Supplemental Table 1: Transcripts up-regulated in spleens from Triple KO mice compared to spleens from WT mice

Shown are a total of 2023 transcripts that were up-regulated in Triple KO mice spleens as compared to WT spleens in the RNA-Seq dataset. GeneChrom refers to the gene symbol, with a chromosome suffix to make gene entries unique. Columns B through E (eg. WT_v1) represent each sample group FPKM value, i.e., sequence read fragments per kilobase per million mapped reads, where pair-end reads are counted as one fragment. FloorLog2FC represents log2 fold change after applying a noise floor, which resolves infinite fold changes produced by cuff-diff. Fold Change represents the fold change over the respective WT samples. The p value is derived from the Cuffdiff statistical t test with negative binomial distribution, and the q value represents the FDR adjusted p value.

GeneChrom	WT_v1	DoubleKO	WT_v2	TripleKO	floorLog2FC DoubleKO vsWT	Fold Change DoubleKO vs WT	floorLog2FC TripleKO vsWT	Fold Change TripleKO vs WT	p_value DoubleKO vsWT	p_value TripleKO vsWT	q_value DoubleKO vsWT	q_value TripleKO vsWT
1190002F15Rik_chr6	3	2	1	11	-0.3	1.2	3.2	9.4	6.23E-01	5.00E-05	1.00E+00	2.82E-04
1300017J02Rik_chr9	0	0	1	21	0.0	1.0	4.4	21.0	8.15E-01	5.00E-05	1.00E+00	2.85E-04
1700001L05Rik_chr15	1	1	1	4	0.0	1.0	1.6	3.0	9.92E-01	5.00E-05	1.00E+00	2.82E-04
1700020L24Rik_chr11	1	1	1	2	0.0	1.0	1.1	2.1	9.70E-01	3.00E-04	1.00E+00	1.47E-03
1810011H11Rik_chr14	3	4	4	7	0.1	1.1	0.9	1.9	7.14E-01	5.00E-05	1.00E+00	2.85E-04
2810417H13Rik_chr9	6	8	7	33	0.4	1.3	2.2	4.8	3.46E-01	5.00E-05	9.98E-01	2.85E-04
4930579G24Rik_chr3	1	2	2	6	0.2	1.2	1.4	2.6	6.15E-01	5.00E-05	1.00E+00	2.85E-04
5730508B09Rik_chr3	5	5	5	20	0.0	1.0	2.0	4.0	9.09E-01	5.00E-05	1.00E+00	2.85E-04
6030468B19Rik_chr11	1	1	1	3	0.0	1.0	1.7	3.3	8.71E-01	5.00E-05	1.00E+00	2.85E-04
A530064D06Rik_chr17	1	1	1	4	0.0	1.0	1.4	2.7	8.77E-01	5.00E-05	1.00E+00	2.85E-04
AA467197_chr2	0	0	0	2	0.0	1.0	1.1	2.2	3.95E-01	3.40E-02	1.00E+00	8.68E-02
Aars_chr8	8	12	18	34	0.6	1.5	1.0	2.0	1.34E-02	5.00E-05	5.29E-01	2.85E-04
Aatk_chr11	1	2	4	6	0.1	1.1	0.7	1.7	7.09E-01	6.25E-05	1.00E+00	3.41E-04
Abcb10_chr8	6	7	12	90	0.4	1.3	2.9	7.5	1.10E-01	5.00E-05	9.38E-01	2.85E-04
Abcb4_chr5	4	4	8	38	0.0	1.0	2.2	4.8	9.71E-01	5.00E-05	1.00E+00	2.85E-04
