	5	1.89E+02	3.06E+01	1.66E-02	3.46E-01	1.15E+00	0.21	1.15	2.92E+01	2.53E+01
Mynn	3	9.79E+01	1.58E+01	5.84E-03	3.33E-01	1.15E+00	0.21	1.15	1.51E+01	1.31E+01
Gm9531	9	1.71E+02	2.73E+01	1.94E-02	3.49E-01	1.15E+00	0.21	1.15	2.65E+01	2.30E+01
Oaz1	10	7.40E+02	1.18E+02	3.20E-03	3.13E-01	1.15E+00	0.21	1.15	1.14E+02	9.91E+01
Cdk12	11	1.78E+02	2.89E+01	3.29E-02	3.71E-01	1.15E+00	0.21	1.15	2.75E+01	2.39E+01
Mob4	1	2.62E+02	4.20E+01	4.03E-03	3.13E-01	1.15E+00	0.21	1.15	4.05E+01	3.51E+01
Tomm70a	16	6.57E+02	1.05E+02	3.06E-02	3.61E-01	1.15E+00	0.20	1.15	1.02E+02	8.81E+01
1810037117Rik	3	1.67E+02	2.70E+01	1.84E-02	3.49E-01	1.15E+00	0.20	1.15	2.58E+01	2.24E+01
Ranbp3	17	1.61E+02	2.64E+01	3.26E-02	3.70E-01	1.15E+00	0.20	1.15	2.49E+01	2.16E+01
Cox6c	15	2.70E+03	4.44E+02	4.06E-02	3.87E-01	1.15E+00	0.20	1.15	4.17E+02	3.62E+02
Znfx1	2	4.36E+02	7.20E+01	9.00E-03	3.33E-01	1.15E+00	0.20	1.15	6.74E+01	5.85E+01
Trmt1	8	1.22E+02	1.97E+01	4.94E-02	4.03E-01	1.15E+00	0.20	1.15	1.89E+01	1.64E+01
Cox5a	9	2.46E+03	3.93E+02	9.96E-03	3.33E-01	1.15E+00	0.20	1.15	3.81E+02	3.31E+02
Eya3	4	1.50E+02	2.47E+01	1.21E-02	3.33E-01	1.15E+00	0.20	1.15	2.32E+01	2.01E+01
Sra1	18	1.59E+02	2.64E+01	4.30E-02	3.92E-01	1.15E+00	0.20	1.15	2.45E+01	2.13E+01
Ftsj1	X	7.44E+01	1.18E+01	1.47E-02	3.40E-01	1.15E+00	0.20	1.15	1.15E+01	9.98E+00
Pno1	11	1.89E+02	3.02E+01	4.09E-04	3.13E-01	1.15E+00	0.20	1.15	2.92E+01	2.54E+01
Ube2d3	3	1.21E+03	1.94E+02	2.11E-02	3.52E-01	1.15E+00	0.20	1.15	1.87E+02	1.63E+02
Orc4	2	1.26E+02	2.04E+01	3.86E-02	3.85E-01	1.15E+00	0.20	1.15	1.95E+01	1.70E+01
Ctbp1	5	5.33E+02	8.42E+01	6.56E-03	3.33E-01	1.15E+00	0.20	1.15	8.23E+01	7.16E+01
Nsd3	8	2.34E+02	3.67E+01	6.41E-03	3.33E-01	1.15E+00	0.20	1.15	3.61E+01	3.14E+01
Gm4459	7	7.31E+02	1.22E+02	4.75E-02	4.02E-01	1.15E+00	0.20	1.15	1.13E+02	9.82E+01
Tank	2	2.27E+02	3.66E+01	4.46E-02	3.95E-01	1.15E+00	0.20	1.15	3.50E+01	3.05E+01
Cnih1	14	3.80E+02	6.04E+01	9.46E-03	3.33E-01	1.15E+00	0.20	1.15	5.86E+01	5.11E+01
Edrf1	7	9.43E+01	1.53E+01	2.82E-02	3.54E-01	1.15E+00	0.20	1.15	1.45E+01	1.27E+01
Zc3h7a	16	1.76E+02	2.90E+01	3.17E-02	3.66E-01	1.15E+00	0.20	1.15	2.72E+01	2.37E+01
Mfsd14b	13	2.11E+02	3.43E+01	7.07E-03	3.33E-01	1.15E+00	0.20	1.15	3.26E+01	2.84E+01
Upf3b	X	7.97E+01	1.28E+01	3.35E-02	3.73E-01	1.15E+00	0.20	1.15	1.23E+01	1.07E+01

Pias2	18	1.61E+02	2.53E+01	3.12E-02	3.64E-01	1.15E+00	0.20	1.15	2.48E+01	2.16E+01
Tmed4	11	3.46E+02	5.58E+01	3.43E-02	3.77E-01	1.15E+00	0.20	1.15	5.33E+01	4.65E+01
Ppp1cc	5	2.19E+02	3.54E+01	1.92E-02	3.49E-01	1.15E+00	0.20	1.15	3.38E+01	2.95E+01
Chtop	3	3.67E+02	5.77E+01	2.82E-03	3.13E-01	1.15E+00	0.20	1.15	5.65E+01	4.93E+01
Prpf39	12	2.25E+02	3.53E+01	1.75E-02	3.49E-01	1.15E+00	0.20	1.15	3.47E+01	3.03E+01
Ndfip2	14	1.56E+02	2.52E+01	3.25E-02	3.69E-01	1.14E+00	0.19	1.14	2.40E+01	2.10E+01
Cxadr	16	4.96E+02	8.04E+01	4.87E-02	4.02E-01	1.14E+00	0.19	1.14	7.63E+01	6.67E+01
Scap	9	2.54E+02	4.05E+01	2.96E-02	3.58E-01	1.14E+00	0.19	1.14	3.90E+01	3.41E+01
Cflar	1	5.72E+02	9.01E+01	3.70E-04	3.13E-01	1.14E+00	0.19	1.14	8.80E+01	7.70E+01
Anapc11	11	7.95E+01	1.27E+01	3.57E-03	3.13E-01	1.14E+00	0.19	1.14	1.22E+01	1.07E+01
1810009A15Rik	19	5.58E+01	9.33E+00	1.91E-02	3.49E-01	1.14E+00	0.19	1.14	8.59E+00	7.52E+00
Esf1	2	7.89E+01	1.25E+01	1.53E-02	3.40E-01	1.14E+00	0.19	1.14	1.21E+01	1.06E+01
Tor2a	2	1.12E+02	1.89E+01	4.61E-02	3.97E-01	1.14E+00	0.19	1.14	1.72E+01	1.51E+01
Fkbp8	8	5.23E+02	8.50E+01	2.28E-02	3.52E-01	1.14E+00	0.19	1.14	8.04E+01	7.04E+01
Ccdc186	19	1.35E+02	2.19E+01	4.84E-02	4.02E-01	1.14E+00	0.19	1.14	2.08E+01	1.82E+01
Eny2	15	1.84E+02	3.04E+01	3.99E-02	3.86E-01	1.14E+00	0.19	1.14	2.84E+01	2.48E+01
Ubl3	5	5.74E+02	9.19E+01	3.18E-02	3.66E-01	1.14E+00	0.19	1.14	8.82E+01	7.73E+01
Gm7535	17	2.45E+01	3.86E+00	4.14E-03	3.14E-01	1.14E+00	0.19	1.14	3.76E+00	3.30E+00
Eif6	2	1.43E+02	2.30E+01	1.64E-02	3.46E-01	1.14E+00	0.19	1.14	2.20E+01	1.93E+01
Slc39a7	17	3.68E+02	5.89E+01	1.91E-02	3.49E-01	1.14E+00	0.19	1.14	5.66E+01	4.96E+01
Rabl6	2	3.41E+02	5.40E+01	1.82E-02	3.49E-01	1.14E+00	0.19	1.14	5.24E+01	4.59E+01
Kmt5b	19	2.72E+02	4.25E+01	2.27E-02	3.52E-01	1.14E+00	0.19	1.14	4.18E+01	3.67E+01
Psme3	11	4.35E+02	6.86E+01	2.96E-03	3.13E-01	1.14E+00	0.19	1.14	6.68E+01	5.86E+01
Nol11	11	1.01E+02	1.66E+01	4.76E-02	4.02E-01	1.14E+00	0.19	1.14	1.56E+01	1.37E+01
Wdr45b	11	2.07E+02	3.28E+01	2.42E-02	3.52E-01	1.14E+00	0.19	1.14	3.18E+01	2.79E+01
Wdr34	2	4.84E+01	8.00E+00	4.51E-02	3.95E-01	1.14E+00	0.19	1.14	7.44E+00	6.53E+00
Gabpb1	2	4.70E+01	7.45E+00	3.85E-03	3.13E-01	1.14E+00	0.19	1.14	7.22E+00	6.33E+00
Smad4	18	2.01E+02	3.25E+01	3.70E-02	3.82E-01	1.14E+00	0.19	1.14	3.08E+01	2.71E+01
Psmb1	17	4.28E+02	6.67E+01	3.02E-03	3.13E-01	1.14E+00	0.19	1.14	6.57E+01	5.78E+01
Frs2	10	2.02E+02	3.39E+01	4.39E-02	3.93E-01	1.14E+00	0.19	1.14	3.09E+01	2.72E+01
Erap1	13	2.56E+02	4.24E+01	4.07E-02	3.87E-01	1.14E+00	0.19	1.14	3.92E+01	3.45E+01

Rps24	14	6.40E+02	1.01E+02	4.77E-02	4.02E-01	1.14E+00	0.19	1.14	9.82E+01	8.63E+01
Tmx3	18	2.44E+02	4.13E+01	4.83E-02	4.02E-01	1.14E+00	0.18	1.14	3.75E+01	3.30E+01
Ssr1	13	3.74E+02	5.94E+01	1.19E-02	3.33E-01	1.14E+00	0.18	1.14	5.74E+01	5.05E+01
Brpf3	17	2.48E+02	3.86E+01	1.31E-03	3.13E-01	1.14E+00	0.18	1.14	3.81E+01	3.35E+01
Atrx	X	4.46E+02	7.43E+01	4.94E-02	4.03E-01	1.14E+00	0.18	1.14	6.84E+01	6.02E+01
Il6st	13	9.12E+02	1.46E+02	8.91E-03	3.33E-01	1.13E+00	0.18	1.13	1.40E+02	1.23E+02
Rpl22	4	3.29E+02	5.26E+01	1.36E-02	3.36E-01	1.13E+00	0.18	1.13	5.04E+01	4.44E+01
Eif3b	5	5.78E+02	8.91E+01	7.15E-03	3.33E-01	1.13E+00	0.18	1.13	8.86E+01	7.81E+01
Gtf3c6	10	1.19E+02	1.96E+01	3.96E-02	3.86E-01	1.13E+00	0.18	1.13	1.83E+01	1.61E+01
Bnip2	9	4.14E+02	6.62E+01	9.39E-03	3.33E-01	1.13E+00	0.18	1.13	6.35E+01	5.60E+01
Brf1	12	1.18E+02	1.90E+01	3.56E-02	3.80E-01	1.13E+00	0.18	1.13	1.81E+01	1.60E+01
Calu	6	1.17E+03	1.86E+02	1.73E-02	3.49E-01	1.13E+00	0.18	1.13	1.79E+02	1.58E+02
Tm9sf1	14	2.49E+02	4.06E+01	1.92E-02	3.49E-01	1.13E+00	0.18	1.13	3.82E+01	3.37E+01
Rad54l2	9	2.20E+02	3.47E+01	3.47E-02	3.77E-01	1.13E+00	0.18	1.13	3.36E+01	2.97E+01
Dmxl2	9	1.02E+02	1.67E+01	4.07E-02	3.87E-01	1.13E+00	0.18	1.13	1.55E+01	1.37E+01
Cog8	8	1.50E+02	2.39E+01	3.18E-02	3.66E-01	1.13E+00	0.18	1.13	2.29E+01	2.03E+01
Axin1	17	1.62E+02	2.58E+01	4.84E-02	4.02E-01	1.13E+00	0.18	1.13	2.48E+01	2.20E+01
Ddx6	9	8.77E+02	1.35E+02	4.75E-03	3.17E-01	1.13E+00	0.18	1.13	1.34E+02	1.19E+02
Ubqln1	13	8.50E+02	1.37E+02	1.69E-02	3.49E-01	1.13E+00	0.18	1.13	1.30E+02	1.15E+02
Dhx16	17	1.35E+02	2.08E+01	8.20E-03	3.33E-01	1.13E+00	0.17	1.13	2.07E+01	1.83E+01
Ss18	18	2.71E+02	4.41E+01	2.57E-02	3.52E-01	1.13E+00	0.17	1.13	4.14E+01	3.67E+01
Usp45	4	1.54E+02	2.44E+01	3.01E-03	3.13E-01	1.13E+00	0.17	1.13	2.35E+01	2.08E+01
G3bp1	11	3.65E+02	5.76E+01	6.26E-03	3.33E-01	1.13E+00	0.17	1.13	5.58E+01	4.95E+01
Mff	1	5.33E+02	8.50E+01	4.13E-02	3.90E-01	1.13E+00	0.17	1.13	8.15E+01	7.22E+01
Dalrd3	9	1.69E+02	2.61E+01	4.79E-02	4.02E-01	1.13E+00	0.17	1.13	2.58E+01	2.29E+01
Pogz	3	1.30E+02	2.07E+01	1.88E-02	3.49E-01	1.13E+00	0.17	1.13	1.99E+01	1.76E+01
Arl6ip5	6	1.66E+02	2.65E+01	2.58E-02	3.52E-01	1.13E+00	0.17	1.13	2.54E+01	2.25E+01
Serbp1	6	7.91E+02	1.28E+02	2.58E-02	3.52E-01	1.13E+00	0.17	1.13	1.21E+02	1.07E+02
Ndufb3	1	1.04E+03	1.60E+02	2.99E-03	3.13E-01	1.13E+00	0.17	1.13	1.58E+02	1.40E+02
Suz12	11	2.71E+02	4.27E+01	1.97E-02	3.49E-01	1.13E+00	0.17	1.13	4.14E+01	3.68E+01
Kmt2b	7	2.65E+02	4.37E+01	3.09E-02	3.63E-01	1.13E+00	0.17	1.13	4.05E+01	3.60E+01

Hdhd5	6	1.29E+02	2.04E+01	1.22E-02	3.33E-01	1.13E+00	0.17	1.13	1.97E+01	1.75E+01
Pafah1b2	9	3.36E+02	5.53E+01	3.20E-02	3.66E-01	1.13E+00	0.17	1.13	5.12E+01	4.55E+01
Braf	6	2.22E+02	3.51E+01	1.10E-02	3.33E-01	1.12E+00	0.17	1.12	3.39E+01	3.01E+01
Casp8ap2	4	7.16E+01	1.12E+01	3.30E-02	3.71E-01	1.12E+00	0.17	1.12	1.09E+01	9.71E+00
Gcdh	8	3.78E+02	6.12E+01	4.23E-02	3.90E-01	1.12E+00	0.17	1.12	5.76E+01	5.13E+01
Uap1	1	4.00E+02	6.52E+01	3.34E-02	3.72E-01	1.12E+00	0.17	1.12	6.10E+01	5.43E+01
Phc3	3	2.26E+02	3.54E+01	1.16E-02	3.33E-01	1.12E+00	0.17	1.12	3.45E+01	3.07E+01
Syncrip	9	4.69E+02	7.45E+01	2.69E-02	3.52E-01	1.12E+00	0.17	1.12	7.15E+01	6.36E+01
Usp1	4	1.42E+02	2.20E+01	5.10E-03	3.27E-01	1.12E+00	0.17	1.12	2.17E+01	1.93E+01
Rab11a	9	3.68E+02	5.62E+01	7.93E-03	3.33E-01	1.12E+00	0.17	1.12	5.60E+01	4.99E+01
Tmem234	4	3.39E+02	5.21E+01	1.10E-02	3.33E-01	1.12E+00	0.17	1.12	5.17E+01	4.60E+01
Tbl1xr1	3	2.23E+02	3.44E+01	2.12E-02	3.52E-01	1.12E+00	0.17	1.12	3.40E+01	3.03E+01
Prrc2c	1	5.07E+02	8.01E+01	1.40E-02	3.36E-01	1.12E+00	0.16	1.12	7.72E+01	6.89E+01
Naa10	X	1.50E+02	2.37E+01	7.68E-03	3.33E-01	1.12E+00	0.16	1.12	2.28E+01	2.04E+01
Pde1a	2	1.89E+02	3.11E+01	3.23E-02	3.68E-01	1.12E+00	0.16	1.12	2.88E+01	2.57E+01
Pip5k1a	3	1.39E+02	2.28E+01	4.20E-02	3.90E-01	1.12E+00	0.16	1.12	2.12E+01	1.89E+01
Oaz1-ps	17	8.30E+02	1.31E+02	3.77E-02	3.83E-01	1.12E+00	0.16	1.12	1.26E+02	1.13E+02
Tmem126a	7	1.47E+02	2.33E+01	4.92E-02	4.03E-01	1.12E+00	0.16	1.12	2.24E+01	2.00E+01
Tmem246	4	1.89E+02	2.93E+01	2.74E-02	3.52E-01	1.12E+00	0.16	1.12	2.87E+01	2.57E+01
Akap10	11	1.53E+02	2.39E+01	9.16E-03	3.33E-01	1.12E+00	0.16	1.12	2.32E+01	2.08E+01
U2surp	9	3.13E+02	4.95E+01	2.84E-02	3.55E-01	1.12E+00	0.16	1.12	4.75E+01	4.26E+01
Prdx5	19	1.15E+03	1.81E+02	8.65E-03	3.33E-01	1.12E+00	0.16	1.12	1.75E+02	1.57E+02
Usp7	16	4.21E+02	6.70E+01	4.55E-02	3.95E-01	1.12E+00	0.16	1.12	6.39E+01	5.73E+01
Erg28	12	4.76E+01	7.72E+00	3.62E-02	3.80E-01	1.11E+00	0.16	1.11	7.22E+00	6.48E+00
Asb6	2	5.82E+01	8.94E+00	4.03E-02	3.87E-01	1.11E+00	0.16	1.11	8.83E+00	7.92E+00
Rasal2	1	1.28E+02	2.05E+01	3.29E-02	3.71E-01	1.11E+00	0.16	1.11	1.94E+01	1.74E+01
Cisd1	10	7.74E+02	1.21E+02	2.27E-02	3.52E-01	1.11E+00	0.15	1.11	1.17E+02	1.05E+02
Daxx	17	9.05E+01	1.44E+01	4.01E-02	3.87E-01	1.11E+00	0.15	1.11	1.37E+01	1.23E+01
Otud7b	3	2.07E+02	3.18E+01	1.03E-02	3.33E-01	1.11E+00	0.15	1.11	3.13E+01	2.82E+01
Chp1	2	2.42E+03	3.72E+02	7.07E-03	3.33E-01	1.11E+00	0.15	1.11	3.67E+02	3.30E+02
Zfp706	15	3.67E+02	5.65E+01	4.71E-02	4.01E-01	1.11E+00	0.15	1.11	5.57E+01	5.01E+01

9530068E07Rik	11	5.12E+02	7.79E+01	2.44E-02	3.52E-01	1.11E+00	0.15	1.11	7.76E+01	6.98E+01
Ube2r2	4	4.04E+02	6.36E+01	1.11E-02	3.33E-01	1.11E+00	0.15	1.11	6.12E+01	5.50E+01
Pttg1ip	10	7.93E+02	1.27E+02	2.79E-02	3.53E-01	1.11E+00	0.15	1.11	1.20E+02	1.08E+02
Capza1	3	4.38E+02	6.90E+01	2.74E-02	3.52E-01	1.11E+00	0.15	1.11	6.63E+01	5.98E+01
Cherp	8	1.74E+02	2.74E+01	7.81E-03	3.33E-01	1.11E+00	0.15	1.11	2.63E+01	2.37E+01
Mea1	17	2.03E+02	3.08E+01	1.98E-02	3.49E-01	1.11E+00	0.15	1.11	3.08E+01	2.78E+01
Nono	X	4.19E+02	6.58E+01	2.64E-02	3.52E-01	1.11E+00	0.15	1.11	6.33E+01	5.72E+01
Gpank1	17	3.82E+01	5.97E+00	1.03E-02	3.33E-01	1.11E+00	0.15	1.11	5.77E+00	5.21E+00
Dnajc14	10	3.81E+02	6.05E+01	1.30E-02	3.33E-01	1.11E+00	0.15	1.11	5.76E+01	5.21E+01
Eef2	10	6.05E+03	9.32E+02	1.31E-02	3.33E-01	1.10E+00	0.14	1.10	9.14E+02	8.27E+02
Lnpep	17	8.23E+02	1.28E+02	1.75E-02	3.49E-01	1.10E+00	0.14	1.10	1.24E+02	1.13E+02
Kmt2e	5	4.66E+02	7.08E+01	3.68E-02	3.82E-01	1.10E+00	0.14	1.10	7.03E+01	6.37E+01
Qsox2	2	7.01E+01	1.08E+01	3.96E-02	3.86E-01	1.10E+00	0.14	1.10	1.06E+01	9.59E+00
Ube3a	7	6.07E+02	9.55E+01	3.99E-02	3.86E-01	1.10E+00	0.14	1.10	9.17E+01	8.30E+01
Wdr36	18	1.51E+02	2.36E+01	4.62E-02	3.97E-01	1.10E+00	0.14	1.10	2.27E+01	2.06E+01
Ncaph2	15	3.01E+02	4.82E+01	3.98E-02	3.86E-01	1.10E+00	0.14	1.10	4.55E+01	4.12E+01
Snrpd3	10	1.74E+02	2.71E+01	2.95E-02	3.58E-01	1.10E+00	0.14	1.10	2.63E+01	2.38E+01
Git2	5	2.14E+02	3.43E+01	1.83E-02	3.49E-01	1.10E+00	0.14	1.10	3.23E+01	2.93E+01
Nop14	5	1.06E+02	1.66E+01	1.19E-02	3.33E-01	1.10E+00	0.14	1.10	1.59E+01	1.45E+01
Mapk1	16	6.67E+02	1.04E+02	1.17E-02	3.33E-01	1.10E+00	0.14	1.10	1.01E+02	9.14E+01
Selenop	15	3.27E+03	4.98E+02	9.67E-03	3.33E-01	1.10E+00	0.14	1.10	4.93E+02	4.48E+02
Chmp4b	2	4.75E+02	7.37E+01	2.00E-02	3.50E-01	1.10E+00	0.14	1.10	7.15E+01	6.51E+01
Polr2c	8	1.06E+02	1.66E+01	1.67E-02	3.46E-01	1.10E+00	0.14	1.10	1.60E+01	1.45E+01
Taf3	2	6.51E+01	1.02E+01	3.83E-02	3.83E-01	1.10E+00	0.14	1.10	9.80E+00	8.92E+00
Mrpl14	17	1.26E+02	1.95E+01	9.66E-03	3.33E-01	1.10E+00	0.14	1.10	1.89E+01	1.72E+01
Rhot1	11	3.98E+02	6.16E+01	2.40E-02	3.52E-01	1.10E+00	0.13	1.10	5.99E+01	5.46E+01
Ranbp9	13	3.38E+02	5.17E+01	1.32E-02	3.35E-01	1.10E+00	0.13	1.10	5.08E+01	4.63E+01
Pex5	6	8.09E+02	1.23E+02	2.80E-03	3.13E-01	1.10E+00	0.13	1.10	1.22E+02	1.11E+02
Mrps28	3	1.28E+02	1.98E+01	1.06E-02	3.33E-01	1.10E+00	0.13	1.10	1.93E+01	1.76E+01
Arhgap21	2	3.67E+02	5.59E+01	6.07E-03	3.33E-01	1.10E+00	0.13	1.10	5.52E+01	5.04E+01
Hnrnpul2	19	6.78E+02	1.05E+02	4.32E-02	3.92E-01	1.09E+00	0.13	1.09	1.02E+02	9.32E+01