Abcb6_chr1	2	2	4	19	0.4	1.3	2.3	5.1	2.48E-01	5.00E-05	9.92E-01	2.85E-04
Abcg2_chr6	5	6	8	25	0.1	1.1	1.7	3.2	7.81E-01	5.00E-05	1.00E+00	2.85E-04
Abcg4_chr9	0	0	0	17	0.0	1.0	4.1	17.0	5.73E-01	5.00E-05	1.00E+00	2.85E-04
Abhd5_chr9	4	4	5	12	-0.1	1.0	1.2	2.2	8.24E-01	5.00E-05	1.00E+00	2.85E-04
Ache_chr5	1	2	3	25	0.4	1.3	3.1	8.6	3.33E-01	5.00E-05	9.98E-01	2.85E-04
Ackr1_chr1	0	1	1	8	0.0	1.0	2.9	7.5	1.14E-01	5.00E-05	9.43E-01	2.85E-04
Acmsd_chr1	0	0	0	4	0.0	1.0	1.9	3.8	5.69E-01	5.00E-05	1.00E+00	2.85E-04
Acp1_chr12	4	4	4	21	0.1	1.1	2.2	4.5	6.93E-01	5.00E-05	1.00E+00	2.92E-04
Acsl1_chr8	6	8	14	41	0.4	1.3	1.6	3.0	1.09E-01	5.00E-05	9.38E-01	2.85E-04
Acsl6_chr11	0	0	0	2	0.0	1.0	0.9	1.9	7.58E-01	5.00E-05	1.00E+00	2.49E-04
Ada_chr2	3	4	5	9	0.1	1.1	0.9	1.9	7.77E-01	5.00E-05	1.00E+00	2.85E-04
Add2_chr6	1	1	2	55	0.3	1.2	4.8	27.7	2.69E-01	5.00E-05	9.75E-01	2.85E-04
Adpgk_chr9	13	14	19	40	0.1	1.1	1.1	2.1	5.96E-01	5.00E-05	1.00E+00	2.85E-04
AI607873_chr1	4	6	8	29	0.5	1.4	1.8	3.5	6.25E-02	5.00E-05	8.76E-01	2.85E-04
Alad_chr4	10	7	19	55	-0.5	1.4	1.5	2.9	1.29E-01	5.00E-05	9.54E-01	2.85E-04
Alas2_chrX	62	103	110	392	0.8	1.7	1.8	3.6	5.14E-02	8.00E-04	5.08E-01	3.37E-03
Aldh1a1_chr19	6	9	9	55	0.5	1.4	2.6	5.9	7.69E-02	5.00E-05	9.03E-01	2.85E-04
Alox5ap_chr5	19	26	28	64	0.4	1.3	1.2	2.3	1.16E-01	5.00E-05	9.45E-01	2.85E-04
Ampd3_chr7	5	6	11	27	0.2	1.2	1.2	2.3	3.14E-01	5.00E-05	9.97E-01	2.85E-04
Angptl4_chr17	3	4	5	9	0.4	1.3	0.9	1.8	2.29E-01	5.00E-05	9.91E-01	2.85E-04
Ankle1_chr8	1	1	1	21	0.2	1.1	4.0	16.5	3.09E-01	5.00E-05	9.97E-01	2.85E-04
Ankrd9_chr12	0	0	1	3	0.0	1.0	1.7	3.2	4.55E-01	5.00E-05	1.00E+00	2.85E-04
Anxa1_chr19	27	30	29	145	0.2	1.1	2.3	5.0	4.23E-01	5.00E-05	1.00E+00	2.85E-04
Anxa2_chr9	37	45	47	81	0.3	1.2	0.8	1.7	2.01E-01	5.00E-05	9.87E-01	2.85E-04
Ap3s1_chr18	13	13	13	33	0.0	1.0	1.3	2.5	9.61E-01	5.00E-05	1.00E+00	2.85E-04
Apoc1_chr7	3	5	1	4	0.8	1.7	1.6	2.9	1.49E-01	5.00E-05	9.70E-01	2.85E-04
Apol10a_chr15	0	0	0	22	0.0	1.0	4.5	22.3	8.40E-02	1.30E-02	1.00E+00	3.91E-02
Apol11b_chr15	0	3	0	367	1.8	3.5	8.5	367.4	6.30E-10	5.00E-05	3.75E-07	2.85E-04
Apol8_chr15	0	0	0	38	0.0	1.0	5.2	37.7	1.31E-01	5.00E-05	1.00E+00	2.85E-04
Apold1_chr6	1	1	1	2	0.0	1.0	1.2	2.3	4.92E-01	5.00E-05	1.00E+00	2.85E-04
Aqp1_chr6	10	10	18	207	0.0	1.0	3.5	11.3	8.46E-01	5.00E-05	1.00E+00	2.85E-04