Lztr1	16	2.80E+02	4.24E+01	3.71E-02	3.82E-01	1.09E+00	0.13	1.09	4.20E+01	3.84E+01
Csnk1d	11	4.77E+02	7.47E+01	2.31E-02	3.52E-01	1.09E+00	0.13	1.09	7.16E+01	6.55E+01
Triap1	5	1.32E+02	2.03E+01	3.63E-02	3.80E-01	1.09E+00	0.13	1.09	1.97E+01	1.81E+01
Usp47	7	5.37E+02	8.26E+01	2.50E-02	3.52E-01	1.09E+00	0.12	1.09	8.06E+01	7.39E+01
Tmem185a	X	1.63E+02	2.58E+01	4.86E-02	4.02E-01	1.09E+00	0.12	1.09	2.44E+01	2.24E+01
Nemf	12	2.20E+02	3.43E+01	1.07E-02	3.33E-01	1.09E+00	0.12	1.09	3.30E+01	3.03E+01
Mob2	7	1.64E+02	2.58E+01	1.94E-02	3.49E-01	1.09E+00	0.12	1.09	2.45E+01	2.25E+01
Zbtb41	1	2.33E+02	3.67E+01	4.47E-02	3.95E-01	1.09E+00	0.12	1.09	3.49E+01	3.21E+01
Hdac2	10	2.95E+02	4.49E+01	4.92E-02	4.03E-01	1.09E+00	0.12	1.09	4.42E+01	4.07E+01
Nlk	11	1.38E+02	2.11E+01	1.76E-02	3.49E-01	1.09E+00	0.12	1.09	2.07E+01	1.91E+01
Preb	5	3.67E+02	5.55E+01	2.58E-02	3.52E-01	1.09E+00	0.12	1.09	5.49E+01	5.06E+01
Naa15	3	3.41E+02	5.24E+01	1.40E-02	3.36E-01	1.09E+00	0.12	1.09	5.10E+01	4.69E+01
Ppp1ccb	7	2.11E+02	3.22E+01	2.12E-02	3.52E-01	1.09E+00	0.12	1.09	3.15E+01	2.91E+01
Kif5b	18	6.67E+02	1.02E+02	4.91E-02	4.03E-01	1.09E+00	0.12	1.09	9.98E+01	9.19E+01
Rab11b	17	4.78E+02	7.26E+01	1.86E-02	3.49E-01	1.08E+00	0.12	1.08	7.14E+01	6.58E+01
Tmem115	9	1.22E+02	1.86E+01	1.14E-02	3.33E-01	1.08E+00	0.12	1.08	1.83E+01	1.69E+01
Atp1b3	9	8.71E+02	1.33E+02	4.03E-02	3.87E-01	1.08E+00	0.12	1.08	1.30E+02	1.20E+02
Gpbp1l1	4	4.60E+02	7.24E+01	2.54E-02	3.52E-01	1.08E+00	0.12	1.08	6.87E+01	6.34E+01
Mycbp	4	1.35E+02	2.11E+01	3.82E-02	3.83E-01	1.08E+00	0.12	1.08	2.01E+01	1.86E+01
Nudt3	17	3.34E+02	5.16E+01	1.83E-02	3.49E-01	1.08E+00	0.12	1.08	4.99E+01	4.61E+01
Mtdh	15	4.68E+02	7.13E+01	2.64E-02	3.52E-01	1.08E+00	0.11	1.08	7.00E+01	6.46E+01
Klhl12	1	1.34E+02	2.02E+01	4.47E-02	3.95E-01	1.08E+00	0.11	1.08	2.00E+01	1.85E+01
Bms1	6	1.47E+02	2.26E+01	3.56E-02	3.80E-01	1.08E+00	0.11	1.08	2.19E+01	2.03E+01
Ostm1	10	1.25E+02	1.94E+01	4.51E-02	3.95E-01	1.08E+00	0.11	1.08	1.87E+01	1.73E+01
Glr3	7	2.38E+02	3.67E+01	1.81E-02	3.49E-01	1.08E+00	0.11	1.08	3.56E+01	3.29E+01
Gm20716	2	5.69E+02	8.63E+01	1.99E-02	3.50E-01	1.08E+00	0.11	1.08	8.48E+01	7.86E+01
Utp15	13	6.12E+01	9.30E+00	3.41E-02	3.76E-01	1.08E+00	0.11	1.08	9.12E+00	8.45E+00
Rprd1b	2	1.53E+02	2.32E+01	2.57E-02	3.52E-01	1.08E+00	0.11	1.08	2.27E+01	2.11E+01
Gapvd1	2	2.81E+02	4.37E+01	1.21E-02	3.33E-01	1.08E+00	0.11	1.08	4.18E+01	3.89E+01
Pafah1b1	11	9.07E+02	1.42E+02	4.28E-02	3.92E-01	1.08E+00	0.11	1.08	1.35E+02	1.26E+02
Higd2a	13	3.85E+02	5.87E+01	1.07E-02	3.33E-01	1.07E+00	0.10	1.07	5.73E+01	5.33E+01

Ddx19a	8	1.38E+02	2.15E+01	4.93E-02	4.03E-01	1.07E+00	0.10	1.07	2.05E+01	1.91E+01
Efr3a	15	3.25E+02	4.96E+01	1.30E-02	3.33E-01	1.07E+00	0.10	1.07	4.82E+01	4.50E+01
Kctd20	17	3.24E+02	4.96E+01	3.70E-02	3.82E-01	1.07E+00	0.09	1.07	4.81E+01	4.50E+01
Sec23ip	7	1.34E+02	2.06E+01	2.74E-02	3.52E-01	1.07E+00	0.09	1.07	1.99E+01	1.87E+01
Zc3h13	14	1.59E+02	2.39E+01	4.48E-03	3.17E-01	1.06E+00	0.09	1.06	2.34E+01	2.21E+01
Slc25a19	11	1.99E+03	2.95E+02	8.89E-03	3.33E-01	1.06E+00	0.09	1.06	2.94E+02	2.77E+02
Nsd1	13	6.37E+02	9.52E+01	2.92E-02	3.58E-01	1.05E+00	0.07	1.05	9.36E+01	8.91E+01
Slc36a2	11	3.62E+03	5.41E+02	2.21E-02	3.52E-01	1.05E+00	0.06	1.05	5.31E+02	5.07E+02
Uqcc1	2	9.34E+02	1.40E+02	2.53E-02	3.52E-01	9.54E-01	-0.07	-1.05	1.30E+02	1.36E+02
Csnk2a3	1	4.47E+02	6.75E+01	1.66E-02	3.46E-01	9.37E-01	-0.09	-1.07	6.14E+01	6.56E+01
Nmt1	11	5.48E+02	8.18E+01	2.57E-02	3.52E-01	9.33E-01	-0.10	-1.07	7.52E+01	8.06E+01
Ubl7	9	1.88E+02	2.88E+01	3.43E-02	3.77E-01	9.33E-01	-0.10	-1.07	2.58E+01	2.77E+01
Mrpl50	4	5.66E+02	8.72E+01	4.47E-02	3.95E-01	9.32E-01	-0.10	-1.07	7.75E+01	8.32E+01
Degs1	1	2.77E+02	4.17E+01	4.53E-02	3.95E-01	9.31E-01	-0.10	-1.07	3.79E+01	4.08E+01
Nap1l4	7	6.97E+02	1.07E+02	2.64E-02	3.52E-01	9.24E-01	-0.11	-1.08	9.51E+01	1.03E+02
Nckap1	2	1.03E+03	1.58E+02	2.29E-02	3.52E-01	9.24E-01	-0.11	-1.08	1.40E+02	1.52E+02
Acad10	5	3.03E+02	4.56E+01	7.67E-04	3.13E-01	9.24E-01	-0.11	-1.08	4.13E+01	4.47E+01
Gm10093	17	1.35E+02	2.08E+01	2.62E-02	3.52E-01	9.22E-01	-0.12	-1.08	1.84E+01	1.99E+01
Chmp5	4	2.76E+02	4.19E+01	1.04E-02	3.33E-01	9.22E-01	-0.12	-1.08	3.77E+01	4.09E+01
Pmpca	2	8.25E+02	1.24E+02	7.66E-04	3.13E-01	9.21E-01	-0.12	-1.09	1.12E+02	1.22E+02
Nudc-ps1	8	3.96E+01	6.07E+00	3.32E-02	3.72E-01	9.20E-01	-0.12	-1.09	5.39E+00	5.85E+00
Dennd5a	7	1.21E+03	1.88E+02	3.99E-02	3.86E-01	9.18E-01	-0.12	-1.09	1.65E+02	1.80E+02
Sdha	13	1.58E+04	2.40E+03	1.62E-02	3.44E-01	9.17E-01	-0.12	-1.09	2.15E+03	2.35E+03
Rere	4	8.36E+02	1.27E+02	1.30E-02	3.33E-01	9.17E-01	-0.12	-1.09	1.14E+02	1.24E+02
Ndufs1	1	4.20E+03	6.46E+02	3.35E-02	3.73E-01	9.16E-01	-0.13	-1.09	5.70E+02	6.23E+02
Sugp1	8	9.20E+01	1.41E+01	3.78E-03	3.13E-01	9.16E-01	-0.13	-1.09	1.25E+01	1.36E+01
Ptgr2	12	1.87E+03	2.90E+02	1.11E-02	3.33E-01	9.13E-01	-0.13	-1.09	2.53E+02	2.77E+02
Nol6	4	2.60E+02	4.05E+01	2.69E-02	3.52E-01	9.13E-01	-0.13	-1.10	3.52E+01	3.85E+01
Ess2	16	6.69E+01	1.06E+01	3.28E-02	3.71E-01	9.13E-01	-0.13	-1.10	9.06E+00	9.92E+00
Trim26	17	1.81E+02	2.87E+01	3.56E-02	3.80E-01	9.13E-01	-0.13	-1.10	2.45E+01	2.68E+01
Memo1	17	2.69E+02	4.18E+01	8.07E-03	3.33E-01	9.12E-01	-0.13	-1.10	3.64E+01	3.99E+01

Gmfb	14	6.85E+02	1.05E+02	4.74E-02	4.02E-01	9.09E-01	-0.14	-1.10	9.25E+01	1.02E+02
Dhodh	8	1.15E+02	1.82E+01	1.55E-02	3.40E-01	9.08E-01	-0.14	-1.10	1.56E+01	1.71E+01
Poc1a	9	2.70E+01	4.15E+00	7.11E-03	3.33E-01	9.08E-01	-0.14	-1.10	3.65E+00	4.02E+00
Nfe2l1	11	3.75E+03	5.83E+02	2.52E-02	3.52E-01	9.06E-01	-0.14	-1.10	5.06E+02	5.59E+02
Fbxw5	2	4.69E+02	7.26E+01	2.25E-02	3.52E-01	9.04E-01	-0.15	-1.11	6.32E+01	6.99E+01
Arl8a	1	1.37E+02	2.11E+01	3.77E-02	3.83E-01	9.03E-01	-0.15	-1.11	1.85E+01	2.05E+01
Plcg1	2	4.76E+02	7.56E+01	1.24E-02	3.33E-01	9.02E-01	-0.15	-1.11	6.40E+01	7.09E+01
Sirt3	7	3.56E+02	5.45E+01	7.56E-03	3.33E-01	9.01E-01	-0.15	-1.11	4.78E+01	5.31E+01
Gga2	7	3.05E+02	4.71E+01	8.04E-03	3.33E-01	9.01E-01	-0.15	-1.11	4.10E+01	4.55E+01
Fbxl4	4	1.37E+02	2.18E+01	4.03E-02	3.87E-01	8.99E-01	-0.15	-1.11	1.84E+01	2.04E+01
Lrrc40	3	7.03E+01	1.10E+01	3.60E-02	3.80E-01	8.99E-01	-0.15	-1.11	9.44E+00	1.05E+01
Zfp398	6	7.84E+01	1.19E+01	8.73E-03	3.33E-01	8.98E-01	-0.15	-1.11	1.05E+01	1.17E+01
Rfc2	5	6.42E+01	9.94E+00	1.45E-02	3.38E-01	8.97E-01	-0.16	-1.11	8.61E+00	9.60E+00
Ip6k2	9	6.54E+01	1.00E+01	1.16E-03	3.13E-01	8.96E-01	-0.16	-1.12	8.77E+00	9.79E+00
Ldlrap1	4	1.94E+02	3.02E+01	2.40E-02	3.52E-01	8.95E-01	-0.16	-1.12	2.59E+01	2.90E+01
Eif2ak3	6	9.38E+01	1.48E+01	2.40E-02	3.52E-01	8.95E-01	-0.16	-1.12	1.26E+01	1.40E+01
Prorp	12	9.40E+01	1.45E+01	3.34E-02	3.72E-01	8.94E-01	-0.16	-1.12	1.26E+01	1.41E+01
Atg10	13	1.13E+02	1.77E+01	1.85E-02	3.49E-01	8.92E-01	-0.17	-1.12	1.51E+01	1.70E+01
Fam45a	19	1.25E+02	1.91E+01	2.51E-03	3.13E-01	8.91E-01	-0.17	-1.12	1.67E+01	1.88E+01
Nudcd3	11	3.49E+02	5.59E+01	1.39E-02	3.36E-01	8.90E-01	-0.17	-1.12	4.65E+01	5.23E+01
Iqsec1	6	1.04E+03	1.64E+02	4.31E-02	3.92E-01	8.90E-01	-0.17	-1.12	1.39E+02	1.56E+02
Lap3	5	4.90E+02	7.67E+01	4.18E-03	3.14E-01	8.89E-01	-0.17	-1.12	6.53E+01	7.35E+01
Acsf2	11	6.43E+02	1.02E+02	2.70E-02	3.52E-01	8.88E-01	-0.17	-1.13	8.57E+01	9.65E+01
Coa5	1	2.83E+03	4.40E+02	2.51E-02	3.52E-01	8.87E-01	-0.17	-1.13	3.77E+02	4.25E+02
Akt2-ps	11	5.15E+02	8.00E+01	2.32E-02	3.52E-01	8.86E-01	-0.17	-1.13	6.86E+01	7.74E+01
Phf20	2	1.55E+02	2.45E+01	3.16E-02	3.66E-01	8.85E-01	-0.18	-1.13	2.06E+01	2.32E+01
Pef1	4	2.94E+02	4.69E+01	1.55E-02	3.40E-01	8.85E-01	-0.18	-1.13	3.91E+01	4.42E+01
Clip1	5	3.39E+02	5.31E+01	6.81E-03	3.33E-01	8.85E-01	-0.18	-1.13	4.51E+01	5.10E+01
Cog4	8	5.33E+02	8.23E+01	2.37E-02	3.52E-01	8.85E-01	-0.18	-1.13	7.09E+01	8.01E+01
Acaa2	18	9.69E+03	1.53E+03	2.13E-02	3.52E-01	8.84E-01	-0.18	-1.13	1.29E+03	1.46E+03
Hddc3	7	6.20E+01	9.79E+00	2.45E-02	3.52E-01	8.83E-01	-0.18	-1.13	8.23E+00	9.32E+00

Eef1akmt2	7	5.24E+01	8.34E+00	1.17E-02	3.33E-01	8.80E-01	-0.18	-1.14	6.95E+00	7.90E+00
Vps52	17	2.31E+02	3.66E+01	2.46E-02	3.52E-01	8.80E-01	-0.18	-1.14	3.07E+01	3.48E+01
Strn	17	1.84E+02	2.99E+01	4.03E-02	3.87E-01	8.77E-01	-0.19	-1.14	2.43E+01	2.77E+01
Ccar2	14	1.58E+02	2.42E+01	4.21E-02	3.90E-01	8.77E-01	-0.19	-1.14	2.09E+01	2.38E+01
Zfand1	3	1.32E+02	2.07E+01	2.93E-02	3.58E-01	8.75E-01	-0.19	-1.14	1.74E+01	1.98E+01
Adprm	11	5.43E+01	8.59E+00	4.50E-02	3.95E-01	8.74E-01	-0.19	-1.14	7.16E+00	8.19E+00
Fggy	4	9.85E+01	1.59E+01	3.78E-02	3.83E-01	8.74E-01	-0.19	-1.14	1.30E+01	1.49E+01
Fam20b	1	4.53E+02	7.14E+01	2.81E-02	3.54E-01	8.73E-01	-0.20	-1.14	5.98E+01	6.84E+01
Pmpcb	5	1.07E+03	1.70E+02	1.32E-02	3.35E-01	8.71E-01	-0.20	-1.15	1.41E+02	1.61E+02
Nmnat1	4	9.87E+01	1.63E+01	3.92E-02	3.86E-01	8.71E-01	-0.20	-1.15	1.30E+01	1.49E+01
Aktip	8	2.61E+02	4.03E+01	2.36E-02	3.52E-01	8.71E-01	-0.20	-1.15	3.44E+01	3.95E+01
Ppm1f	16	3.70E+02	5.99E+01	4.20E-02	3.90E-01	8.71E-01	-0.20	-1.15	4.88E+01	5.60E+01
Lonp1	17	1.33E+03	2.06E+02	2.94E-02	3.58E-01	8.70E-01	-0.20	-1.15	1.76E+02	2.02E+02
Ipo13	4	2.22E+02	3.67E+01	3.97E-02	3.86E-01	8.69E-01	-0.20	-1.15	2.92E+01	3.36E+01
Gstm5	3	1.24E+02	2.03E+01	1.45E-02	3.39E-01	8.69E-01	-0.20	-1.15	1.63E+01	1.87E+01
Oma1	4	5.61E+01	9.30E+00	3.80E-02	3.83E-01	8.69E-01	-0.20	-1.15	7.38E+00	8.49E+00
Phactr2	10	1.87E+02	2.98E+01	2.77E-02	3.53E-01	8.68E-01	-0.20	-1.15	2.46E+01	2.84E+01
Mtx3	13	3.62E+02	5.65E+01	2.33E-02	3.52E-01	8.68E-01	-0.20	-1.15	4.75E+01	5.48E+01
Vps41	13	3.19E+02	5.15E+01	2.93E-02	3.58E-01	8.66E-01	-0.21	-1.15	4.19E+01	4.83E+01
Kif3b	2	1.83E+02	2.85E+01	1.63E-03	3.13E-01	8.65E-01	-0.21	-1.16	2.40E+01	2.78E+01
Etfrf1	6	1.20E+03	1.97E+02	3.88E-02	3.86E-01	8.64E-01	-0.21	-1.16	1.58E+02	1.82E+02
Rab3gap2	1	1.74E+02	2.82E+01	4.08E-02	3.87E-01	8.63E-01	-0.21	-1.16	2.28E+01	2.65E+01
Zkscan8	13	1.44E+02	2.36E+01	2.31E-02	3.52E-01	8.63E-01	-0.21	-1.16	1.89E+01	2.19E+01
Washc2	6	3.16E+02	5.14E+01	2.96E-02	3.58E-01	8.63E-01	-0.21	-1.16	4.14E+01	4.80E+01
Ankrd40	11	1.13E+03	1.86E+02	2.06E-02	3.52E-01	8.62E-01	-0.21	-1.16	1.48E+02	1.71E+02
Nudt7	8	9.32E+02	1.49E+02	3.69E-02	3.82E-01	8.62E-01	-0.21	-1.16	1.22E+02	1.41E+02
Pdhb	14	4.80E+03	7.83E+02	2.29E-02	3.52E-01	8.62E-01	-0.21	-1.16	6.27E+02	7.28E+02
Wdr53	16	3.67E+01	6.12E+00	4.84E-02	4.02E-01	8.61E-01	-0.22	-1.16	4.80E+00	5.58E+00
Eftud2	11	1.52E+02	2.43E+01	3.93E-02	3.86E-01	8.61E-01	-0.22	-1.16	1.99E+01	2.32E+01
Exosc9	3	7.95E+01	1.26E+01	8.27E-03	3.33E-01	8.60E-01	-0.22	-1.16	1.04E+01	1.21E+01
Vac14	8	1.66E+02	2.60E+01	1.29E-02	3.33E-01	8.60E-01	-0.22	-1.16	2.17E+01	2.52E+01

Uhrf1bp1	17	3.46E+02	5.59E+01	2.60E-02	3.52E-01	8.60E-01	-0.22	-1.16	4.52E+01	5.26E+01
Slc44a2	9	1.29E+02	2.05E+01	1.01E-02	3.33E-01	8.59E-01	-0.22	-1.16	1.68E+01	1.96E+01
Ikbkg	X	3.34E+02	5.49E+01	1.40E-02	3.36E-01	8.58E-01	-0.22	-1.16	4.37E+01	5.09E+01
Frg2f1	4	4.21E+01	6.61E+00	1.45E-02	3.38E-01	8.57E-01	-0.22	-1.17	5.50E+00	6.41E+00
1110032A03Rik	9	3.70E+02	6.29E+01	2.00E-02	3.50E-01	8.57E-01	-0.22	-1.17	4.83E+01	5.64E+01
Anxa5	3	1.73E+03	2.77E+02	2.69E-02	3.52E-01	8.56E-01	-0.22	-1.17	2.25E+02	2.63E+02
Zfp932	5	5.65E+01	9.11E+00	2.08E-02	3.52E-01	8.56E-01	-0.22	-1.17	7.36E+00	8.60E+00
Mroh1	15	2.93E+02	4.74E+01	4.54E-02	3.95E-01	8.55E-01	-0.23	-1.17	3.82E+01	4.47E+01
Ddo	10	5.72E+02	9.52E+01	4.68E-02	3.99E-01	8.55E-01	-0.23	-1.17	7.45E+01	8.71E+01
St6galnac2	11	7.03E+01	1.10E+01	1.94E-03	3.13E-01	8.55E-01	-0.23	-1.17	9.16E+00	1.07E+01
Vps53	11	1.07E+02	1.79E+01	2.47E-02	3.52E-01	8.55E-01	-0.23	-1.17	1.40E+01	1.64E+01
C1rl	6	2.02E+02	3.41E+01	4.44E-02	3.95E-01	8.54E-01	-0.23	-1.17	2.63E+01	3.08E+01
Gsta4	9	2.34E+02	3.69E+01	8.69E-04	3.13E-01	8.54E-01	-0.23	-1.17	3.04E+01	3.57E+01
Sorbs3	14	2.60E+02	4.21E+01	4.54E-02	3.95E-01	8.53E-01	-0.23	-1.17	3.38E+01	3.96E+01
Snap47	11	1.44E+02	2.37E+01	2.56E-02	3.52E-01	8.52E-01	-0.23	-1.17	1.88E+01	2.20E+01
Capns1	7	1.66E+03	2.70E+02	5.71E-03	3.33E-01	8.52E-01	-0.23	-1.17	2.16E+02	2.53E+02
Plcb1	2	1.09E+02	1.74E+01	4.69E-02	3.99E-01	8.51E-01	-0.23	-1.17	1.41E+01	1.66E+01
Fas	19	8.84E+01	1.39E+01	3.36E-02	3.74E-01	8.51E-01	-0.23	-1.17	1.15E+01	1.35E+01
Mpc1-ps	12	8.80E+02	1.43E+02	4.57E-02	3.96E-01	8.50E-01	-0.24	-1.18	1.14E+02	1.34E+02
Trmt6	2	6.89E+01	1.08E+01	1.77E-02	3.49E-01	8.49E-01	-0.24	-1.18	8.93E+00	1.05E+01
Ets1	9	4.10E+02	6.92E+01	2.53E-02	3.52E-01	8.49E-01	-0.24	-1.18	5.32E+01	6.27E+01
Cd151	7	8.48E+02	1.39E+02	2.41E-02	3.52E-01	8.48E-01	-0.24	-1.18	1.10E+02	1.30E+02
Glod4	11	1.81E+02	2.90E+01	2.52E-02	3.52E-01	8.48E-01	-0.24	-1.18	2.35E+01	2.77E+01
Hspbap1	16	1.42E+01	2.25E+00	2.41E-03	3.13E-01	8.48E-01	-0.24	-1.18	1.85E+00	2.18E+00
Trim16	11	1.75E+02	2.95E+01	1.51E-02	3.40E-01	8.47E-01	-0.24	-1.18	2.27E+01	2.68E+01
Zfp113	5	6.03E+01	9.97E+00	1.35E-02	3.36E-01	8.46E-01	-0.24	-1.18	7.80E+00	9.22E+00
Dcps	9	4.10E+01	6.52E+00	2.67E-02	3.52E-01	8.45E-01	-0.24	-1.18	5.30E+00	6.28E+00
A130010J15Rik	1	3.27E+01	5.16E+00	9.75E-03	3.33E-01	8.43E-01	-0.25	-1.19	4.23E+00	5.01E+00
Mast4	13	1.37E+02	2.14E+01	3.48E-02	3.77E-01	8.41E-01	-0.25	-1.19	1.77E+01	2.10E+01
Tbcel	9	1.15E+02	1.93E+01	1.38E-02	3.36E-01	8.40E-01	-0.25	-1.19	1.49E+01	1.77E+01
Gbe1	16	2.07E+03	3.26E+02	1.09E-02	3.33E-01	8.40E-01	-0.25	-1.19	2.67E+02	3.18E+02

D10Wsu102e	10	9.22E+01	1.53E+01	4.66E-02	3.98E-01	8.40E-01	-0.25	-1.19	1.19E+01	1.41E+01
Mpzl1	1	3.66E+01	6.13E+00	4.08E-02	3.87E-01	8.38E-01	-0.25	-1.19	4.71E+00	5.63E+00
Zfp709	8	1.91E+01	3.10E+00	2.50E-03	3.13E-01	8.38E-01	-0.26	-1.19	2.46E+00	2.93E+00
Cryzl1	16	1.52E+02	2.38E+01	2.35E-05	2.22E-01	8.36E-01	-0.26	-1.20	1.96E+01	2.34E+01
Prkd1	12	1.55E+02	2.53E+01	1.45E-02	3.39E-01	8.36E-01	-0.26	-1.20	1.99E+01	2.38E+01
Zfp65	13	3.93E+01	6.34E+00	1.70E-02	3.49E-01	8.35E-01	-0.26	-1.20	5.04E+00	6.04E+00
Tab1	15	6.47E+01	1.04E+01	4.20E-03	3.14E-01	8.35E-01	-0.26	-1.20	8.30E+00	9.94E+00
Rrm1	7	1.47E+02	2.50E+01	2.49E-02	3.52E-01	8.35E-01	-0.26	-1.20	1.89E+01	2.26E+01
Sox13	1	7.68E+01	1.32E+01	4.54E-02	3.95E-01	8.34E-01	-0.26	-1.20	9.86E+00	1.18E+01
Plekha2	8	7.34E+01	1.19E+01	3.66E-02	3.82E-01	8.34E-01	-0.26	-1.20	9.42E+00	1.13E+01
Tle5	10	1.39E+03	2.35E+02	4.24E-02	3.90E-01	8.33E-01	-0.26	-1.20	1.79E+02	2.14E+02
Cpsf3	12	1.86E+02	3.16E+01	2.93E-02	3.58E-01	8.32E-01	-0.27	-1.20	2.38E+01	2.86E+01
Idh1	1	1.74E+03	2.79E+02	2.23E-02	3.52E-01	8.32E-01	-0.27	-1.20	2.23E+02	2.68E+02
Zadh2	18	1.42E+03	2.31E+02	1.20E-02	3.33E-01	8.31E-01	-0.27	-1.20	1.82E+02	2.18E+02
Wdr59	8	1.04E+02	1.69E+01	2.21E-02	3.52E-01	8.31E-01	-0.27	-1.20	1.34E+01	1.61E+01
Atp9a	2	6.24E+02	1.01E+02	1.04E-02	3.33E-01	8.31E-01	-0.27	-1.20	7.98E+01	9.60E+01
Dus4l	12	2.44E+01	3.92E+00	3.46E-02	3.77E-01	8.31E-01	-0.27	-1.20	3.12E+00	3.76E+00
Gm13502	2	6.84E+01	1.10E+01	1.70E-02	3.49E-01	8.30E-01	-0.27	-1.20	8.75E+00	1.05E+01
Sorbs1	19	1.20E+03	2.13E+02	2.80E-02	3.53E-01	8.29E-01	-0.27	-1.21	1.54E+02	1.86E+02
Zfp426	9	7.41E+01	1.19E+01	7.26E-03	3.33E-01	8.29E-01	-0.27	-1.21	9.46E+00	1.14E+01
Gm6644	1	1.36E+02	2.28E+01	4.48E-02	3.95E-01	8.28E-01	-0.27	-1.21	1.73E+01	2.09E+01
Dlg3	X	5.98E+01	1.06E+01	4.97E-02	4.04E-01	8.28E-01	-0.27	-1.21	7.63E+00	9.22E+00
Pde10a	17	3.60E+01	5.99E+00	2.59E-02	3.52E-01	8.27E-01	-0.27	-1.21	4.59E+00	5.55E+00
Gm7072	17	6.66E+01	1.12E+01	2.54E-02	3.52E-01	8.27E-01	-0.27	-1.21	8.49E+00	1.03E+01
Poll	19	6.48E+01	1.09E+01	4.87E-02	4.02E-01	8.26E-01	-0.28	-1.21	8.26E+00	1.00E+01
Cd59a	2	6.10E+02	1.03E+02	6.43E-03	3.33E-01	8.26E-01	-0.28	-1.21	7.78E+01	9.42E+01
Chpt1	10	1.14E+04	1.82E+03	4.45E-02	3.95E-01	8.26E-01	-0.28	-1.21	1.45E+03	1.76E+03
Nln	13	2.43E+02	4.08E+01	8.75E-03	3.33E-01	8.25E-01	-0.28	-1.21	3.09E+01	3.75E+01
Lpin2	17	1.15E+02	1.90E+01	2.72E-02	3.52E-01	8.24E-01	-0.28	-1.21	1.46E+01	1.77E+01
Gstm1	3	5.32E+02	9.31E+01	1.73E-02	3.49E-01	8.24E-01	-0.28	-1.21	6.77E+01	8.21E+01
A430018G15Rik	2	3.71E+01	6.11E+00	3.98E-02	3.86E-01	8.23E-01	-0.28	-1.21	4.72E+00	5.74E+00

Txnrd2	16	3.45E+02	5.83E+01	8.37E-03	3.33E-01	8.23E-01	-0.28	-1.21	4.38E+01	5.32E+01
Ap1g2	14	1.47E+02	2.32E+01	4.58E-04	3.13E-01	8.22E-01	-0.28	-1.22	1.86E+01	2.27E+01
Ano10	9	3.05E+02	5.07E+01	2.55E-02	3.52E-01	8.22E-01	-0.28	-1.22	3.88E+01	4.72E+01
Pex1	5	1.81E+02	3.00E+01	1.57E-02	3.41E-01	8.21E-01	-0.28	-1.22	2.30E+01	2.80E+01
Cpt1a	19	1.30E+02	2.18E+01	3.16E-02	3.66E-01	8.21E-01	-0.28	-1.22	1.65E+01	2.00E+01
Abhd18	3	7.49E+01	1.26E+01	3.07E-02	3.61E-01	8.21E-01	-0.29	-1.22	9.51E+00	1.16E+01
Vwa8	14	3.13E+03	5.31E+02	4.26E-02	3.91E-01	8.20E-01	-0.29	-1.22	3.98E+02	4.85E+02
Ap5z1	5	7.22E+01	1.20E+01	1.96E-02	3.49E-01	8.19E-01	-0.29	-1.22	9.16E+00	1.12E+01
Neurl1b	17	4.35E+01	6.97E+00	1.43E-03	3.13E-01	8.18E-01	-0.29	-1.22	5.52E+00	6.74E+00
Sec14l4	11	1.78E+02	2.95E+01	2.03E-03	3.13E-01	8.18E-01	-0.29	-1.22	2.26E+01	2.76E+01
1600014C10Rik	7	6.35E+02	1.09E+02	3.04E-02	3.59E-01	8.18E-01	-0.29	-1.22	8.05E+01	9.84E+01
Gnao1	8	5.56E+02	9.37E+01	4.80E-02	4.02E-01	8.18E-01	-0.29	-1.22	7.05E+01	8.61E+01
Spg7	8	6.53E+02	1.06E+02	7.39E-03	3.33E-01	8.18E-01	-0.29	-1.22	8.28E+01	1.01E+02
Prnp	2	7.82E+02	1.28E+02	9.50E-03	3.33E-01	8.18E-01	-0.29	-1.22	9.91E+01	1.21E+02
Zfp141	7	2.44E+01	3.96E+00	4.07E-02	3.87E-01	8.16E-01	-0.29	-1.23	3.09E+00	3.78E+00
Pcca	14	1.60E+03	2.67E+02	1.43E-02	3.38E-01	8.16E-01	-0.29	-1.23	2.02E+02	2.48E+02
Vps35l	7	2.25E+02	3.62E+01	1.27E-02	3.33E-01	8.15E-01	-0.29	-1.23	2.85E+01	3.49E+01
H6pd	4	1.51E+03	2.53E+02	1.92E-02	3.49E-01	8.15E-01	-0.30	-1.23	1.91E+02	2.35E+02
Gm6123	1	6.74E+02	1.14E+02	1.29E-02	3.33E-01	8.14E-01	-0.30	-1.23	8.52E+01	1.05E+02
Ctnnbl1	2	8.86E+01	1.41E+01	6.90E-05	2.22E-01	8.13E-01	-0.30	-1.23	1.12E+01	1.38E+01
Mtor	4	1.35E+03	2.34E+02	7.66E-03	3.33E-01	8.13E-01	-0.30	-1.23	1.71E+02	2.10E+02
Vps26c	16	1.28E+02	2.25E+01	4.78E-02	4.02E-01	8.13E-01	-0.30	-1.23	1.62E+01	2.00E+01
Rmdn2	17	3.82E+01	6.23E+00	6.81E-03	3.33E-01	8.12E-01	-0.30	-1.23	4.82E+00	5.94E+00
Gm13131	4	2.09E+01	3.45E+00	1.87E-02	3.49E-01	8.12E-01	-0.30	-1.23	2.64E+00	3.25E+00
Tmem216	19	3.24E+01	5.81E+00	3.26E-02	3.69E-01	8.12E-01	-0.30	-1.23	4.09E+00	5.04E+00
Gm5540	3	2.44E+02	3.99E+01	1.36E-02	3.36E-01	8.10E-01	-0.30	-1.23	3.07E+01	3.79E+01
Pm20d1	1	2.10E+02	3.59E+01	1.67E-02	3.46E-01	8.10E-01	-0.30	-1.24	2.64E+01	3.27E+01
Clybl	14	8.43E+02	1.37E+02	5.09E-03	3.27E-01	8.10E-01	-0.30	-1.24	1.06E+02	1.31E+02
Gapdh	6	1.65E+03	2.97E+02	4.46E-02	3.95E-01	8.09E-01	-0.31	-1.24	2.08E+02	2.57E+02
Gpd2	2	8.23E+03	1.44E+03	3.62E-02	3.80E-01	8.09E-01	-0.31	-1.24	1.04E+03	1.28E+03
Dus2	8	6.94E+01	1.11E+01	3.63E-03	3.13E-01	8.09E-01	-0.31	-1.24	8.74E+00	1.08E+01

Zfp512	5	7.22E+01	1.17E+01	4.40E-02	3.93E-01	8.06E-01	-0.31	-1.24	9.07E+00	1.13E+01
Agl	3	1.01E+03	1.70E+02	2.96E-02	3.58E-01	8.05E-01	-0.31	-1.24	1.27E+02	1.57E+02
Pls3	X	2.86E+02	4.59E+01	1.10E-02	3.33E-01	8.04E-01	-0.31	-1.24	3.59E+01	4.46E+01
Dhdh	7	1.81E+03	2.92E+02	3.89E-02	3.86E-01	8.04E-01	-0.31	-1.24	2.26E+02	2.82E+02
Gpr146	5	3.89E+02	6.21E+01	3.67E-03	3.13E-01	8.04E-01	-0.32	-1.24	4.88E+01	6.07E+01
Zfyve26	12	2.36E+02	3.78E+01	2.06E-02	3.52E-01	8.04E-01	-0.32	-1.24	2.96E+01	3.69E+01
Mtus1	8	1.16E+03	1.91E+02	3.59E-02	3.80E-01	8.03E-01	-0.32	-1.24	1.46E+02	1.82E+02
Lpcat1	13	5.08E+01	8.95E+00	3.11E-02	3.64E-01	8.03E-01	-0.32	-1.25	6.36E+00	7.92E+00
Tmem209	6	7.86E+01	1.33E+01	1.35E-02	3.36E-01	8.03E-01	-0.32	-1.25	9.84E+00	1.23E+01
Osbpl5	7	1.42E+02	2.50E+01	1.29E-02	3.33E-01	8.02E-01	-0.32	-1.25	1.78E+01	2.21E+01
Thnsl2	6	5.26E+01	9.09E+00	1.98E-02	3.49E-01	8.02E-01	-0.32	-1.25	6.58E+00	8.21E+00
Sparc	11	4.03E+03	7.04E+02	3.25E-02	3.69E-01	8.01E-01	-0.32	-1.25	5.05E+02	6.30E+02
Cep162	9	2.68E+01	4.83E+00	2.78E-02	3.53E-01	8.01E-01	-0.32	-1.25	3.35E+00	4.19E+00
Ppp1r21	17	7.90E+01	1.30E+01	1.91E-02	3.49E-01	8.00E-01	-0.32	-1.25	9.88E+00	1.23E+01
Ttc8	12	8.32E+01	1.38E+01	4.44E-02	3.95E-01	8.00E-01	-0.32	-1.25	1.04E+01	1.30E+01
Epb41l5	1	1.04E+02	1.74E+01	1.93E-03	3.13E-01	8.00E-01	-0.32	-1.25	1.30E+01	1.62E+01
Gdpgp1	7	2.44E+01	4.04E+00	3.73E-02	3.83E-01	7.99E-01	-0.32	-1.25	3.05E+00	3.82E+00
Hps3	3	7.52E+01	1.25E+01	2.60E-02	3.52E-01	7.99E-01	-0.32	-1.25	9.40E+00	1.18E+01
Gm3555	1	2.76E+01	4.58E+00	3.00E-03	3.13E-01	7.98E-01	-0.33	-1.25	3.44E+00	4.31E+00
Aatf	11	3.70E+01	6.30E+00	2.70E-02	3.52E-01	7.98E-01	-0.33	-1.25	4.62E+00	5.79E+00
Tlr4	4	4.49E+01	7.61E+00	4.93E-02	4.03E-01	7.97E-01	-0.33	-1.25	5.60E+00	7.02E+00
Cry2	2	2.86E+02	4.66E+01	2.86E-02	3.55E-01	7.97E-01	-0.33	-1.25	3.57E+01	4.48E+01
Prpf19	19	3.51E+02	5.97E+01	5.26E-03	3.32E-01	7.97E-01	-0.33	-1.25	4.38E+01	5.50E+01
Hacl1	14	2.69E+02	4.52E+01	4.90E-03	3.20E-01	7.96E-01	-0.33	-1.26	3.35E+01	4.20E+01
Hspa12b	2	2.36E+02	4.12E+01	1.80E-02	3.49E-01	7.95E-01	-0.33	-1.26	2.94E+01	3.70E+01
Optn	2	5.38E+02	9.58E+01	1.53E-02	3.40E-01	7.95E-01	-0.33	-1.26	6.69E+01	8.42E+01
Odf2l	3	7.76E+01	1.30E+01	4.23E-02	3.90E-01	7.94E-01	-0.33	-1.26	9.66E+00	1.22E+01
Exoc4	6	1.81E+02	3.00E+01	7.01E-03	3.33E-01	7.94E-01	-0.33	-1.26	2.26E+01	2.84E+01
Nacc2	2	5.58E+02	9.46E+01	4.94E-02	4.03E-01	7.94E-01	-0.33	-1.26	6.94E+01	8.74E+01
Elk3	10	1.50E+02	2.81E+01	4.03E-02	3.87E-01	7.94E-01	-0.33	-1.26	1.87E+01	2.36E+01
Tada2a	11	3.07E+01	5.01E+00	1.07E-03	3.13E-01	7.92E-01	-0.34	-1.26	3.81E+00	4.81E+00

Mrto4-ps1	12	1.09E+01	1.90E+00	4.49E-02	3.95E-01	7.92E-01	-0.34	-1.26	1.35E+00	1.71E+00
Tkfc	19	7.36E+01	1.33E+01	4.57E-02	3.96E-01	7.92E-01	-0.34	-1.26	9.14E+00	1.15E+01
Nod1	6	1.21E+02	2.01E+01	2.40E-02	3.52E-01	7.92E-01	-0.34	-1.26	1.51E+01	1.91E+01
Pwwp2b	7	1.01E+02	1.75E+01	2.79E-02	3.53E-01	7.91E-01	-0.34	-1.26	1.25E+01	1.58E+01
Wbp2	11	5.62E+02	9.12E+01	1.62E-02	3.44E-01	7.91E-01	-0.34	-1.26	6.98E+01	8.82E+01
Tceanc	X	3.78E+01	6.30E+00	5.71E-03	3.33E-01	7.91E-01	-0.34	-1.26	4.69E+00	5.93E+00
Rsu1	2	1.83E+02	3.09E+01	1.18E-02	3.33E-01	7.90E-01	-0.34	-1.27	2.26E+01	2.87E+01
Commd10	18	8.48E+01	1.48E+01	2.60E-02	3.52E-01	7.88E-01	-0.34	-1.27	1.05E+01	1.33E+01
Add1	5	5.40E+02	9.44E+01	4.20E-02	3.90E-01	7.88E-01	-0.34	-1.27	6.69E+01	8.49E+01
Ajuba	14	5.80E+01	1.01E+01	2.30E-02	3.52E-01	7.88E-01	-0.34	-1.27	7.18E+00	9.12E+00
Hrct1	4	3.12E+01	5.27E+00	6.75E-03	3.33E-01	7.87E-01	-0.34	-1.27	3.86E+00	4.90E+00
Zfp26	9	7.68E+01	1.29E+01	1.16E-03	3.13E-01	7.87E-01	-0.35	-1.27	9.50E+00	1.21E+01
Shpk	11	1.13E+02	1.87E+01	3.32E-03	3.13E-01	7.87E-01	-0.35	-1.27	1.39E+01	1.77E+01
Casp2	6	4.71E+01	8.30E+00	4.58E-02	3.96E-01	7.86E-01	-0.35	-1.27	5.82E+00	7.40E+00
Gm14026	2	6.55E+01	1.14E+01	4.77E-02	4.02E-01	7.86E-01	-0.35	-1.27	8.09E+00	1.03E+01
Lrig3	10	2.68E+01	4.85E+00	1.92E-02	3.49E-01	7.85E-01	-0.35	-1.27	3.31E+00	4.22E+00
Sparcl1	5	9.82E+02	1.68E+02	1.53E-02	3.40E-01	7.85E-01	-0.35	-1.27	1.21E+02	1.55E+02
Iqcc	4	5.07E+01	9.01E+00	3.54E-02	3.79E-01	7.83E-01	-0.35	-1.28	6.25E+00	7.98E+00
Ap5s1	2	9.51E+01	1.63E+01	3.47E-02	3.77E-01	7.83E-01	-0.35	-1.28	1.17E+01	1.50E+01
Vstm4	14	3.25E+01	5.36E+00	3.70E-03	3.13E-01	7.81E-01	-0.36	-1.28	4.00E+00	5.13E+00
Akr1e1	13	1.39E+02	2.38E+01	1.26E-02	3.33E-01	7.80E-01	-0.36	-1.28	1.71E+01	2.19E+01
Parva	7	4.50E+02	8.31E+01	4.35E-02	3.93E-01	7.80E-01	-0.36	-1.28	5.53E+01	7.09E+01
Magi2	5	1.25E+01	2.13E+00	2.53E-02	3.52E-01	7.79E-01	-0.36	-1.28	1.54E+00	1.98E+00
Ttc30b	2	1.46E+02	2.60E+01	3.67E-02	3.82E-01	7.78E-01	-0.36	-1.29	1.80E+01	2.31E+01
Ggta1	2	1.42E+02	2.48E+01	1.66E-02	3.46E-01	7.77E-01	-0.36	-1.29	1.75E+01	2.25E+01
Ppip5k1	2	1.09E+03	1.79E+02	3.51E-04	3.13E-01	7.77E-01	-0.36	-1.29	1.33E+02	1.72E+02
Copg2	6	2.09E+02	3.54E+01	4.81E-02	4.02E-01	7.76E-01	-0.37	-1.29	2.56E+01	3.31E+01
Lipe	7	8.15E+03	1.40E+03	3.08E-02	3.62E-01	7.73E-01	-0.37	-1.29	9.97E+02	1.29E+03
Gm12854	4	5.63E+01	1.03E+01	3.53E-02	3.79E-01	7.72E-01	-0.37	-1.30	6.88E+00	8.91E+00
P2rx6	16	7.26E+01	1.25E+01	3.60E-02	3.80E-01	7.71E-01	-0.37	-1.30	8.87E+00	1.15E+01
Nsdhl	X	4.28E+02	7.53E+01	4.89E-03	3.20E-01	7.71E-01	-0.38	-1.30	5.23E+01	6.78E+01

Gmpr2	14	7.25E+01	1.42E+01	4.42E-02	3.94E-01	7.70E-01	-0.38	-1.30	8.85E+00	1.15E+01
Zfp958	8	2.52E+01	4.28E+00	2.50E-02	3.52E-01	7.70E-01	-0.38	-1.30	3.08E+00	4.00E+00
Orm1	4	4.37E+02	8.08E+01	3.76E-02	3.83E-01	7.68E-01	-0.38	-1.30	5.32E+01	6.93E+01
Shld2	14	5.16E+01	9.74E+00	2.97E-02	3.58E-01	7.68E-01	-0.38	-1.30	6.28E+00	8.18E+00
Mapt	11	3.26E+02	5.77E+01	3.61E-02	3.80E-01	7.66E-01	-0.38	-1.31	3.96E+01	5.17E+01
Exog	9	1.64E+01	2.69E+00	1.01E-02	3.33E-01	7.66E-01	-0.38	-1.31	1.99E+00	2.60E+00
Cdk20	13	2.01E+01	3.28E+00	7.92E-03	3.33E-01	7.62E-01	-0.39	-1.31	2.44E+00	3.20E+00
Iffo1	6	4.76E+01	8.28E+00	4.53E-02	3.95E-01	7.62E-01	-0.39	-1.31	5.76E+00	7.57E+00
Zfp120	2	6.17E+01	1.06E+01	5.80E-03	3.33E-01	7.61E-01	-0.39	-1.31	7.48E+00	9.82E+00
Colca2	9	3.15E+01	5.36E+00	5.85E-03	3.33E-01	7.60E-01	-0.40	-1.32	3.81E+00	5.02E+00
Tmem237	1	1.70E+01	3.03E+00	5.39E-03	3.33E-01	7.60E-01	-0.40	-1.32	2.06E+00	2.71E+00
4930581F22Rik	9	2.22E+01	3.80E+00	4.91E-02	4.03E-01	7.59E-01	-0.40	-1.32	2.69E+00	3.54E+00
Cyp4v3	8	3.80E+02	6.75E+01	3.71E-02	3.82E-01	7.59E-01	-0.40	-1.32	4.59E+01	6.05E+01
Zfp229	17	6.11E+01	1.06E+01	9.52E-03	3.33E-01	7.58E-01	-0.40	-1.32	7.38E+00	9.73E+00
Ezh1	11	3.25E+02	6.18E+01	2.55E-02	3.52E-01	7.57E-01	-0.40	-1.32	3.92E+01	5.18E+01
Ampd3	7	3.42E+02	5.72E+01	3.72E-03	3.13E-01	7.57E-01	-0.40	-1.32	4.13E+01	5.46E+01
Eno1	4	8.26E+03	1.55E+03	1.56E-02	3.41E-01	7.57E-01	-0.40	-1.32	9.97E+02	1.32E+03
Arntl2	6	3.58E+01	6.59E+00	2.40E-02	3.52E-01	7.56E-01	-0.40	-1.32	4.32E+00	5.72E+00
Fdps	3	2.65E+02	4.69E+01	3.54E-02	3.79E-01	7.54E-01	-0.41	-1.33	3.19E+01	4.23E+01
Zfp101	17	4.47E+01	7.80E+00	2.40E-02	3.52E-01	7.54E-01	-0.41	-1.33	5.38E+00	7.13E+00
Ankrd27	7	1.99E+02	3.67E+01	3.47E-02	3.77E-01	7.53E-01	-0.41	-1.33	2.40E+01	3.19E+01
BC035947	1	1.68E+01	3.02E+00	3.53E-02	3.79E-01	7.53E-01	-0.41	-1.33	2.02E+00	2.69E+00
Gm3571	10	7.81E+01	1.36E+01	2.68E-02	3.52E-01	7.53E-01	-0.41	-1.33	9.40E+00	1.25E+01
Rpgr	X	2.82E+01	5.22E+00	3.69E-02	3.82E-01	7.53E-01	-0.41	-1.33	3.39E+00	4.51E+00
Fzd6	15	7.35E+01	1.24E+01	1.12E-02	3.33E-01	7.52E-01	-0.41	-1.33	8.84E+00	1.17E+01
Tns2	15	1.04E+03	1.77E+02	1.19E-02	3.33E-01	7.50E-01	-0.42	-1.33	1.25E+02	1.67E+02
Fhit	14	8.90E+00	1.72E+00	3.59E-02	3.80E-01	7.45E-01	-0.43	-1.34	1.06E+00	1.43E+00
Haus8	8	1.04E+01	1.85E+00	2.84E-02	3.55E-01	7.44E-01	-0.43	-1.34	1.24E+00	1.67E+00
Zfp953	13	1.72E+01	3.16E+00	4.60E-02	3.97E-01	7.44E-01	-0.43	-1.34	2.05E+00	2.76E+00
Spata7	12	1.17E+01	1.98E+00	3.17E-02	3.66E-01	7.43E-01	-0.43	-1.35	1.40E+00	1.89E+00
Ugp2	11	1.35E+03	2.37E+02	3.23E-03	3.13E-01	7.43E-01	-0.43	-1.35	1.61E+02	2.17E+02

Gm49284	15	2.23E+01	3.92E+00	1.75E-02	3.49E-01	7.42E-01	-0.43	-1.35	2.66E+00	3.58E+00
Acsf3	8	7.83E+02	1.37E+02	1.04E-03	3.13E-01	7.41E-01	-0.43	-1.35	9.32E+01	1.26E+02
9030407P2ORik	7	1.52E+01	2.58E+00	2.87E-02	3.56E-01	7.39E-01	-0.44	-1.35	1.81E+00	2.44E+00
Plag1	4	1.59E+01	2.78E+00	1.98E-02	3.49E-01	7.39E-01	-0.44	-1.35	1.89E+00	2.56E+00
B430212C06Rik	18	4.27E+01	7.35E+00	3.81E-02	3.83E-01	7.39E-01	-0.44	-1.35	5.08E+00	6.87E+00
Anapc4	5	1.45E+02	2.64E+01	3.04E-02	3.59E-01	7.39E-01	-0.44	-1.35	1.72E+01	2.33E+01
Lrrc61	6	1.28E+02	2.35E+01	1.43E-02	3.38E-01	7.38E-01	-0.44	-1.35	1.52E+01	2.06E+01
Enpp5	17	2.99E+02	5.33E+01	2.64E-02	3.52E-01	7.38E-01	-0.44	-1.36	3.56E+01	4.82E+01
Tril	6	2.05E+01	3.92E+00	2.14E-02	3.52E-01	7.38E-01	-0.44	-1.36	2.43E+00	3.29E+00
Eno1b	18	6.34E+03	1.18E+03	3.48E-02	3.77E-01	7.38E-01	-0.44	-1.36	7.52E+02	1.02E+03
Gm43205	3	2.04E+01	3.83E+00	4.56E-02	3.96E-01	7.38E-01	-0.44	-1.36	2.42E+00	3.28E+00
Thsd1	8	3.06E+01	5.60E+00	8.56E-03	3.33E-01	7.37E-01	-0.44	-1.36	3.63E+00	4.93E+00
Abcd1	X	2.56E+02	4.51E+01	4.25E-02	3.91E-01	7.37E-01	-0.44	-1.36	3.04E+01	4.12E+01
Cers4	8	1.04E+02	1.98E+01	4.01E-02	3.87E-01	7.36E-01	-0.44	-1.36	1.23E+01	1.68E+01
Atg4a-ps	3	5.05E+01	9.14E+00	1.72E-02	3.49E-01	7.36E-01	-0.44	-1.36	5.98E+00	8.13E+00
Ttc30a1	2	1.81E+01	3.24E+00	4.03E-02	3.87E-01	7.35E-01	-0.44	-1.36	2.14E+00	2.91E+00
Arsb	13	3.16E+02	5.76E+01	3.08E-02	3.62E-01	7.35E-01	-0.44	-1.36	3.74E+01	5.09E+01
Tpmt	13	6.40E+01	1.18E+01	3.45E-02	3.77E-01	7.31E-01	-0.45	-1.37	7.55E+00	1.03E+01
Txnip	3	6.67E+03	1.29E+03	4.46E-02	3.95E-01	7.30E-01	-0.45	-1.37	7.87E+02	1.08E+03
Zfp984	4	2.98E+01	5.64E+00	1.05E-02	3.33E-01	7.30E-01	-0.45	-1.37	3.52E+00	4.82E+00
Gm7336	7	6.38E+03	1.23E+03	2.68E-02	3.52E-01	7.29E-01	-0.46	-1.37	7.52E+02	1.03E+03
Mecom	3	8.64E+01	1.63E+01	1.90E-02	3.49E-01	7.29E-01	-0.46	-1.37	1.02E+01	1.40E+01
Glb1l	1	4.06E+01	7.42E+00	5.62E-03	3.33E-01	7.28E-01	-0.46	-1.37	4.78E+00	6.57E+00
Shc2	10	1.00E+01	1.89E+00	4.66E-02	3.98E-01	7.28E-01	-0.46	-1.37	1.18E+00	1.62E+00
Gm4735	2	6.49E+03	1.21E+03	1.02E-02	3.33E-01	7.28E-01	-0.46	-1.37	7.64E+02	1.05E+03
Gpi1	7	3.78E+03	7.05E+02	6.41E-03	3.33E-01	7.28E-01	-0.46	-1.37	4.45E+02	6.12E+02
Pfkl	10	4.28E+03	7.88E+02	2.57E-02	3.52E-01	7.26E-01	-0.46	-1.38	5.03E+02	6.93E+02
4933431E2ORik	3	4.69E+01	8.23E+00	1.16E-03	3.13E-01	7.26E-01	-0.46	-1.38	5.51E+00	7.58E+00
Gm49331	12	7.83E+00	1.43E+00	1.12E-02	3.33E-01	7.26E-01	-0.46	-1.38	9.20E-01	1.27E+00
Cd300a	11	8.17E+00	1.63E+00	3.44E-02	3.77E-01	7.25E-01	-0.46	-1.38	9.59E-01	1.32E+00
Anxa9	3	7.64E+00	1.37E+00	3.48E-02	3.77E-01	7.24E-01	-0.47	-1.38	8.97E-01	1.24E+00

Fn3k	11	6.93E+01	1.25E+01	1.02E-02	3.33E-01	7.24E-01	-0.47	-1.38	8.13E+00	1.12E+01
Tctn3	19	1.39E+01	2.69E+00	4.75E-02	4.02E-01	7.23E-01	-0.47	-1.38	1.63E+00	2.26E+00
Slc25a53	X	2.08E+01	3.68E+00	2.33E-02	3.52E-01	7.23E-01	-0.47	-1.38	2.44E+00	3.37E+00
Slc8b1	5	8.13E+01	1.55E+01	2.56E-02	3.52E-01	7.20E-01	-0.47	-1.39	9.50E+00	1.32E+01
Gm1840	8	1.15E+03	2.17E+02	8.85E-03	3.33E-01	7.19E-01	-0.48	-1.39	1.34E+02	1.87E+02
Eaf2	16	1.30E+01	2.39E+00	1.05E-02	3.33E-01	7.19E-01	-0.48	-1.39	1.52E+00	2.12E+00
Gm45470	8	1.97E+02	4.01E+01	3.87E-02	3.86E-01	7.18E-01	-0.48	-1.39	2.30E+01	3.21E+01
Tnfaip3	10	1.91E+01	3.85E+00	3.48E-02	3.77E-01	7.18E-01	-0.48	-1.39	2.23E+00	3.11E+00
Kif26a	12	1.20E+02	2.19E+01	2.78E-02	3.53E-01	7.17E-01	-0.48	-1.39	1.40E+01	1.95E+01
Meox1	11	2.92E+01	5.25E+00	1.48E-02	3.40E-01	7.16E-01	-0.48	-1.40	3.40E+00	4.75E+00
Zbtb5	4	1.12E+02	2.02E+01	4.36E-02	3.93E-01	7.15E-01	-0.48	-1.40	1.30E+01	1.82E+01
Gm6728	6	8.60E+00	1.46E+00	2.99E-03	3.13E-01	7.15E-01	-0.48	-1.40	1.00E+00	1.40E+00
Pwwp3a	10	1.96E+02	3.62E+01	4.51E-02	3.95E-01	7.13E-01	-0.49	-1.40	2.28E+01	3.19E+01
Pola1	X	1.99E+01	3.87E+00	2.53E-02	3.52E-01	7.12E-01	-0.49	-1.40	2.30E+00	3.24E+00
Slx1b	7	5.35E+01	9.52E+00	4.29E-02	3.92E-01	7.09E-01	-0.50	-1.41	6.19E+00	8.74E+00
Mapk11	15	1.75E+01	3.15E+00	2.67E-02	3.52E-01	7.09E-01	-0.50	-1.41	2.03E+00	2.86E+00
4921536K21Rik	11	1.17E+01	2.23E+00	4.38E-02	3.93E-01	7.08E-01	-0.50	-1.41	1.36E+00	1.92E+00
Gcfc2	6	1.07E+01	1.93E+00	2.41E-02	3.52E-01	7.08E-01	-0.50	-1.41	1.24E+00	1.75E+00
Tmem71	15	1.26E+01	2.14E+00	2.28E-02	3.52E-01	7.08E-01	-0.50	-1.41	1.45E+00	2.05E+00
Rin2	2	1.96E+02	3.45E+01	2.40E-02	3.52E-01	7.08E-01	-0.50	-1.41	2.26E+01	3.20E+01
Gm47593	10	3.05E+01	5.95E+00	2.58E-02	3.52E-01	7.05E-01	-0.50	-1.42	3.52E+00	4.99E+00
Zfp788	7	4.56E+01	8.28E+00	2.45E-02	3.52E-01	7.05E-01	-0.50	-1.42	5.26E+00	7.46E+00
Aldoa	7	1.91E+04	3.62E+03	4.27E-02	3.91E-01	7.05E-01	-0.50	-1.42	2.20E+03	3.12E+03
Gm47483	10	4.51E+01	9.16E+00	1.92E-02	3.49E-01	7.03E-01	-0.51	-1.42	5.19E+00	7.37E+00
Gpr17	18	3.47E+01	6.59E+00	4.76E-03	3.17E-01	7.02E-01	-0.51	-1.42	3.99E+00	5.68E+00
Zfp955b	17	5.90E+01	1.05E+01	4.87E-02	4.02E-01	7.01E-01	-0.51	-1.43	6.78E+00	9.68E+00
Zfp799	17	4.06E+01	7.38E+00	1.62E-02	3.44E-01	7.00E-01	-0.51	-1.43	4.66E+00	6.65E+00
Hfe	13	1.98E+02	3.44E+01	2.70E-03	3.13E-01	6.99E-01	-0.52	-1.43	2.27E+01	3.25E+01
Gm37691	1	3.38E+01	6.03E+00	1.85E-02	3.49E-01	6.99E-01	-0.52	-1.43	3.87E+00	5.54E+00
Adh1	3	4.17E+02	8.01E+01	4.20E-02	3.90E-01	6.94E-01	-0.53	-1.44	4.75E+01	6.85E+01
Cpeb1	7	1.71E+02	3.55E+01	2.48E-02	3.52E-01	6.93E-01	-0.53	-1.44	1.95E+01	2.81E+01

Dchs1	7	5.08E+01	1.01E+01	1.47E-02	3.40E-01	6.92E-01	-0.53	-1.45	5.79E+00	8.37E+00
Mccc1os	3	7.78E+00	1.46E+00	4.06E-02	3.87E-01	6.88E-01	-0.54	-1.45	8.83E-01	1.28E+00
Plk2	13	6.26E+01	1.12E+01	1.86E-03	3.13E-01	6.85E-01	-0.55	-1.46	7.08E+00	1.03E+01
Aox1	1	5.85E+02	1.04E+02	4.55E-03	3.17E-01	6.84E-01	-0.55	-1.46	6.62E+01	9.67E+01
Pgd	4	2.79E+03	5.82E+02	3.82E-02	3.83E-01	6.83E-01	-0.55	-1.46	3.15E+02	4.61E+02
Ephx1	1	1.75E+02	3.25E+01	1.26E-02	3.33E-01	6.82E-01	-0.55	-1.47	1.97E+01	2.90E+01
Pkm	9	1.16E+04	2.09E+03	3.07E-03	3.13E-01	6.81E-01	-0.55	-1.47	1.31E+03	1.92E+03
Klf10	15	3.67E+02	7.40E+01	4.74E-02	4.02E-01	6.81E-01	-0.55	-1.47	4.14E+01	6.08E+01
Kng2	16	4.02E+02	7.68E+01	5.86E-03	3.33E-01	6.80E-01	-0.56	-1.47	4.53E+01	6.66E+01
6430562O15Rik	13	9.45E+00	2.09E+00	3.44E-02	3.77E-01	6.79E-01	-0.56	-1.47	1.06E+00	1.57E+00
Gm6560	5	1.14E+03	2.09E+02	2.69E-03	3.13E-01	6.78E-01	-0.56	-1.48	1.28E+02	1.90E+02
Zfp128	7	1.74E+01	3.28E+00	4.78E-03	3.17E-01	6.75E-01	-0.57	-1.48	1.95E+00	2.89E+00
Zfp28	7	5.74E+01	1.09E+01	2.28E-02	3.52E-01	6.74E-01	-0.57	-1.48	6.43E+00	9.53E+00
Nynrin	14	3.56E+01	6.32E+00	2.13E-02	3.52E-01	6.71E-01	-0.58	-1.49	3.97E+00	5.92E+00
Gm47451	13	9.68E+00	1.75E+00	1.80E-02	3.49E-01	6.71E-01	-0.58	-1.49	1.08E+00	1.61E+00
2010007H06Rik	9	4.04E+01	8.57E+00	4.11E-02	3.89E-01	6.70E-01	-0.58	-1.49	4.50E+00	6.72E+00
Zfp825	13	2.01E+01	3.48E+00	3.83E-04	3.13E-01	6.68E-01	-0.58	-1.50	2.24E+00	3.35E+00
A030001D20Rik	7	2.05E+01	3.68E+00	1.50E-02	3.40E-01	6.68E-01	-0.58	-1.50	2.29E+00	3.42E+00
Zfp975	7	2.35E+01	4.26E+00	4.09E-03	3.14E-01	6.67E-01	-0.58	-1.50	2.61E+00	3.92E+00
Col4a3	1	8.70E+00	1.50E+00	4.54E-02	3.95E-01	6.67E-01	-0.58	-1.50	9.67E-01	1.45E+00
Hgf	5	1.12E+01	2.38E+00	3.58E-02	3.80E-01	6.65E-01	-0.59	-1.50	1.24E+00	1.86E+00
Sema4c	1	7.37E+01	1.41E+01	3.79E-03	3.13E-01	6.65E-01	-0.59	-1.50	8.17E+00	1.23E+01
Rapgef5	12	1.55E+02	3.04E+01	1.20E-02	3.33E-01	6.65E-01	-0.59	-1.50	1.72E+01	2.59E+01
Cd46	1	2.07E+01	3.80E+00	1.37E-03	3.13E-01	6.54E-01	-0.61	-1.53	2.27E+00	3.47E+00
Rassf9	10	6.31E+01	1.36E+01	2.89E-02	3.57E-01	6.53E-01	-0.61	-1.53	6.91E+00	1.06E+01
Ccdc114	7	1.34E+01	2.75E+00	3.13E-02	3.65E-01	6.53E-01	-0.62	-1.53	1.47E+00	2.25E+00
Zscan2	7	8.94E+00	1.89E+00	2.74E-02	3.52E-01	6.53E-01	-0.62	-1.53	9.79E-01	1.50E+00
Zfp712	13	9.59E+00	2.04E+00	2.99E-02	3.58E-01	6.51E-01	-0.62	-1.54	1.05E+00	1.61E+00
Hoga1	19	1.20E+01	2.33E+00	1.99E-02	3.49E-01	6.50E-01	-0.62	-1.54	1.31E+00	2.02E+00
Cxxc4	3	1.60E+01	3.22E+00	6.85E-03	3.33E-01	6.47E-01	-0.63	-1.55	1.74E+00	2.69E+00
Tchp	5	2.85E+01	5.86E+00	4.12E-02	3.89E-01	6.45E-01	-0.63	-1.55	3.10E+00	4.80E+00

Jrk	15	1.83E+01	3.85E+00	4.59E-02	3.96E-01	6.42E-01	-0.64	-1.56	1.98E+00	3.09E+00
Mettl27	5	4.06E+01	8.03E+00	4.16E-02	3.90E-01	6.39E-01	-0.65	-1.57	4.38E+00	6.86E+00
Zfp90	8	1.13E+01	2.33E+00	3.10E-02	3.63E-01	6.39E-01	-0.65	-1.57	1.22E+00	1.91E+00
Efnb2	8	1.11E+02	2.11E+01	1.30E-03	3.13E-01	6.39E-01	-0.65	-1.57	1.20E+01	1.87E+01
Fabp5	3	4.88E+02	1.06E+02	2.27E-02	3.52E-01	6.31E-01	-0.66	-1.58	5.23E+01	8.29E+01
Smyd4	11	1.04E+02	2.10E+01	1.48E-02	3.40E-01	6.30E-01	-0.67	-1.59	1.11E+01	1.77E+01
4930481A15Rik	19	6.97E+01	1.29E+01	4.22E-02	3.90E-01	6.25E-01	-0.68	-1.60	7.41E+00	1.19E+01
4931428F04Rik	8	1.44E+01	2.76E+00	1.30E-02	3.33E-01	6.23E-01	-0.68	-1.60	1.53E+00	2.45E+00
Zfp759	13	2.06E+01	3.73E+00	4.56E-02	3.96E-01	6.23E-01	-0.68	-1.60	2.19E+00	3.51E+00
5930430L01Rik	5	3.30E+01	7.05E+00	2.59E-02	3.52E-01	6.23E-01	-0.68	-1.61	3.51E+00	5.63E+00
Fuca2	10	6.97E+01	1.57E+01	3.94E-02	3.86E-01	6.22E-01	-0.69	-1.61	7.39E+00	1.19E+01
Gm12070	11	1.80E+01	3.41E+00	1.86E-03	3.13E-01	6.21E-01	-0.69	-1.61	1.91E+00	3.07E+00
Fam53b	7	7.32E+02	1.45E+02	2.12E-02	3.52E-01	6.16E-01	-0.70	-1.62	7.70E+01	1.25E+02
Gm46430	13	3.00E+01	5.74E+00	2.11E-03	3.13E-01	6.16E-01	-0.70	-1.62	3.16E+00	5.13E+00
Tctn1	5	3.63E+01	7.32E+00	8.60E-03	3.33E-01	6.14E-01	-0.70	-1.63	3.82E+00	6.21E+00
Zfp982	4	1.78E+02	3.52E+01	1.21E-02	3.33E-01	6.11E-01	-0.71	-1.64	1.87E+01	3.05E+01
Gm21092	8	7.79E+00	1.58E+00	2.74E-02	3.52E-01	6.09E-01	-0.71	-1.64	8.14E-01	1.34E+00
Gm9776	13	1.40E+01	2.74E+00	2.31E-02	3.52E-01	6.08E-01	-0.72	-1.65	1.46E+00	2.40E+00
Snx32	19	4.44E+01	9.07E+00	2.37E-02	3.52E-01	6.06E-01	-0.72	-1.65	4.62E+00	7.63E+00
Neurl3	1	1.54E+01	3.28E+00	3.15E-02	3.66E-01	6.03E-01	-0.73	-1.66	1.60E+00	2.65E+00
Gemin8	X	8.12E+00	1.60E+00	4.62E-03	3.17E-01	6.03E-01	-0.73	-1.66	8.44E-01	1.40E+00
Aldoat1	4	4.87E+01	1.08E+01	1.28E-02	3.33E-01	6.02E-01	-0.73	-1.66	5.05E+00	8.39E+00
Bhlhe41	6	1.31E+02	2.92E+01	3.66E-02	3.82E-01	6.01E-01	-0.73	-1.66	1.36E+01	2.26E+01
Zbed5	5	7.90E+00	1.69E+00	3.99E-02	3.86E-01	5.94E-01	-0.75	-1.68	8.12E-01	1.37E+00
Afmid	11	1.01E+01	2.14E+00	4.20E-03	3.14E-01	5.86E-01	-0.77	-1.71	1.03E+00	1.76E+00
Gm7329	1	2.46E+01	5.03E+00	4.35E-02	3.92E-01	5.86E-01	-0.77	-1.71	2.50E+00	4.27E+00
Gm32200	1	4.46E+01	1.02E+01	1.13E-02	3.33E-01	5.84E-01	-0.78	-1.71	4.53E+00	7.76E+00
Me1	9	5.34E+03	1.19E+03	4.05E-02	3.87E-01	5.84E-01	-0.78	-1.71	5.42E+02	9.28E+02
Slc22a2	17	1.63E+01	3.79E+00	4.89E-02	4.02E-01	5.83E-01	-0.78	-1.72	1.65E+00	2.84E+00
Zfp72	13	2.21E+01	4.86E+00	1.94E-02	3.49E-01	5.76E-01	-0.80	-1.74	2.23E+00	3.87E+00
Haghl	17	2.03E+01	4.44E+00	4.04E-02	3.87E-01	5.75E-01	-0.80	-1.74	2.03E+00	3.54E+00

Ano1	7	3.83E+02	7.36E+01	1.49E-02	3.40E-01	5.73E-01	-0.80	-1.75	3.83E+01	6.69E+01
Gm11266	4	1.56E+01	3.09E+00	9.48E-03	3.33E-01	5.72E-01	-0.81	-1.75	1.56E+00	2.73E+00
Gm31166	19	8.39E+00	1.63E+00	3.81E-02	3.83E-01	5.67E-01	-0.82	-1.76	8.35E-01	1.47E+00
Zfp960	17	1.55E+01	3.14E+00	2.73E-02	3.52E-01	5.61E-01	-0.83	-1.78	1.53E+00	2.73E+00
Prelp	1	2.71E+03	5.17E+02	1.64E-03	3.13E-01	5.58E-01	-0.84	-1.79	2.66E+02	4.77E+02
Ropn1l	15	1.39E+01	3.20E+00	1.25E-02	3.33E-01	5.57E-01	-0.84	-1.80	1.36E+00	2.45E+00
Gm13610	2	7.50E+00	1.90E+00	3.94E-02	3.86E-01	5.54E-01	-0.85	-1.80	7.35E-01	1.33E+00
Ccr5	9	8.62E+00	1.71E+00	3.31E-03	3.13E-01	5.50E-01	-0.86	-1.82	8.40E-01	1.53E+00
Gm6166	9	6.28E+01	1.35E+01	5.94E-03	3.33E-01	5.49E-01	-0.87	-1.82	6.10E+00	1.11E+01
Spaca1	4	1.61E+01	4.15E+00	4.94E-02	4.03E-01	5.47E-01	-0.87	-1.83	1.57E+00	2.86E+00
Gm7049	13	1.22E+03	2.76E+02	2.20E-02	3.52E-01	5.43E-01	-0.88	-1.84	1.18E+02	2.17E+02
Gm5276	3	8.22E+00	1.83E+00	1.32E-02	3.35E-01	5.41E-01	-0.89	-1.85	7.91E-01	1.46E+00
Map3k8	18	1.30E+01	2.83E+00	3.10E-03	3.13E-01	5.40E-01	-0.89	-1.85	1.25E+00	2.32E+00
Nat1	8	1.06E+01	2.54E+00	3.38E-02	3.75E-01	5.35E-01	-0.90	-1.87	1.01E+00	1.90E+00
Lrrc20	10	1.25E+02	2.90E+01	1.08E-02	3.33E-01	5.31E-01	-0.91	-1.88	1.19E+01	2.24E+01
Zfp763	17	1.94E+01	4.63E+00	4.19E-02	3.90E-01	5.31E-01	-0.91	-1.88	1.84E+00	3.46E+00
Gm48795	13	1.18E+02	2.99E+01	3.27E-02	3.71E-01	5.30E-01	-0.92	-1.89	1.12E+01	2.11E+01
Gm10699	8	7.71E+00	1.87E+00	4.77E-02	4.02E-01	5.29E-01	-0.92	-1.89	7.30E-01	1.38E+00
F3	3	2.75E+02	6.20E+01	2.90E-02	3.57E-01	5.27E-01	-0.92	-1.90	2.60E+01	4.93E+01
BC043934	9	3.79E+01	8.05E+00	4.48E-02	3.95E-01	5.24E-01	-0.93	-1.91	3.56E+00	6.80E+00
S100b	10	4.70E+02	1.06E+02	2.41E-02	3.52E-01	5.16E-01	-0.96	-1.94	4.37E+01	8.48E+01
Ak4	4	3.68E+01	9.72E+00	4.17E-02	3.90E-01	5.10E-01	-0.97	-1.96	3.39E+00	6.65E+00
Hpgd	8	3.09E+01	6.65E+00	9.73E-03	3.33E-01	5.09E-01	-0.97	-1.96	2.85E+00	5.60E+00
Ccdc9b	2	5.61E+01	1.19E+01	1.00E-02	3.33E-01	5.05E-01	-0.99	-1.98	5.13E+00	1.02E+01
Abhd1	5	1.39E+01	2.81E+00	1.25E-03	3.13E-01	5.01E-01	-1.00	-2.00	1.26E+00	2.52E+00
Gm32687	10	8.41E+00	1.79E+00	1.05E-02	3.33E-01	5.00E-01	-1.00	-2.00	7.65E-01	1.53E+00
H2ac19	3	2.35E+01	5.53E+00	4.32E-02	3.92E-01	4.96E-01	-1.01	-2.02	2.13E+00	4.28E+00
Eppk1	15	6.63E+01	1.38E+01	2.02E-02	3.51E-01	4.94E-01	-1.02	-2.02	5.97E+00	1.21E+01
Acox2	14	1.92E+01	4.24E+00	9.39E-03	3.33E-01	4.78E-01	-1.07	-2.09	1.69E+00	3.53E+00
E430024I08Rik	13	9.66E+00	2.33E+00	2.80E-02	3.53E-01	4.71E-01	-1.09	-2.12	8.40E-01	1.79E+00
Ttc25	11	9.54E+01	2.89E+01	2.96E-02	3.58E-01	4.70E-01	-1.09	-2.13	8.29E+00	1.76E+01

Ntsr2	12	1.38E+01	3.35E+00	1.93E-02	3.49E-01	4.62E-01	-1.12	-2.17	1.18E+00	2.57E+00
Zkscan4	13	1.59E+01	4.31E+00	2.35E-02	3.52E-01	4.59E-01	-1.12	-2.18	1.36E+00	2.97E+00
Pnlcd1	17	1.35E+02	3.23E+01	3.93E-03	3.13E-01	4.39E-01	-1.19	-2.28	1.11E+01	2.53E+01
Hpgds	6	1.22E+01	3.90E+00	2.84E-02	3.55E-01	4.21E-01	-1.25	-2.37	9.72E-01	2.31E+00
Cyp2f2	7	9.13E+00	2.42E+00	3.68E-02	3.82E-01	4.00E-01	-1.32	-2.50	7.02E-01	1.76E+00
Zfp605	5	1.74E+01	3.90E+00	2.67E-03	3.13E-01	3.95E-01	-1.34	-2.53	1.33E+00	3.36E+00
Egf	3	8.36E+00	2.53E+00	2.73E-02	3.52E-01	3.85E-01	-1.38	-2.59	6.25E-01	1.62E+00
Dcst1	3	9.51E+00	2.45E+00	1.75E-02	3.49E-01	3.60E-01	-1.48	-2.78	6.73E-01	1.87E+00
Nup210	6	1.20E+01	3.09E+00	3.41E-02	3.76E-01	3.56E-01	-1.49	-2.81	8.42E-01	2.37E+00
Wscd2	5	1.68E+01	4.55E+00	3.93E-02	3.86E-01	3.53E-01	-1.50	-2.83	1.17E+00	3.32E+00
Ryr2	13	2.60E+01	7.66E+00	1.82E-03	3.13E-01	3.23E-01	-1.63	-3.10	1.69E+00	5.24E+00
Ncan	8	4.34E+01	1.04E+01	1.10E-02	3.33E-01	2.97E-01	-1.75	-3.36	2.64E+00	8.87E+00
Slc15a5	6	1.43E+01	4.79E+00	1.87E-02	3.49E-01	1.65E-01	-2.60	-6.08	5.22E-01	3.18E+00

Statistical analysis at Partek Flow software: ANOVA; only genes with a $p < 0.05$ are shown; total counts is the number of reads overlapping a specific gene.

Table S6- Gene set enrichment analysis of differentially expressed genes in adult BAT-D3KO iBAT.

Gene set	Description	Enrichment score	P-value
GO:1990904	ribonucleoprotein complex	68.9	1.14E-30
GO:0043231	intracellular membrane-bounded organelle	66.4	1.46E-29
GO:0043227	membrane-bounded organelle	58.6	3.38E-26
GO:0003723	RNA binding	57.0	1.73E-25
GO:0016070	RNA metabolic process	57.0	1.77E-25
GO:0034641	cellular nitrogen compound metabolic process	56.6	2.52E-25
GO:0005634	nucleus	55.6	7.15E-25
GO:0043226	organelle	55.0	1.26E-24
GO:0006396	RNA processing	54.8	1.52E-24
GO:0043229	intracellular organelle	54.7	1.74E-24
GO:0032991	protein-containing complex	51.6	4.06E-23
GO:0003676	nucleic acid binding	49.7	2.61E-22
GO:0044237	cellular metabolic process	46.6	5.63E-21
GO:0043170	macromolecule metabolic process	44.1	7.15E-20
GO:0008152	metabolic process	43.9	8.41E-20
GO:0006139	nucleobase-containing compound metabolic process	43.7	1.05E-19
GO:0090304	nucleic acid metabolic process	43.0	2.21E-19
GO:0044238	primary metabolic process	41.5	9.22E-19
GO:0006807	nitrogen compound metabolic process	41.0	1.52E-18
GO:0016071	mRNA metabolic process	39.9	4.56E-18
GO:0006397	mRNA processing	39.8	5.02E-18
GO:0003735	structural constituent of ribosome	39.8	5.20E-18
GO:0005840	ribosome	39.7	5.48E-18
GO:0044391	ribosomal subunit	39.0	1.10E-17
GO:0046483	heterocycle metabolic process	39.0	1.20E-17
GO:0071704	organic substance metabolic process	38.4	2.07E-17
GO:0006725	cellular aromatic compound metabolic process	38.0	3.20E-17
GO:1901360	organic cyclic compound metabolic process	33.6	2.49E-15
GO:0008380	RNA splicing	32.0	1.26E-14
GO:0097159	organic cyclic compound binding	29.3	1.97E-13
GO:1901363	heterocyclic compound binding	29.0	2.67E-13
GO:0044271	cellular nitrogen compound biosynthetic process	28.4	4.62E-13
GO:0005681	spliceosomal complex	28.2	5.54E-13
GO:1902494	catalytic complex	27.0	1.87E-12
GO:0019219	regulation of nucleobase-containing compound metabolic process	26.5	3.00E-12
GO:0009059	macromolecule biosynthetic process	26.1	4.57E-12
GO:0022625	cytosolic large ribosomal subunit	26.1	4.69E-12
GO:0010468	regulation of gene expression	25.8	6.05E-12
GO:0051252	regulation of RNA metabolic process	25.6	7.79E-12
GO:0003729	mRNA binding	24.7	1.79E-11

GO:0044260	cellular macromolecule metabolic process	24.2	3.10E-11
GO:0034645	cellular macromolecule biosynthetic process	23.8	4.39E-11
GO:0005654	nucleoplasm	23.5	6.44E-11
GO:0006412	translation	22.6	1.47E-10
GO:0015934	large ribosomal subunit	22.6	1.50E-10
GO:0043043	peptide biosynthetic process	21.6	4.33E-10
GO:2000112	regulation of cellular macromolecule biosynthetic process	21.6	4.37E-10
GO:0005730	nucleolus	21.3	5.42E-10
GO:1901576	organic substance biosynthetic process	21.2	5.97E-10
GO:0009058	biosynthetic process	21.2	6.04E-10
GO:0036002	pre-mRNA binding	21.1	7.07E-10
GO:0050684	regulation of mRNA processing	20.7	1.01E-09
GO:0010556	regulation of macromolecule biosynthetic process	20.3	1.53E-09
GO:0000377	RNA splicing, via transesterification reactions with bulged adenosine as nucleophile	20.3	1.55E-09
GO:0000398	mRNA splicing, via spliceosome	20.3	1.55E-09
GO:0000375	RNA splicing, via transesterification reactions	20.1	1.90E-09
GO:0006518	peptide metabolic process	20.1	1.92E-09
GO:0031326	regulation of cellular biosynthetic process	19.9	2.29E-09
GO:0010628	positive regulation of gene expression	19.9	2.36E-09
GO:0015935	small ribosomal subunit	19.8	2.51E-09
GO:0009889	regulation of biosynthetic process	19.7	2.88E-09
GO:0016607	nuclear speck	19.6	3.10E-09
GO:0022627	cytosolic small ribosomal subunit	19.1	4.98E-09
GO:0044249	cellular biosynthetic process	19.0	5.40E-09
GO:1903311	regulation of mRNA metabolic process	18.4	9.72E-09
GO:0045935	positive regulation of nucleobase-containing compound metabolic process	18.4	1.01E-08
GO:0006364	rRNA processing	18.4	1.04E-08
GO:0016072	rRNA metabolic process	18.3	1.11E-08
GO:0044267	cellular protein metabolic process	17.8	1.88E-08
GO:0019222	regulation of metabolic process	17.8	1.93E-08
GO:0071826	ribonucleoprotein complex subunit organization	17.6	2.17E-08
GO:0031328	positive regulation of cellular biosynthetic process	17.5	2.43E-08
GO:0006355	regulation of transcription, DNA-templated	17.5	2.53E-08
GO:0050657	nucleic acid transport	17.5	2.54E-08
GO:0050658	RNA transport	17.5	2.54E-08
GO:0034470	ncRNA processing	17.4	2.78E-08
GO:0060255	regulation of macromolecule metabolic process	17.3	3.18E-08
GO:0009891	positive regulation of biosynthetic process	17.2	3.51E-08
GO:1903506	regulation of nucleic acid-templated transcription	17.2	3.55E-08
GO:0051236	establishment of RNA localization	17.1	3.77E-08
GO:0010557	positive regulation of macromolecule biosynthetic process	17.1	3.79E-08
GO:2001141	regulation of RNA biosynthetic process	17.0	4.02E-08

GO:0080090	regulation of primary metabolic process	17.0	4.24E-08
GO:0043484	regulation of RNA splicing	16.6	6.18E-08
GO:0043604	amide biosynthetic process	16.5	6.73E-08
GO:0031323	regulation of cellular metabolic process	16.5	7.14E-08
GO:0022618	ribonucleoprotein complex assembly	16.4	7.44E-08
GO:0051254	positive regulation of RNA metabolic process	16.3	8.00E-08
GO:0016604	nuclear body	16.3	8.05E-08
GO:0051171	regulation of nitrogen compound metabolic process	16.3	8.49E-08
GO:0048024	regulation of mRNA splicing, via spliceosome	16.1	1.01E-07
GO:1990234	transferase complex	15.5	1.79E-07
GO:0000381	regulation of alternative mRNA splicing, via spliceosome	15.0	2.98E-07
GO:0071013	catalytic step 2 spliceosome	14.9	3.46E-07
GO:0045893	positive regulation of transcription, DNA-templated	14.9	3.48E-07
GO:0034708	methyltransferase complex	14.8	3.66E-07
GO:0034660	ncRNA metabolic process	14.8	3.88E-07
GO:1903508	positive regulation of nucleic acid-templated transcription	14.7	4.05E-07
GO:1902680	positive regulation of RNA biosynthetic process	14.7	4.27E-07
GO:0009893	positive regulation of metabolic process	14.6	4.53E-07
GO:0015931	nucleobase-containing compound transport	14.3	5.90E-07
GO:0006357	regulation of transcription by RNA polymerase II	14.3	6.02E-07
GO:0003712	transcription coregulator activity	14.3	6.35E-07
GO:0003677	DNA binding	14.2	6.92E-07
GO:0022613	ribonucleoprotein complex biogenesis	14.1	7.42E-07
GO:0042274	ribosomal small subunit biogenesis	13.8	1.00E-06
GO:0043565	sequence-specific DNA binding	13.7	1.16E-06
GO:0140110	transcription regulator activity	13.6	1.30E-06
GO:0010604	positive regulation of macromolecule metabolic process	13.6	1.30E-06
GO:0010629	negative regulation of gene expression	13.5	1.38E-06
GO:0051253	negative regulation of RNA metabolic process	13.4	1.54E-06
GO:0019538	protein metabolic process	13.3	1.66E-06
GO:0044085	cellular component biogenesis	13.2	1.93E-06
GO:0009987	cellular process	12.9	2.42E-06
GO:0110165	cellular anatomical entity	12.3	4.35E-06
GO:0006091	generation of precursor metabolites and energy	12.2	4.87E-06
GO:0043021	ribonucleoprotein complex binding	12.2	5.04E-06
GO:0010605	negative regulation of macromolecule metabolic process	12.1	5.41E-06
GO:0001067	regulatory region nucleic acid binding	12.1	5.83E-06
GO:0005739	mitochondrion	12.0	6.22E-06
GO:0034654	nucleobase-containing compound biosynthetic process	12.0	6.29E-06
GO:1901566	organonitrogen compound biosynthetic process	11.9	6.53E-06
GO:0045934	negative regulation of nucleobase-containing compound metabolic process	11.8	7.28E-06
GO:0031325	positive regulation of cellular metabolic process	11.8	7.30E-06
GO:0006457	protein folding	11.8	7.78E-06

GO:0043603	cellular amide metabolic process	11.7	8.28E-06
GO:0051173	positive regulation of nitrogen compound metabolic process	11.6	8.87E-06
GO:0032774	RNA biosynthetic process	11.6	9.09E-06
GO:0018130	heterocycle biosynthetic process	11.6	9.53E-06
GO:0005488	binding	11.5	1.05E-05
GO:0051028	mRNA transport	11.4	1.07E-05
GO:0005198	structural molecule activity	11.4	1.12E-05
GO:0044212	transcription regulatory region DNA binding	11.3	1.29E-05
GO:0030684	preribosome	11.2	1.34E-05
GO:0000976	transcription regulatory region sequence-specific DNA binding	11.1	1.52E-05
GO:0000987	cis-regulatory region sequence-specific DNA binding	11.0	1.65E-05
GO:0008134	transcription factor binding	11.0	1.71E-05
GO:0019438	aromatic compound biosynthetic process	11.0	1.74E-05
GO:1990837	sequence-specific double-stranded DNA binding	10.9	1.91E-05
GO:1901564	organonitrogen compound metabolic process	10.9	1.92E-05
GO:0051172	negative regulation of nitrogen compound metabolic process	10.8	1.99E-05
GO:0000977	RNA polymerase II regulatory region sequence-specific DNA binding	10.7	2.15E-05
GO:0000978	RNA polymerase II cis-regulatory region sequence-specific DNA binding	10.7	2.25E-05
GO:1903312	negative regulation of mRNA metabolic process	10.6	2.49E-05
GO:0035326	cis-regulatory region binding	10.6	2.51E-05
GO:0018205	peptidyl-lysine modification	10.3	3.38E-05
GO:0001012	RNA polymerase II regulatory region DNA binding	10.3	3.47E-05
GO:0051169	nuclear transport	10.3	3.51E-05
GO:0006913	nucleocytoplasmic transport	10.3	3.51E-05
GO:2000113	negative regulation of cellular macromolecule biosynthetic process	10.2	3.74E-05
GO:0005622	intracellular	10.2	3.76E-05
GO:1901362	organic cyclic compound biosynthetic process	10.2	3.78E-05
GO:0003682	chromatin binding	10.2	3.85E-05
GO:0045944	positive regulation of transcription by RNA polymerase II	10.1	4.02E-05
GO:0034622	cellular protein-containing complex assembly	10.0	4.48E-05
GO:0002181	cytoplasmic translation	9.8	5.29E-05
GO:0098798	mitochondrial protein complex	9.8	5.37E-05
GO:0019899	enzyme binding	9.7	5.88E-05
GO:0006325	chromatin organization	9.7	6.13E-05
GO:0045892	negative regulation of transcription, DNA-templated	9.5	7.50E-05
GO:0005849	mRNA cleavage factor complex	9.4	8.10E-05
GO:0005829	cytosol	9.4	8.13E-05
GO:0009892	negative regulation of metabolic process	9.4	8.66E-05
GO:0050686	negative regulation of mRNA processing	9.4	8.70E-05
GO:1903507	negative regulation of nucleic acid-templated transcription	9.3	8.97E-05
GO:0016569	covalent chromatin modification	9.3	9.01E-05
GO:1902679	negative regulation of RNA biosynthetic process	9.3	9.38E-05
GO:0097157	pre-mRNA intronic binding	9.3	9.56E-05

GO:0016570	histone modification	9.2	9.91E-05
GO:0005847	mRNA cleavage and polyadenylation specificity factor complex	9.2	1.01E-04
GO:0035264	multicellular organism growth	9.2	1.04E-04
GO:0000956	nuclear-transcribed mRNA catabolic process	9.1	1.09E-04
GO:0045292	mRNA cis splicing, via spliceosome	9.0	1.22E-04
GO:0010558	negative regulation of macromolecule biosynthetic process	9.0	1.24E-04
GO:0034655	nucleobase-containing compound catabolic process	9.0	1.26E-04
GO:0061077	chaperone-mediated protein folding	9.0	1.26E-04
GO:0051082	unfolded protein binding	9.0	1.29E-04
GO:0035097	histone methyltransferase complex	8.8	1.52E-04
GO:0003690	double-stranded DNA binding	8.8	1.52E-04
GO:0065003	protein-containing complex assembly	8.8	1.54E-04
GO:0006351	transcription, DNA-templated	8.7	1.59E-04
GO:0005685	U1 snRNP	8.7	1.60E-04
GO:0030518	intracellular steroid hormone receptor signaling pathway	8.7	1.62E-04
GO:0097659	nucleic acid-templated transcription	8.7	1.74E-04
GO:0098732	macromolecule deacylation	8.5	1.94E-04
GO:0035601	protein deacylation	8.5	1.94E-04
GO:0019843	rRNA binding	8.5	2.07E-04
GO:0003713	transcription coactivator activity	8.5	2.09E-04
GO:0050685	positive regulation of mRNA processing	8.4	2.17E-04
GO:0043933	protein-containing complex subunit organization	8.4	2.21E-04
GO:0031324	negative regulation of cellular metabolic process	8.4	2.26E-04
GO:0043232	intracellular non-membrane-bounded organelle	8.4	2.28E-04
GO:0009890	negative regulation of biosynthetic process	8.4	2.35E-04
GO:0043228	non-membrane-bounded organelle	8.3	2.40E-04
GO:0044270	cellular nitrogen compound catabolic process	8.3	2.48E-04
GO:0006405	RNA export from nucleus	8.2	2.71E-04
GO:0005684	U2-type spliceosomal complex	8.2	2.78E-04
GO:0032040	small-subunit processome	8.2	2.86E-04
GO:0043412	macromolecule modification	8.1	2.92E-04
GO:1990247	N6-methyladenosine-containing RNA binding	8.1	3.01E-04
GO:1990446	U1 snRNP binding	8.1	3.01E-04
GO:0140296	general transcription initiation factor binding	8.1	3.08E-04
GO:0006476	protein deacetylation	8.1	3.13E-04
GO:0010608	posttranscriptional regulation of gene expression	8.0	3.28E-04
GO:0000470	maturation of LSU-rRNA	8.0	3.30E-04
GO:0031327	negative regulation of cellular biosynthetic process	8.0	3.47E-04
GO:0006997	nucleus organization	8.0	3.52E-04
GO:0006376	mRNA splice site selection	7.9	3.61E-04
GO:0035259	glucocorticoid receptor binding	7.9	3.64E-04
GO:0019439	aromatic compound catabolic process	7.9	3.73E-04
GO:0031490	chromatin DNA binding	7.8	4.16E-04

GO:0006402	mRNA catabolic process	7.8	4.28E-04
GO:0046907	intracellular transport	7.7	4.34E-04
GO:0071705	nitrogen compound transport	7.7	4.39E-04
GO:0051168	nuclear export	7.7	4.41E-04
GO:0031056	regulation of histone modification	7.7	4.51E-04
GO:0006986	response to unfolded protein	7.7	4.65E-04
GO:0006473	protein acetylation	7.7	4.71E-04
GO:0017069	snRNA binding	7.6	4.82E-04
GO:1900363	regulation of mRNA polyadenylation	7.6	4.93E-04
GO:0000028	ribosomal small subunit assembly	7.6	4.93E-04
GO:0000380	alternative mRNA splicing, via spliceosome	7.6	4.93E-04
GO:0016575	histone deacetylation	7.6	4.94E-04
GO:0001825	blastocyst formation	7.6	4.98E-04
GO:0030515	snoRNA binding	7.6	4.98E-04
GO:0045454	cell redox homeostasis	7.5	5.58E-04
GO:0098803	respiratory chain complex	7.5	5.76E-04
GO:0030521	androgen receptor signaling pathway	7.4	6.11E-04
GO:0043401	steroid hormone mediated signaling pathway	7.4	6.15E-04
GO:0046700	heterocycle catabolic process	7.3	6.76E-04
GO:0032182	ubiquitin-like protein binding	7.3	6.80E-04
GO:0000122	negative regulation of transcription by RNA polymerase II	7.3	6.87E-04
GO:0090311	regulation of protein deacetylation	7.2	7.65E-04
GO:0061629	RNA polymerase II-specific DNA-binding transcription factor binding	7.2	7.73E-04
GO:0055024	regulation of cardiac muscle tissue development	7.1	7.90E-04
GO:0043435	response to corticotropin-releasing hormone	7.1	7.98E-04
GO:0071376	cellular response to corticotropin-releasing hormone stimulus	7.1	7.98E-04
GO:0033119	negative regulation of RNA splicing	7.0	8.97E-04
GO:0000785	chromatin	7.0	9.14E-04
GO:0034250	positive regulation of cellular amide metabolic process	7.0	9.49E-04
GO:0062105	RNA 2'-O-methyltransferase activity	7.0	9.51E-04
GO:0048025	negative regulation of mRNA splicing, via spliceosome	6.9	1.02E-03
GO:0048026	positive regulation of mRNA splicing, via spliceosome	6.9	1.02E-03
GO:0031396	regulation of protein ubiquitination	6.9	1.04E-03
GO:2001252	positive regulation of chromosome organization	6.9	1.04E-03
GO:0016278	lysine N-methyltransferase activity	6.8	1.07E-03
GO:0016279	protein-lysine N-methyltransferase activity	6.8	1.07E-03
GO:0006401	RNA catabolic process	6.8	1.13E-03
GO:0043022	ribosome binding	6.8	1.15E-03
GO:0019103	pyrimidine nucleotide binding	6.8	1.16E-03
GO:0070990	snRNP binding	6.8	1.16E-03
GO:0005667	transcription factor complex	6.8	1.16E-03
GO:0042788	polysomal ribosome	6.7	1.18E-03
GO:0051085	chaperone cofactor-dependent protein refolding	6.7	1.18E-03

GO:0055021	regulation of cardiac muscle tissue growth	6.7	1.20E-03
GO:0018024	histone-lysine N-methyltransferase activity	6.7	1.21E-03
GO:0019217	regulation of fatty acid metabolic process	6.7	1.22E-03
GO:1901361	organic cyclic compound catabolic process	6.6	1.30E-03
GO:0005689	U12-type spliceosomal complex	6.6	1.38E-03
GO:0032784	regulation of DNA-templated transcription, elongation	6.6	1.40E-03
GO:0046034	ATP metabolic process	6.5	1.44E-03
GO:0010942	positive regulation of cell death	6.5	1.45E-03
GO:0035770	ribonucleoprotein granule	6.5	1.49E-03
GO:0042254	ribosome biogenesis	6.5	1.51E-03
GO:0018394	peptidyl-lysine acetylation	6.5	1.51E-03
GO:0140098	catalytic activity, acting on RNA	6.5	1.53E-03
GO:1902493	acetyltransferase complex	6.5	1.57E-03
GO:0031248	protein acetyltransferase complex	6.5	1.57E-03
GO:0006464	cellular protein modification process	6.4	1.66E-03
GO:0036211	protein modification process	6.4	1.66E-03
GO:0042054	histone methyltransferase activity	6.4	1.69E-03
GO:0007623	circadian rhythm	6.4	1.72E-03
GO:0010941	regulation of cell death	6.3	1.75E-03
GO:0006090	pyruvate metabolic process	6.3	1.81E-03
GO:0033044	regulation of chromosome organization	6.3	1.84E-03
GO:0009055	electron transfer activity	6.3	1.88E-03
GO:0022900	electron transport chain	6.3	1.90E-03
GO:1903320	regulation of protein modification by small protein conjugation or removal	6.3	1.92E-03
GO:0046620	regulation of organ growth	6.3	1.93E-03
GO:0042382	paraspeckles	6.2	2.06E-03
GO:0070569	uridylyltransferase activity	6.2	2.06E-03
GO:0046976	histone methyltransferase activity (H3-K27 specific)	6.2	2.06E-03
GO:0048332	mesoderm morphogenesis	6.2	2.06E-03
GO:0032525	somite rostral/caudal axis specification	6.2	2.06E-03
GO:1902275	regulation of chromatin organization	6.2	2.08E-03
GO:0016676	oxidoreductase activity, acting on a heme group of donors, oxygen as acceptor	6.2	2.11E-03
GO:0004129	cytochrome-c oxidase activity	6.2	2.11E-03
GO:0035145	exon-exon junction complex	6.2	2.11E-03
GO:0015002	heme-copper terminal oxidase activity	6.2	2.11E-03
GO:1901861	regulation of muscle tissue development	6.1	2.14E-03
GO:0090501	RNA phosphodiester bond hydrolysis	6.1	2.14E-03
GO:0045727	positive regulation of translation	6.1	2.15E-03
GO:0035966	response to topologically incorrect protein	6.1	2.17E-03
GO:0070647	protein modification by small protein conjugation or removal	6.1	2.18E-03
GO:0060420	regulation of heart growth	6.1	2.20E-03
GO:0001675	acrosome assembly	6.1	2.24E-03

GO:0032183	SUMO binding	6.1	2.24E-03
GO:0035098	ESC/E(Z) complex	6.1	2.24E-03
GO:0036464	cytoplasmic ribonucleoprotein granule	6.1	2.32E-03
GO:0043543	protein acylation	6.0	2.36E-03
GO:0031440	regulation of mRNA 3'-end processing	6.0	2.40E-03
GO:0008023	transcription elongation factor complex	6.0	2.41E-03
GO:0046320	regulation of fatty acid oxidation	6.0	2.46E-03
GO:0003730	mRNA 3'-UTR binding	6.0	2.48E-03
GO:0003714	transcription corepressor activity	6.0	2.56E-03
GO:0035257	nuclear hormone receptor binding	6.0	2.56E-03
GO:0035258	steroid hormone receptor binding	5.9	2.83E-03
GO:0016675	oxidoreductase activity, acting on a heme group of donors	5.9	2.86E-03
GO:0010155	regulation of proton transport	5.9	2.86E-03
GO:0003727	single-stranded RNA binding	5.8	2.91E-03
GO:0031625	ubiquitin protein ligase binding	5.8	2.93E-03
GO:0022904	respiratory electron transport chain	5.8	2.96E-03
GO:0045444	fat cell differentiation	5.8	2.96E-03
GO:0016151	nickel cation binding	5.8	2.97E-03
GO:0017150	tRNA dihydrouridine synthase activity	5.8	2.97E-03
GO:0044530	supraspliceosomal complex	5.8	2.97E-03
GO:0070898	RNA polymerase III preinitiation complex assembly	5.8	2.97E-03
GO:0072531	pyrimidine-containing compound transmembrane transport	5.8	2.97E-03
GO:0000126	transcription factor TFIIIB complex	5.8	2.97E-03
GO:0000243	commitment complex	5.8	2.97E-03
GO:0001025	RNA polymerase III general transcription initiation factor binding	5.8	2.97E-03
GO:1905323	telomerase holoenzyme complex assembly	5.8	2.97E-03
GO:0005672	transcription factor TFIIA complex	5.8	2.97E-03
GO:0031508	pericentric heterochromatin assembly	5.8	2.97E-03
GO:0015031	protein transport	5.8	3.07E-03
GO:1903846	positive regulation of cellular response to transforming growth factor beta stimulus	5.8	3.09E-03
GO:0030511	positive regulation of transforming growth factor beta receptor signaling pathway	5.8	3.09E-03
GO:0009948	anterior/posterior axis specification	5.8	3.09E-03
GO:0034101	erythrocyte homeostasis	5.8	3.10E-03
GO:0006006	glucose metabolic process	5.7	3.22E-03
GO:0016202	regulation of striated muscle tissue development	5.7	3.40E-03
GO:0006417	regulation of translation	5.7	3.51E-03
GO:0033120	positive regulation of RNA splicing	5.6	3.54E-03
GO:1900407	regulation of cellular response to oxidative stress	5.6	3.65E-03
GO:0051147	regulation of muscle cell differentiation	5.6	3.72E-03
GO:0000469	cleavage involved in rRNA processing	5.6	3.78E-03
GO:0043067	regulation of programmed cell death	5.6	3.80E-03

GO:0000184	nuclear-transcribed mRNA catabolic process, nonsense-mediated decay	5.6	3.81E-03
GO:0051084	'de novo' posttranslational protein folding	5.6	3.81E-03
GO:1903748	negative regulation of establishment of protein localization to mitochondrion	5.6	3.81E-03
GO:0001016	RNA polymerase III regulatory region DNA binding	5.6	3.81E-03
GO:1904732	regulation of electron transfer activity	5.6	3.81E-03
GO:0055114	oxidation-reduction process	5.6	3.81E-03
GO:0016573	histone acetylation	5.5	3.91E-03
GO:0004407	histone deacetylase activity	5.5	3.93E-03
GO:0048634	regulation of muscle organ development	5.5	4.07E-03
GO:0018193	peptidyl-amino acid modification	5.5	4.08E-03
GO:0008170	N-methyltransferase activity	5.5	4.13E-03
GO:0045184	establishment of protein localization	5.5	4.15E-03
GO:0015833	peptide transport	5.5	4.21E-03
GO:1902882	regulation of response to oxidative stress	5.4	4.39E-03
GO:0046321	positive regulation of fatty acid oxidation	5.4	4.41E-03
GO:0032239	regulation of nucleobase-containing compound transport	5.4	4.41E-03
GO:0032922	circadian regulation of gene expression	5.4	4.60E-03
GO:0071280	cellular response to copper ion	5.4	4.66E-03
GO:0055026	negative regulation of cardiac muscle tissue development	5.4	4.66E-03
GO:0006458	'de novo' protein folding	5.4	4.66E-03
GO:1905269	positive regulation of chromatin organization	5.4	4.73E-03
GO:0051427	hormone receptor binding	5.3	4.80E-03
GO:0044389	ubiquitin-like protein ligase binding	5.3	4.89E-03
GO:0031060	regulation of histone methylation	5.3	4.91E-03
GO:0000578	embryonic axis specification	5.3	4.92E-03
GO:0031058	positive regulation of histone modification	5.3	4.92E-03
GO:0033558	protein deacetylase activity	5.3	4.93E-03
GO:0046031	ADP metabolic process	5.3	0.01
GO:0120114	Sm-like protein family complex	5.3	0.01
GO:2001242	regulation of intrinsic apoptotic signaling pathway	5.3	0.01
GO:0009798	axis specification	5.2	0.01
GO:0043068	positive regulation of programmed cell death	5.2	0.01
GO:0006096	glycolytic process	5.2	0.01
GO:0006757	ATP generation from ADP	5.2	0.01
GO:0080135	regulation of cellular response to stress	5.1	0.01
GO:0042886	amide transport	5.1	0.01
GO:0070182	DNA polymerase binding	5.1	0.01
GO:0005732	small nucleolar ribonucleoprotein complex	5.1	0.01
GO:0031998	regulation of fatty acid beta-oxidation	5.1	0.01
GO:0034248	regulation of cellular amide metabolic process	5.1	0.01
GO:2000725	regulation of cardiac muscle cell differentiation	5.1	0.01
GO:0018393	internal peptidyl-lysine acetylation	5.1	0.01

GO:0048589	developmental growth	5.1	0.01
GO:0045843	negative regulation of striated muscle tissue development	5.1	0.01
GO:0044183	protein folding chaperone	5.1	0.01
GO:0001671	ATPase activator activity	5.1	0.01
GO:0042752	regulation of circadian rhythm	5.1	0.01
GO:0035520	monoubiquitinated protein deubiquitination	5.1	0.01
GO:0030522	intracellular receptor signaling pathway	5.0	0.01
GO:0043065	positive regulation of apoptotic process	5.0	0.01
GO:0070935	3'-UTR-mediated mRNA stabilization	5.0	0.01
GO:0061000	negative regulation of dendritic spine development	5.0	0.01
GO:0070940	dephosphorylation of RNA polymerase II C-terminal domain	5.0	0.01
GO:0071256	translocon complex	5.0	0.01
GO:0045875	negative regulation of sister chromatid cohesion	5.0	0.01
GO:1900034	regulation of cellular response to heat	5.0	0.01
GO:0097342	riposome	5.0	0.01
GO:0000395	mRNA 5'-splice site recognition	5.0	0.01
GO:0051450	myoblast proliferation	5.0	0.01
GO:0005784	Sec61 translocon complex	5.0	0.01
GO:0031415	NatA complex	5.0	0.01
GO:0032557	pyrimidine ribonucleotide binding	5.0	0.01
GO:0034715	pICln-Sm protein complex	5.0	0.01
GO:0060623	regulation of chromosome condensation	5.0	0.01
GO:0035666	TRIF-dependent toll-like receptor signaling pathway	5.0	0.01
GO:0090370	negative regulation of cholesterol efflux	5.0	0.01
GO:0002039	p53 binding	5.0	0.01
GO:0015980	energy derivation by oxidation of organic compounds	5.0	0.01
GO:0000123	histone acetyltransferase complex	5.0	0.01
GO:0048635	negative regulation of muscle organ development	4.9	0.01
GO:0043414	macromolecule methylation	4.9	0.01
GO:0009792	embryo development ending in birth or egg hatching	4.9	0.01
GO:0016627	oxidoreductase activity, acting on the CH-CH group of donors	4.9	0.01
GO:0140297	DNA-binding transcription factor binding	4.9	0.01
GO:0031329	regulation of cellular catabolic process	4.9	0.01
GO:0001701	in utero embryonic development	4.9	0.01
GO:0042981	regulation of apoptotic process	4.9	0.01
GO:0031072	heat shock protein binding	4.9	0.01
GO:0005996	monosaccharide metabolic process	4.9	0.01
GO:0040007	growth	4.9	0.01
GO:0019318	hexose metabolic process	4.9	0.01
GO:2000757	negative regulation of peptidyl-lysine acetylation	4.8	0.01
GO:0001091	RNA polymerase II general transcription initiation factor binding	4.8	0.01
GO:0006368	transcription elongation from RNA polymerase II promoter	4.8	0.01
GO:0009755	hormone-mediated signaling pathway	4.8	0.01

GO:1902175	regulation of oxidative stress-induced intrinsic apoptotic signaling pathway	4.8	0.01
GO:0032369	negative regulation of lipid transport	4.8	0.01
GO:0048255	mRNA stabilization	4.8	0.01
GO:0030490	maturation of SSU-rRNA	4.8	0.01
GO:0060590	ATPase regulator activity	4.8	0.01
GO:1901862	negative regulation of muscle tissue development	4.8	0.01
GO:0030532	small nuclear ribonucleoprotein complex	4.8	0.01
GO:0005737	cytoplasm	4.8	0.01
GO:0006366	transcription by RNA polymerase II	4.8	0.01
GO:0019866	organelle inner membrane	4.8	0.01
GO:0006475	internal protein amino acid acetylation	4.8	0.01
GO:0043966	histone H3 acetylation	4.8	0.01
GO:0051879	Hsp90 protein binding	4.8	0.01
GO:0031519	PcG protein complex	4.8	0.01
GO:0046872	metal ion binding	4.8	0.01
GO:0048522	positive regulation of cellular process	4.8	0.01
GO:0003725	double-stranded RNA binding	4.8	0.01
GO:0051641	cellular localization	4.8	0.01
GO:0016922	nuclear receptor binding	4.8	0.01
GO:0070104	negative regulation of interleukin-6-mediated signaling pathway	4.8	0.01
GO:0019255	glucose 1-phosphate metabolic process	4.8	0.01
GO:0106050	tRNA 2'-O-methyltransferase activity	4.8	0.01
GO:0106140	P-TEFb complex binding	4.8	0.01
GO:0022605	mammalian oogenesis stage	4.8	0.01
GO:0072737	response to diamide	4.8	0.01
GO:0072738	cellular response to diamide	4.8	0.01
GO:1902340	negative regulation of chromosome condensation	4.8	0.01
GO:0099609	microtubule lateral binding	4.8	0.01
GO:0002135	CTP binding	4.8	0.01
GO:0003220	left ventricular cardiac muscle tissue morphogenesis	4.8	0.01
GO:0003977	UDP-N-acetylglucosamine diphosphorylase activity	4.8	0.01
GO:0030627	pre-mRNA 5'-splice site binding	4.8	0.01
GO:0031509	telomeric heterochromatin assembly	4.8	0.01
GO:0006343	establishment of chromatin silencing	4.8	0.01
GO:0031930	mitochondria-nucleus signaling pathway	4.8	0.01
GO:0008078	mesodermal cell migration	4.8	0.01
GO:0008650	rRNA (uridine-2'-O-)-methyltransferase activity	4.8	0.01
GO:0036337	Fas signaling pathway	4.8	0.01
GO:0015234	thiamine transmembrane transporter activity	4.8	0.01
GO:0032269	negative regulation of cellular protein metabolic process	4.7	0.01
GO:0009790	embryo development	4.7	0.01
GO:0050821	protein stabilization	4.7	0.01
GO:0009060	aerobic respiration	4.7	0.01

GO:0071004	U2-type prespliceosome	4.7	0.01
GO:0070897	transcription preinitiation complex assembly	4.7	0.01
GO:0071010	prespliceosome	4.7	0.01
GO:0045793	positive regulation of cell size	4.7	0.01
GO:0005521	lamin binding	4.7	0.01
GO:0034719	SMN-Sm protein complex	4.7	0.01
GO:0090083	regulation of inclusion body assembly	4.7	0.01
GO:2000756	regulation of peptidyl-lysine acetylation	4.7	0.01
GO:0032268	regulation of cellular protein metabolic process	4.7	0.01
GO:0006406	mRNA export from nucleus	4.6	0.01
GO:1904591	positive regulation of protein import	4.6	0.01
GO:0071702	organic substance transport	4.6	0.01
GO:0008757	S-adenosylmethionine-dependent methyltransferase activity	4.6	0.01
GO:0005687	U4 snRNP	4.6	0.01
GO:0045333	cellular respiration	4.6	0.01
GO:2000059	negative regulation of ubiquitin-dependent protein catabolic process	4.6	0.01
GO:0030880	RNA polymerase complex	4.6	0.01
GO:1902235	regulation of endoplasmic reticulum stress-induced intrinsic apoptotic signaling pathway	4.6	0.01
GO:1902884	positive regulation of response to oxidative stress	4.6	0.01
GO:0035198	miRNA binding	4.6	0.01
GO:0016363	nuclear matrix	4.6	0.01
GO:1903201	regulation of oxidative stress-induced cell death	4.6	0.01
GO:2001243	negative regulation of intrinsic apoptotic signaling pathway	4.6	0.01
GO:0034620	cellular response to unfolded protein	4.6	0.01
GO:0098800	inner mitochondrial membrane protein complex	4.6	0.01
GO:0001217	DNA-binding transcription repressor activity	4.6	0.01
GO:0001227	DNA-binding transcription repressor activity, RNA polymerase II-specific	4.6	0.01
GO:0043009	chordate embryonic development	4.6	0.01
GO:0043169	cation binding	4.5	0.01
GO:0097009	energy homeostasis	4.5	0.01
GO:0000979	RNA polymerase II core promoter sequence-specific DNA binding	4.5	0.01
GO:0032435	negative regulation of proteasomal ubiquitin-dependent protein catabolic process	4.5	0.01
GO:0032786	positive regulation of DNA-templated transcription, elongation	4.5	0.01
GO:0097525	spliceosomal snRNP complex	4.5	0.01
GO:0010467	gene expression	4.5	0.01
GO:0007030	Golgi organization	4.5	0.01
GO:1902373	negative regulation of mRNA catabolic process	4.5	0.01
GO:0009135	purine nucleoside diphosphate metabolic process	4.5	0.01
GO:0009179	purine ribonucleoside diphosphate metabolic process	4.5	0.01
GO:0051248	negative regulation of protein metabolic process	4.5	0.01
GO:0043122	regulation of I-kappaB kinase/NF-kappaB signaling	4.4	0.01

GO:0062013	positive regulation of small molecule metabolic process	4.4	0.01
GO:0040029	regulation of gene expression, epigenetic	4.4	0.01
GO:2001233	regulation of apoptotic signaling pathway	4.4	0.01
GO:0070069	cytochrome complex	4.4	0.01
GO:0055022	negative regulation of cardiac muscle tissue growth	4.4	0.01
GO:0006378	mRNA polyadenylation	4.4	0.01
GO:0061050	regulation of cell growth involved in cardiac muscle cell development	4.4	0.01
GO:0061117	negative regulation of heart growth	4.4	0.01
GO:0016779	nucleotidyltransferase activity	4.4	0.01
GO:0070932	histone H3 deacetylation	4.4	0.01
GO:0071243	cellular response to arsenic-containing substance	4.4	0.01
GO:0046831	regulation of RNA export from nucleus	4.4	0.01
GO:0099640	axo-dendritic protein transport	4.4	0.01
GO:0101031	chaperone complex	4.4	0.01
GO:1901984	negative regulation of protein acetylation	4.4	0.01
GO:0071557	histone H3-K27 demethylation	4.4	0.01
GO:0071763	nuclear membrane organization	4.4	0.01
GO:2001015	negative regulation of skeletal muscle cell differentiation	4.4	0.01
GO:0098961	dendritic transport of ribonucleoprotein complex	4.4	0.01
GO:0098963	dendritic transport of messenger ribonucleoprotein complex	4.4	0.01
GO:1903897	regulation of PERK-mediated unfolded protein response	4.4	0.01
GO:0001739	sex chromatin	4.4	0.01
GO:1905634	regulation of protein localization to chromatin	4.4	0.01
GO:0004726	non-membrane spanning protein tyrosine phosphatase activity	4.4	0.01
GO:0031264	death-inducing signaling complex	4.4	0.01
GO:0006048	UDP-N-acetylglucosamine biosynthetic process	4.4	0.01
GO:0034511	U3 snoRNA binding	4.4	0.01
GO:0060669	embryonic placenta morphogenesis	4.4	0.01
GO:0010986	positive regulation of lipoprotein particle clearance	4.4	0.01
GO:0009451	RNA modification	4.3	0.01
GO:1902229	regulation of intrinsic apoptotic signaling pathway in response to DNA damage	4.3	0.01
GO:0031124	mRNA 3'-end processing	4.3	0.01
GO:0006165	nucleoside diphosphate phosphorylation	4.3	0.01
GO:0016571	histone methylation	4.3	0.01
GO:0008276	protein methyltransferase activity	4.3	0.01
GO:0001650	fibrillar center	4.3	0.01
GO:0043124	negative regulation of I-kappaB kinase/NF-kappaB signaling	4.3	0.01
GO:0031491	nucleosome binding	4.3	0.01
GO:0042826	histone deacetylase binding	4.3	0.01
GO:0051087	chaperone binding	4.3	0.01
GO:0009132	nucleoside diphosphate metabolic process	4.3	0.01
GO:0072594	establishment of protein localization to organelle	4.3	0.01

GO:2001234	negative regulation of apoptotic signaling pathway	4.3	0.01
GO:0009894	regulation of catabolic process	4.3	0.01
GO:0019646	aerobic electron transport chain	4.2	0.01
GO:1901033	positive regulation of response to reactive oxygen species	4.2	0.01
GO:0098789	pre-mRNA cleavage required for polyadenylation	4.2	0.01
GO:0006123	mitochondrial electron transport, cytochrome c to oxygen	4.2	0.01
GO:0090576	RNA polymerase III transcription factor complex	4.2	0.01
GO:0032446	protein modification by small protein conjugation	4.2	0.01
GO:0010970	transport along microtubule	4.2	0.01
GO:0048518	positive regulation of biological process	4.2	0.01
GO:1903363	negative regulation of cellular protein catabolic process	4.2	0.01
GO:1903959	regulation of anion transmembrane transport	4.2	0.01
GO:0010614	negative regulation of cardiac muscle hypertrophy	4.2	0.01
GO:0016407	acetyltransferase activity	4.2	0.01
GO:0071011	precatalytic spliceosome	4.2	0.02
GO:0031593	polyubiquitin modification-dependent protein binding	4.2	0.02
GO:0009056	catabolic process	4.2	0.02
GO:0034243	regulation of transcription elongation from RNA polymerase II promoter	4.2	0.02
GO:0055029	nuclear DNA-directed RNA polymerase complex	4.2	0.02
GO:0030705	cytoskeleton-dependent intracellular transport	4.2	0.02
GO:1901983	regulation of protein acetylation	4.1	0.02
GO:0009154	purine ribonucleotide catabolic process	4.1	0.02
GO:0009261	ribonucleotide catabolic process	4.1	0.02
GO:0046890	regulation of lipid biosynthetic process	4.1	0.02
GO:1903313	positive regulation of mRNA metabolic process	4.1	0.02
GO:0045277	respiratory chain complex IV	4.1	0.02
GO:1902176	negative regulation of oxidative stress-induced intrinsic apoptotic signaling pathway	4.1	0.02
GO:0006379	mRNA cleavage	4.1	0.02
GO:0007585	respiratory gaseous exchange by respiratory system	4.1	0.02
GO:0051246	regulation of protein metabolic process	4.1	0.02
GO:0005793	endoplasmic reticulum-Golgi intermediate compartment	4.1	0.02
GO:0006446	regulation of translational initiation	4.1	0.02
GO:0031399	regulation of protein modification process	4.1	0.02
GO:0046939	nucleotide phosphorylation	4.1	0.02
GO:0048193	Golgi vesicle transport	4.0	0.02
GO:0043631	RNA polyadenylation	4.0	0.02
GO:0072599	establishment of protein localization to endoplasmic reticulum	4.0	0.02
GO:0000314	organellar small ribosomal subunit	4.0	0.02
GO:0005763	mitochondrial small ribosomal subunit	4.0	0.02
GO:0016052	carbohydrate catabolic process	4.0	0.02
GO:1990204	oxidoreductase complex	4.0	0.02
GO:0042326	negative regulation of phosphorylation	4.0	0.02

GO:0000428	DNA-directed RNA polymerase complex	4.0	0.02
GO:0009166	nucleotide catabolic process	4.0	0.02
GO:0090305	nucleic acid phosphodiester bond hydrolysis	4.0	0.02
GO:0031062	positive regulation of histone methylation	4.0	0.02
GO:0006576	cellular biogenic amine metabolic process	4.0	0.02
GO:0061980	regulatory RNA binding	4.0	0.02
GO:0010632	regulation of epithelial cell migration	4.0	0.02
GO:0098840	protein transport along microtubule	4.0	0.02
GO:0099118	microtubule-based protein transport	4.0	0.02
GO:0044877	protein-containing complex binding	4.0	0.02
GO:0001933	negative regulation of protein phosphorylation	4.0	0.02
GO:0017038	protein import	3.9	0.02
GO:0031400	negative regulation of protein modification process	3.9	0.02
GO:0043967	histone H4 acetylation	3.9	0.02
GO:0006111	regulation of gluconeogenesis	3.9	0.02
GO:0009185	ribonucleoside diphosphate metabolic process	3.9	0.02
GO:0012501	programmed cell death	3.9	0.02
GO:1900409	positive regulation of cellular response to oxidative stress	3.9	0.02
GO:0046685	response to arsenic-containing substance	3.9	0.02
GO:0090398	cellular senescence	3.9	0.02
GO:0046332	SMAD binding	3.9	0.02
GO:2000644	regulation of receptor catabolic process	3.9	0.02
GO:1901298	regulation of hydrogen peroxide-mediated programmed cell death	3.9	0.02
GO:0098787	mRNA cleavage involved in mRNA processing	3.9	0.02
GO:0098935	dendritic transport	3.9	0.02
GO:0006901	vesicle coating	3.9	0.02
GO:0032259	methylation	3.9	0.02
GO:0006479	protein methylation	3.9	0.02
GO:0008213	protein alkylation	3.9	0.02
GO:0010565	regulation of cellular ketone metabolic process	3.9	0.02
GO:0016830	carbon-carbon lyase activity	3.9	0.02
GO:0001046	core promoter sequence-specific DNA binding	3.9	0.02
GO:0044248	cellular catabolic process	3.9	0.02
GO:0031647	regulation of protein stability	3.9	0.02
GO:0016926	protein desumoylation	3.9	0.02
GO:0016929	SUMO-specific protease activity	3.9	0.02
GO:0070775	H3 histone acetyltransferase complex	3.9	0.02
GO:0070776	MOZ/MORF histone acetyltransferase complex	3.9	0.02
GO:0071439	clathrin complex	3.9	0.02
GO:0050847	progesterone receptor signaling pathway	3.9	0.02
GO:1904959	regulation of cytochrome-c oxidase activity	3.9	0.02
GO:0003223	ventricular compact myocardium morphogenesis	3.9	0.02
GO:0030578	PML body organization	3.9	0.02

GO:0005879	axonemal microtubule	3.9	0.02
GO:0006735	NADH regeneration	3.9	0.02
GO:0032803	regulation of low-density lipoprotein particle receptor catabolic process	3.9	0.02
GO:0008595	anterior/posterior axis specification, embryo	3.9	0.02
GO:0060054	positive regulation of epithelial cell proliferation involved in wound healing	3.9	0.02
GO:0120170	intraciliary transport particle B binding	3.9	0.02
GO:0061621	canonical glycolysis	3.9	0.02
GO:0061718	glucose catabolic process to pyruvate	3.9	0.02
GO:0090084	negative regulation of inclusion body assembly	3.9	0.02
GO:0090241	negative regulation of histone H4 acetylation	3.9	0.02
GO:0022884	macromolecule transmembrane transporter activity	3.9	0.02
GO:0030575	nuclear body organization	3.9	0.02
GO:0005697	telomerase holoenzyme complex	3.9	0.02
GO:0051153	regulation of striated muscle cell differentiation	3.9	0.02
GO:0000387	spliceosomal snRNP assembly	3.9	0.02
GO:0007498	mesoderm development	3.9	0.02
GO:0014741	negative regulation of muscle hypertrophy	3.9	0.02
GO:0044106	cellular amine metabolic process	3.9	0.02
GO:0046621	negative regulation of organ growth	3.9	0.02
GO:0051154	negative regulation of striated muscle cell differentiation	3.9	0.02
GO:0033143	regulation of intracellular steroid hormone receptor signaling pathway	3.8	0.02
GO:0010611	regulation of cardiac muscle hypertrophy	3.8	0.02
GO:0043488	regulation of mRNA stability	3.8	0.02
GO:0006915	apoptotic process	3.8	0.02
GO:0046822	regulation of nucleocytoplasmic transport	3.8	0.02
GO:0051148	negative regulation of muscle cell differentiation	3.8	0.02
GO:0070646	protein modification by small protein removal	3.8	0.02
GO:0006886	intracellular protein transport	3.8	0.02
GO:0050662	coenzyme binding	3.8	0.02
GO:0030374	nuclear receptor transcription coactivator activity	3.8	0.02
GO:0005643	nuclear pore	3.8	0.02
GO:1903362	regulation of cellular protein catabolic process	3.8	0.02
GO:0046824	positive regulation of nucleocytoplasmic transport	3.7	0.02
GO:0042026	protein refolding	3.7	0.02
GO:0032373	positive regulation of sterol transport	3.7	0.02
GO:0032376	positive regulation of cholesterol transport	3.7	0.02
GO:0046889	positive regulation of lipid biosynthetic process	3.7	0.02
GO:0016436	rRNA (uridine) methyltransferase activity	3.7	0.02
GO:0017087	mitochondrial processing peptidase complex	3.7	0.02
GO:0017098	sulfonylurea receptor binding	3.7	0.02
GO:0042799	histone methyltransferase activity (H4-K20 specific)	3.7	0.02
GO:0042866	pyruvate biosynthetic process	3.7	0.02
GO:0043969	histone H2B acetylation	3.7	0.02

GO:0070103	regulation of interleukin-6-mediated signaling pathway	3.7	0.02
GO:0070138	ubiquitin-like protein-specific isopeptidase activity	3.7	0.02
GO:0070140	SUMO-specific isopeptidase activity	3.7	0.02
GO:0019230	proprioception	3.7	0.02
GO:0070428	regulation of nucleotide-binding oligomerization domain containing 1 signaling pathway	3.7	0.02
GO:0045117	azole transmembrane transport	3.7	0.02
GO:0071008	U2-type post-mRNA release spliceosomal complex	3.7	0.02
GO:0046661	male sex differentiation	3.7	0.02
GO:0046881	positive regulation of follicle-stimulating hormone secretion	3.7	0.02
GO:1900923	regulation of glycine import across plasma membrane	3.7	0.02
GO:0047192	1-alkylglycerophosphocholine O-acetyltransferase activity	3.7	0.02
GO:1901329	regulation of odontoblast differentiation	3.7	0.02
GO:0047522	15-oxoprostaglandin 13-oxidase activity	3.7	0.02
GO:0097506	deaminated base DNA N-glycosylase activity	3.7	0.02
GO:1902268	negative regulation of polyamine transmembrane transport	3.7	0.02
GO:1902725	negative regulation of satellite cell differentiation	3.7	0.02
GO:1903093	regulation of protein K48-linked deubiquitination	3.7	0.02
GO:1903108	regulation of mitochondrial transcription	3.7	0.02
GO:1903109	positive regulation of mitochondrial transcription	3.7	0.02
GO:0099178	regulation of retrograde trans-synaptic signaling by endocannabinoid	3.7	0.02
GO:0001097	TFIIH-class transcription factor complex binding	3.7	0.02
GO:1903899	positive regulation of PERK-mediated unfolded protein response	3.7	0.02
GO:0001156	TFIIIC-class transcription factor complex binding	3.7	0.02
GO:0001560	regulation of cell growth by extracellular stimulus	3.7	0.02
GO:0001887	selenium compound metabolic process	3.7	0.02
GO:1905581	positive regulation of low-density lipoprotein particle clearance	3.7	0.02
GO:1905602	positive regulation of receptor-mediated endocytosis involved in cholesterol transport	3.7	0.02
GO:0004844	uracil DNA N-glycosylase activity	3.7	0.02
GO:0140311	protein sequestering activity	3.7	0.02
GO:0140313	molecular sequestering activity	3.7	0.02
GO:0032278	positive regulation of gonadotropin secretion	3.7	0.02
GO:0032417	positive regulation of sodium:proton antiporter activity	3.7	0.02
GO:0032767	copper-dependent protein binding	3.7	0.02
GO:0032804	negative regulation of low-density lipoprotein particle receptor catabolic process	3.7	0.02
GO:0008073	ornithine decarboxylase inhibitor activity	3.7	0.02
GO:0034092	negative regulation of maintenance of sister chromatid cohesion	3.7	0.02
GO:0034140	negative regulation of toll-like receptor 3 signaling pathway	3.7	0.02
GO:0034183	negative regulation of maintenance of mitotic sister chromatid cohesion	3.7	0.02
GO:0034455	t-UTP complex	3.7	0.02
GO:0034457	Mpp10 complex	3.7	0.02

GO:0034673	inhibin-betaglycan-ActRII complex	3.7	0.02
GO:0060416	response to growth hormone	3.7	0.02
GO:0060914	heart formation	3.7	0.02
GO:0036132	13-prostaglandin reductase activity	3.7	0.02
GO:1990108	protein linear deubiquitination	3.7	0.02
GO:0012510	trans-Golgi network transport vesicle membrane	3.7	0.02
GO:1990932	5.8S rRNA binding	3.7	0.02
GO:0090443	FAR/SIN/STRIPAK complex	3.7	0.02
GO:0048511	rhythmic process	3.7	0.02
GO:0070888	E-box binding	3.7	0.02
GO:1905953	negative regulation of lipid localization	3.7	0.02
GO:0032371	regulation of sterol transport	3.7	0.02
GO:0032374	regulation of cholesterol transport	3.7	0.02
GO:0042277	peptide binding	3.7	0.02
GO:0006352	DNA-templated transcription, initiation	3.7	0.03
GO:0016747	transferase activity, transferring acyl groups other than amino-acyl groups	3.7	0.03
GO:0042177	negative regulation of protein catabolic process	3.6	0.03
GO:0099111	microtubule-based transport	3.6	0.03
GO:0045722	positive regulation of gluconeogenesis	3.6	0.03
GO:2000726	negative regulation of cardiac muscle cell differentiation	3.6	0.03
GO:0030878	thyroid gland development	3.6	0.03
GO:0009048	dosage compensation by inactivation of X chromosome	3.6	0.03
GO:0014743	regulation of muscle hypertrophy	3.6	0.03
GO:0042401	cellular biogenic amine biosynthetic process	3.6	0.03
GO:0043023	ribosomal large subunit binding	3.6	0.03
GO:0019908	nuclear cyclin-dependent protein kinase holoenzyme complex	3.6	0.03
GO:0005665	RNA polymerase II, core complex	3.6	0.03
GO:0032785	negative regulation of DNA-templated transcription, elongation	3.6	0.03
GO:0009309	amine biosynthetic process	3.6	0.03
GO:0061615	glycolytic process through fructose-6-phosphate	3.6	0.03
GO:0043489	RNA stabilization	3.6	0.03
GO:0071005	U2-type precatalytic spliceosome	3.6	0.03
GO:0007369	gastrulation	3.6	0.03
GO:0022607	cellular component assembly	3.6	0.03
GO:0033036	macromolecule localization	3.6	0.03
GO:0055006	cardiac cell development	3.6	0.03
GO:0031057	negative regulation of histone modification	3.6	0.03
GO:0010907	positive regulation of glucose metabolic process	3.6	0.03
GO:0000790	nuclear chromatin	3.6	0.03
GO:0044798	nuclear transcription factor complex	3.6	0.03
GO:0008168	methyltransferase activity	3.5	0.03
GO:0070717	poly-purine tract binding	3.5	0.03
GO:0070979	protein K11-linked ubiquitination	3.5	0.03

GO:0005743	mitochondrial inner membrane	3.5	0.03
GO:0005798	Golgi-associated vesicle	3.5	0.03
GO:0001510	RNA methylation	3.5	0.03
GO:0016605	PML body	3.5	0.03
GO:0003697	single-stranded DNA binding	3.5	0.03
GO:0042307	positive regulation of protein import into nucleus	3.5	0.03
GO:0015959	diadenosine polyphosphate metabolic process	3.5	0.03
GO:0070180	large ribosomal subunit rRNA binding	3.5	0.03
GO:0045293	mRNA editing complex	3.5	0.03
GO:0071635	negative regulation of transforming growth factor beta production	3.5	0.03
GO:0046349	amino sugar biosynthetic process	3.5	0.03
GO:1900364	negative regulation of mRNA polyadenylation	3.5	0.03
GO:0046975	histone methyltransferase activity (H3-K36 specific)	3.5	0.03
GO:1901299	negative regulation of hydrogen peroxide-mediated programmed cell death	3.5	0.03
GO:0097677	STAT family protein binding	3.5	0.03
GO:0048208	COPII vesicle coating	3.5	0.03
GO:1902237	positive regulation of endoplasmic reticulum stress-induced intrinsic apoptotic signaling pathway	3.5	0.03
GO:0140268	endoplasmic reticulum-plasma membrane contact site	3.5	0.03
GO:0005742	mitochondrial outer membrane translocase complex	3.5	0.03
GO:0031441	negative regulation of mRNA 3'-end processing	3.5	0.03
GO:0031507	heterochromatin assembly	3.5	0.03
GO:0032372	negative regulation of sterol transport	3.5	0.03
GO:0032375	negative regulation of cholesterol transport	3.5	0.03
GO:0032552	deoxyribonucleotide binding	3.5	0.03
GO:0008024	cyclin/CDK positive transcription elongation factor complex	3.5	0.03
GO:0009950	dorsal/ventral axis specification	3.5	0.03
GO:0035726	common myeloid progenitor cell proliferation	3.5	0.03
GO:0061614	pri-miRNA transcription by RNA polymerase II	3.5	0.03
GO:0061665	SUMO ligase activity	3.5	0.03
GO:0036396	RNA N6-methyladenosine methyltransferase complex	3.5	0.03
GO:0090571	RNA polymerase II transcription repressor complex	3.5	0.03
GO:0001047	core promoter binding	3.5	0.03
GO:1905207	regulation of cardiocyte differentiation	3.5	0.03
GO:0070469	respirasome	3.4	0.03
GO:0043130	ubiquitin binding	3.4	0.03
GO:0098876	vesicle-mediated transport to the plasma membrane	3.4	0.03
GO:0000228	nuclear chromosome	3.4	0.03
GO:0019213	deacetylase activity	3.4	0.03
GO:0070972	protein localization to endoplasmic reticulum	3.4	0.03
GO:0045923	positive regulation of fatty acid metabolic process	3.4	0.03
GO:0034198	cellular response to amino acid starvation	3.4	0.03
GO:0060043	regulation of cardiac muscle cell proliferation	3.4	0.03

GO:0061650	ubiquitin-like protein conjugating enzyme activity	3.4	0.03
GO:0070227	lymphocyte apoptotic process	3.4	0.03
GO:0046688	response to copper ion	3.4	0.03
GO:2001014	regulation of skeletal muscle cell differentiation	3.4	0.03
GO:0051291	protein heterooligomerization	3.4	0.03
GO:0090335	regulation of brown fat cell differentiation	3.4	0.03
GO:2000058	regulation of ubiquitin-dependent protein catabolic process	3.4	0.03
GO:0062012	regulation of small molecule metabolic process	3.4	0.03
GO:1902532	negative regulation of intracellular signal transduction	3.4	0.03
GO:0140101	catalytic activity, acting on a tRNA	3.4	0.03
GO:0030134	COPII-coated ER to Golgi transport vesicle	3.4	0.03
GO:0008104	protein localization	3.4	0.03
GO:0070273	phosphatidylinositol-4-phosphate binding	3.4	0.03
GO:0031063	regulation of histone deacetylation	3.4	0.03
GO:0006195	purine nucleotide catabolic process	3.4	0.03
GO:0008219	cell death	3.4	0.03
GO:0045271	respiratory chain complex I	3.4	0.03
GO:0030964	NADH dehydrogenase complex	3.4	0.03
GO:0005747	mitochondrial respiratory chain complex I	3.4	0.03
GO:0071426	ribonucleoprotein complex export from nucleus	3.4	0.03
GO:0071428	rRNA-containing ribonucleoprotein complex export from nucleus	3.4	0.03
GO:0000054	ribosomal subunit export from nucleus	3.4	0.03
GO:0000463	maturation of LSU-rRNA from tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA)	3.4	0.03
GO:0051131	chaperone-mediated protein complex assembly	3.4	0.03
GO:0055089	fatty acid homeostasis	3.4	0.03
GO:0033750	ribosome localization	3.4	0.03
GO:0060339	negative regulation of type I interferon-mediated signaling pathway	3.4	0.03
GO:0060788	ectodermal placode formation	3.4	0.03
GO:0003700	DNA-binding transcription factor activity	3.4	0.03
GO:0001936	regulation of endothelial cell proliferation	3.4	0.03
GO:0032386	regulation of intracellular transport	3.4	0.03
GO:0016458	gene silencing	3.4	0.04
GO:0001098	basal transcription machinery binding	3.3	0.04
GO:0001099	basal RNA polymerase II transcription machinery binding	3.3	0.04
GO:0033673	negative regulation of kinase activity	3.3	0.04
GO:0034504	protein localization to nucleus	3.3	0.04
GO:1901031	regulation of response to reactive oxygen species	3.3	0.04
GO:0016567	protein ubiquitination	3.3	0.04
GO:1901575	organic substance catabolic process	3.3	0.04
GO:0007005	mitochondrion organization	3.3	0.04
GO:0006606	protein import into nucleus	3.3	0.04
GO:0046622	positive regulation of organ growth	3.3	0.04

GO:1904589	regulation of protein import	3.2	0.04
GO:0043014	alpha-tubulin binding	3.2	0.04
GO:0021955	central nervous system neuron axonogenesis	3.2	0.04
GO:0001707	mesoderm formation	3.2	0.04
GO:0051721	protein phosphatase 2A binding	3.2	0.04
GO:0055013	cardiac muscle cell development	3.2	0.04
GO:0043255	regulation of carbohydrate biosynthetic process	3.2	0.04
GO:0051348	negative regulation of transferase activity	3.2	0.04
GO:0000932	P-body	3.2	0.04
GO:0070530	K63-linked polyubiquitin modification-dependent protein binding	3.2	0.04
GO:0071353	cellular response to interleukin-4	3.2	0.04
GO:1901626	regulation of postsynaptic membrane organization	3.2	0.04
GO:0000413	protein peptidyl-prolyl isomerization	3.2	0.04
GO:0001824	blastocyst development	3.2	0.04
GO:0006119	oxidative phosphorylation	3.2	0.04
GO:0007549	dosage compensation	3.2	0.04
GO:0010592	positive regulation of lamellipodium assembly	3.2	0.04
GO:0070536	protein K63-linked deubiquitination	3.2	0.04
GO:0005637	nuclear inner membrane	3.2	0.04
GO:0006354	DNA-templated transcription, elongation	3.2	0.04
GO:0009266	response to temperature stimulus	3.2	0.04
GO:0007029	endoplasmic reticulum organization	3.2	0.04
GO:0009308	amine metabolic process	3.2	0.04
GO:0009880	embryonic pattern specification	3.2	0.04
GO:0016410	N-acyltransferase activity	3.2	0.04
GO:2001021	negative regulation of response to DNA damage stimulus	3.1	0.04
GO:0140030	modification-dependent protein binding	3.1	0.04
GO:0010634	positive regulation of epithelial cell migration	3.1	0.04
GO:1902369	negative regulation of RNA catabolic process	3.1	0.04
GO:1990841	promoter-specific chromatin binding	3.1	0.04
GO:0016725	oxidoreductase activity, acting on CH or CH2 groups	3.1	0.04
GO:0017062	respiratory chain complex III assembly	3.1	0.04
GO:0017085	response to insecticide	3.1	0.04
GO:0047372	acylglycerol lipase activity	3.1	0.04
GO:0000290	deadenylation-dependent decapping of nuclear-transcribed mRNA	3.1	0.04
GO:1903800	positive regulation of production of miRNAs involved in gene silencing by miRNA	3.1	0.04
GO:1903789	regulation of amino acid transmembrane transport	3.1	0.04
GO:1904393	regulation of skeletal muscle acetylcholine-gated channel clustering	3.1	0.04
GO:0006616	SRP-dependent cotranslational protein targeting to membrane, translocation	3.1	0.04
GO:0007289	spermatid nucleus differentiation	3.1	0.04
GO:0034139	regulation of toll-like receptor 3 signaling pathway	3.1	0.04
GO:0060039	pericardium development	3.1	0.04

GO:0034551	mitochondrial respiratory chain complex III assembly	3.1	0.04
GO:0060638	mesenchymal-epithelial cell signaling	3.1	0.04
GO:0010958	regulation of amino acid import across plasma membrane	3.1	0.04
GO:0061085	regulation of histone H3-K27 methylation	3.1	0.04
GO:0035562	negative regulation of chromatin binding	3.1	0.04
GO:0035686	sperm fibrous sheath	3.1	0.04
GO:0035773	insulin secretion involved in cellular response to glucose stimulus	3.1	0.04
GO:0031398	positive regulation of protein ubiquitination	3.1	0.04
GO:0070231	T cell apoptotic process	3.1	0.04
GO:0044804	autophagy of nucleus	3.1	0.04
GO:1903960	negative regulation of anion transmembrane transport	3.1	0.04
GO:0051156	glucose 6-phosphate metabolic process	3.1	0.04
GO:0051290	protein heterotetramerization	3.1	0.04
GO:1904396	regulation of neuromuscular junction development	3.1	0.04
GO:0051547	regulation of keratinocyte migration	3.1	0.04
GO:0006474	N-terminal protein amino acid acetylation	3.1	0.04
GO:0032516	positive regulation of phosphoprotein phosphatase activity	3.1	0.04
GO:0008320	protein transmembrane transporter activity	3.1	0.04
GO:0061051	positive regulation of cell growth involved in cardiac muscle cell development	3.1	0.04
GO:0018208	peptidyl-proline modification	3.1	0.04
GO:0009408	response to heat	3.1	0.05
GO:0016746	transferase activity, transferring acyl groups	3.1	0.05
GO:0009057	macromolecule catabolic process	3.1	0.05
GO:0016259	selenocysteine metabolic process	3.1	0.05
GO:0016972	thiol oxidase activity	3.1	0.05
GO:0043527	tRNA methyltransferase complex	3.1	0.05
GO:0043654	recognition of apoptotic cell	3.1	0.05
GO:0070086	ubiquitin-dependent endocytosis	3.1	0.05
GO:0070122	isopeptidase activity	3.1	0.05
GO:0019828	aspartic-type endopeptidase inhibitor activity	3.1	0.05
GO:0070934	CRD-mediated mRNA stabilization	3.1	0.05
GO:0045901	positive regulation of translational elongation	3.1	0.05
GO:2000152	regulation of ubiquitin-specific protease activity	3.1	0.05
GO:1900365	positive regulation of mRNA polyadenylation	3.1	0.05
GO:0071947	protein deubiquitination involved in ubiquitin-dependent protein catabolic process	3.1	0.05
GO:2000645	negative regulation of receptor catabolic process	3.1	0.05
GO:0097167	circadian regulation of translation	3.1	0.05
GO:0097452	GAIT complex	3.1	0.05
GO:1901537	positive regulation of DNA demethylation	3.1	0.05
GO:1902202	regulation of hepatocyte growth factor receptor signaling pathway	3.1	0.05
GO:1902512	positive regulation of apoptotic DNA fragmentation	3.1	0.05

GO:0098749	cerebellar neuron development	3.1	0.05
GO:1902774	late endosome to lysosome transport	3.1	0.05
GO:0000015	phosphopyruvate hydratase complex	3.1	0.05
GO:0098904	regulation of AV node cell action potential	3.1	0.05
GO:1902951	negative regulation of dendritic spine maintenance	3.1	0.05
GO:0000720	pyrimidine dimer repair by nucleotide-excision repair	3.1	0.05
GO:1903795	regulation of inorganic anion transmembrane transport	3.1	0.05
GO:1903842	response to arsenite ion	3.1	0.05
GO:1903843	cellular response to arsenite ion	3.1	0.05
GO:1903936	cellular response to sodium arsenite	3.1	0.05
GO:1904059	regulation of locomotor rhythm	3.1	0.05
GO:0051731	polynucleotide 5'-hydroxyl-kinase activity	3.1	0.05
GO:0001875	lipopolysaccharide immune receptor activity	3.1	0.05
GO:0002069	columnar/cuboidal epithelial cell maturation	3.1	0.05
GO:0052042	positive regulation by symbiont of host programmed cell death	3.1	0.05
GO:0002134	UTP binding	3.1	0.05
GO:0052151	positive regulation by symbiont of host apoptotic process	3.1	0.05
GO:0052330	positive regulation by organism of programmed cell death in other organism involved in symbiotic interaction	3.1	0.05
GO:0003433	chondrocyte development involved in endochondral bone morphogenesis	3.1	0.05
GO:0004634	phosphopyruvate hydratase activity	3.1	0.05
GO:0031064	negative regulation of histone deacetylation	3.1	0.05
GO:0031265	CD95 death-inducing signaling complex	3.1	0.05
GO:0005968	Rab-protein geranylgeranyltransferase complex	3.1	0.05
GO:0031499	TRAMP complex	3.1	0.05
GO:0031697	beta-1 adrenergic receptor binding	3.1	0.05
GO:0006344	maintenance of chromatin silencing	3.1	0.05
GO:0032379	positive regulation of intracellular lipid transport	3.1	0.05
GO:0032382	positive regulation of intracellular sterol transport	3.1	0.05
GO:0032385	positive regulation of intracellular cholesterol transport	3.1	0.05
GO:0032415	regulation of sodium:proton antiporter activity	3.1	0.05
GO:0032422	purine-rich negative regulatory element binding	3.1	0.05
GO:0032497	detection of lipopolysaccharide	3.1	0.05
GO:0032564	dATP binding	3.1	0.05
GO:0009051	pentose-phosphate shunt, oxidative branch	3.1	0.05
GO:0120200	rod photoreceptor outer segment	3.1	0.05
GO:0035061	interchromatin granule	3.1	0.05
GO:0060926	cardiac pacemaker cell development	3.1	0.05
GO:0061086	negative regulation of histone H3-K27 methylation	3.1	0.05
GO:0035617	stress granule disassembly	3.1	0.05
GO:0035927	RNA import into mitochondrion	3.1	0.05
GO:1990254	keratin filament binding	3.1	0.05
GO:0090170	regulation of Golgi inheritance	3.1	0.05

GO:0090272	negative regulation of fibroblast growth factor production	3.1	0.05
GO:0015187	glycine transmembrane transporter activity	3.1	0.05
GO:0031966	mitochondrial membrane	3.1	0.05
GO:1905897	regulation of response to endoplasmic reticulum stress	3.1	0.05
GO:0016740	transferase activity	3.1	0.05
GO:0051054	positive regulation of DNA metabolic process	3.1	0.05
GO:0006739	NADP metabolic process	3.1	0.05
GO:0006754	ATP biosynthetic process	3.1	0.05
GO:0035967	cellular response to topologically incorrect protein	3.1	0.05
GO:0006611	protein export from nucleus	3.1	0.05
GO:0043281	regulation of cysteine-type endopeptidase activity involved in apoptotic process	3.1	0.05
GO:0000209	protein polyubiquitination	3.0	0.05
GO:0070412	R-SMAD binding	3.0	0.05
GO:0045736	negative regulation of cyclin-dependent protein serine/threonine kinase activity	3.0	0.05
GO:0045943	positive regulation of transcription by RNA polymerase I	3.0	0.05
GO:0071887	leukocyte apoptotic process	3.0	0.05
GO:1901673	regulation of mitotic spindle assembly	3.0	0.05
GO:0048156	tau protein binding	3.0	0.05
GO:0001702	gastrulation with mouth forming second	3.0	0.05
GO:1905208	negative regulation of cardiocyte differentiation	3.0	0.05
GO:0031307	integral component of mitochondrial outer membrane	3.0	0.05
GO:0007063	regulation of sister chromatid cohesion	3.0	0.05
GO:0032968	positive regulation of transcription elongation from RNA polymerase II promoter	3.0	0.05
GO:0060765	regulation of androgen receptor signaling pathway	3.0	0.05
GO:0010874	regulation of cholesterol efflux	3.0	0.05
GO:0016234	inclusion body	3.0	0.05
GO:1903051	negative regulation of proteolysis involved in cellular protein catabolic process	3.0	0.05
GO:0008088	axo-dendritic transport	3.0	0.05
GO:0035065	regulation of histone acetylation	3.0	0.05
GO:0000315	organellar large ribosomal subunit	3.0	0.05
GO:0005762	mitochondrial large ribosomal subunit	3.0	0.05
GO:0008270	zinc ion binding	3.0	0.05
GO:0044092	negative regulation of molecular function	3.0	0.05
GO:2001020	regulation of response to DNA damage stimulus	3.0	0.05
GO:0043487	regulation of RNA stability	3.0	0.05
GO:0031330	negative regulation of cellular catabolic process	3.0	0.05
GO:0019209	kinase activator activity	3.0	0.05
GO:0045913	positive regulation of carbohydrate metabolic process	3.0	0.05
GO:0050660	flavin adenine dinucleotide binding	3.0	0.05
GO:0004843	thiol-dependent ubiquitin-specific protease activity	3.0	0.05

GO:0072523	purine-containing compound catabolic process	3.0	0.05
GO:0003899	DNA-directed 5'-3' RNA polymerase activity	3.0	0.05
GO:0005048	signal sequence binding	3.0	0.05
GO:0051170	import into nucleus	3.0	0.05
GO:0090100	positive regulation of transmembrane receptor protein serine/threonine kinase signaling pathway	3.0	0.05
GO:0016741	transferase activity, transferring one-carbon groups	3.0	0.05
GO:0043433	negative regulation of DNA-binding transcription factor activity	2.9	0.05
GO:1903202	negative regulation of oxidative stress-induced cell death	2.9	0.05
GO:1990928	response to amino acid starvation	2.9	0.05
GO:0101005	ubiquitinyl hydrolase activity	2.9	0.05
GO:0050678	regulation of epithelial cell proliferation	2.9	0.05
GO:0045773	positive regulation of axon extension	2.9	0.05
GO:1901799	negative regulation of proteasomal protein catabolic process	2.9	0.05
GO:0010662	regulation of striated muscle cell apoptotic process	2.9	0.05
GO:0044265	cellular macromolecule catabolic process	2.9	0.05
GO:0071634	regulation of transforming growth factor beta production	2.9	0.05
GO:1903205	regulation of hydrogen peroxide-induced cell death	2.9	0.05
GO:0016864	intramolecular oxidoreductase activity, transposing S-S bonds	2.9	0.05
GO:0070034	telomerase RNA binding	2.9	0.05
GO:0001056	RNA polymerase III activity	2.9	0.05
GO:0003756	protein disulfide isomerase activity	2.9	0.05
GO:0004675	transmembrane receptor protein serine/threonine kinase activity	2.9	0.05
GO:0004724	magnesium-dependent protein serine/threonine phosphatase activity	2.9	0.05
GO:0032688	negative regulation of interferon-beta production	2.9	0.05
GO:0034063	stress granule assembly	2.9	0.05
GO:0034399	nuclear periphery	2.9	0.05
GO:0060044	negative regulation of cardiac muscle cell proliferation	2.9	0.05
GO:0043467	regulation of generation of precursor metabolites and energy	2.9	0.05
GO:0006338	chromatin remodeling	2.9	0.05

Analysis done using the Partek Flow package. Gene set column contains Gene Ontology identifiers. Enrichment score: negative natural logarithm of the enrichment P-value derived from the Fisher's exact test. The higher the enrichment score, the more overrepresented the GO category is within the input list of significant genes; only gene sets with a $p < 0.05$ are shown.

Table S7- Pathway enrichment analysis of differentially expressed genes in adult BAT-D3KO iBAT.

Gene set	Description	Enrichment score	P-value
path:mmu03010	Ribosome	41.3	1.16E-18
path:mmu03040	Spliceosome	26.0	5.34E-12
path:mmu05016	Huntington disease	8.4	2.34E-04
path:mmu05010	Alzheimer disease	7.2	7.67E-04
path:mmu03015	mRNA surveillance pathway	7.0	9.27E-04
path:mmu03008	Ribosome biogenesis in eukaryotes	5.5	3.90E-03
path:mmu00190	Oxidative phosphorylation	5.5	4.27E-03
path:mmu04714	Thermogenesis	5.2	0.01
path:mmu04066	HIF-1 signaling pathway	5.2	0.01
path:mmu04932	Non-alcoholic fatty liver disease (NAFLD)	5.2	0.01
path:mmu05012	Parkinson disease	4.8	0.01
path:mmu04141	Protein processing in endoplasmic reticulum	4.4	0.01
path:mmu05211	Renal cell carcinoma	3.9	0.02
path:mmu00010	Glycolysis / Gluconeogenesis	3.8	0.02
path:mmu00450	Selenocompound metabolism	3.5	0.03
path:mmu05168	Herpes simplex virus 1 infection	3.5	0.03
path:mmu04152	AMPK signaling pathway	3.4	0.03
path:mmu00310	Lysine degradation	3.3	0.04
path:mmu03018	RNA degradation	3.3	0.04
path:mmu01230	Biosynthesis of amino acids	3.1	0.04
path:mmu04622	RIG-I-like receptor signaling pathway	3.0	0.05

Analysis done using Partek Flow package. Gene set column contains the KEGG pathway ID. Enrichment score: negative natural logarithm of the enrichment p-value derived from the Fisher's exact test. The higher the enrichment score, the more overrepresented the KEGG pathway is within the input list of significant genes. An enrichment score of three is equal to a p-value of 0.05; only pathways with a $p < 0.05$ are shown.