Aqp9_chr9	1	1	2	8	0.2	1.2	2.2	4.6	5.88E-01	5.00E-05	1.00E+00	2.85E-04
Arhgef37_chr18	1	0	1	3	0.0	1.0	1.1	2.2	4.60E-01	5.00E-05	1.00E+00	2.85E-04
Arhgef39_chr4	1	1	1	7	0.0	1.0	2.3	5.0	9.35E-01	5.00E-05	1.00E+00	2.85E-04
Arl11_chr14	2	2	2	5	-0.2	1.1	1.5	2.8	6.90E-01	5.00E-05	1.00E+00	2.85E-04
Art4_chr6	2	2	3	10	-0.1	1.1	1.5	2.9	8.33E-01	5.00E-05	1.00E+00	2.85E-04
Asf1b_chr8	4	6	7	37	0.3	1.3	2.5	5.7	3.07E-01	5.00E-05	9.97E-01	2.85E-04
Asns_chr6	2	2	3	28	0.3	1.2	3.2	9.0	4.52E-01	5.00E-05	1.00E+00	2.85E-04
Aspm_chr1	1	1	2	16	0.0	1.0	3.1	8.3	9.86E-01	5.00E-05	1.00E+00	2.85E-04
Asprv1_chr6	2	2	2	7	0.2	1.2	1.9	3.7	6.13E-01	5.00E-05	1.00E+00	2.85E-04
Atad5_chr11	2	2	4	12	0.0	1.0	1.7	3.2	8.63E-01	5.00E-05	1.00E+00	2.85E-04
Atp2b4_chr1	6	6	14	48	0.0	1.0	1.7	3.3	9.43E-01	5.00E-05	1.00E+00	2.85E-04
Atp7b_chr8	0	0	1	6	0.0	1.0	2.7	6.5	9.82E-01	5.00E-05	1.00E+00	2.85E-04
Atp8b4_chr2	3	3	5	12	0.2	1.2	1.2	2.2	4.44E-01	5.00E-05	1.00E+00	2.85E-04
Atpif1_chr4	37	37	27	128	0.0	1.0	2.2	4.7	9.75E-01	5.00E-05	1.00E+00	2.85E-04
Aurka_chr2	2	3	3	22	0.7	1.7	2.8	7.2	7.58E-02	5.00E-05	9.02E-01	2.85E-04
Aurkb_chr11	3	3	5	27	0.3	1.2	2.5	5.5	4.86E-01	5.00E-05	1.00E+00	2.85E-04
B430306N03Rik_chr17	5	5	9	17	0.0	1.0	0.9	1.9	9.71E-01	5.00E-05	1.00E+00	2.85E-04
B4galt6_chr18	2	2	3	8	0.4	1.3	1.3	2.4	2.23E-01	5.00E-05	9.91E-01	2.85E-04
Bag2_chr1	1	1	2	7	0.1	1.0	2.0	4.1	9.12E-01	5.00E-05	1.00E+00	2.85E-04
Bard1_chr1	1	1	2	8	0.1	1.1	2.2	4.7	8.41E-01	5.00E-05	1.00E+00	2.85E-04
BC030867_chr11	0	0	1	3	0.0	1.0	1.5	2.8	5.08E-01	5.00E-05	1.00E+00	2.85E-04
Bcl2l1_chr2	4	7	8	38	0.7	1.6	2.2	4.7	1.66E-02	5.00E-05	5.86E-01	2.85E-04
Bex4_chrX	0	1	0	4	0.0	1.0	1.9	3.7	7.63E-01	5.00E-05	1.00E+00	2.85E-04
Bhlha15_chr5	1	1	2	5	0.4	1.3	1.3	2.5	2.99E-01	5.00E-05	9.96E-01	2.85E-04
Birc5_chr11	4	5	3	33	0.5	1.4	3.7	13.0	2.84E-01	5.00E-05	9.97E-01	2.92E-04

Blm_chr7	3	3	5	16	-0.1	1.0	1.7	3.3	**8.51E-01**	**5.00E-05**	1.00E+00	2.85E-04
Blvrb_chr7	23	30	24	107	0.4	1.3	2.1	4.4	**1.28E-01**	**5.00E-05**	9.54E-01	2.85E-04
Bmx_chrX	0	0	0	2	0.0	1.0	0.8	1.7	**7.63E-01**	**5.00E-05**	1.00E+00	2.85E-04
Bora_chr14	3	3	5	11	0.0	1.0	1.3	2.5	**9.10E-01**	**5.00E-05**	1.00E+00	2.85E-04
Bpgm_chr6	57	86	77	157	0.6	1.5	1.0	2.0	**5.49E-03**	**5.00E-05**	3.58E-01	2.85E-04
Brca1_chr11	2	2	3	15	0.0	1.0	2.3	4.8	**9.13E-01**	**5.00E-05**	1.00E+00	2.85E-04
Brca2_chr5	1	1	2	7	0.0	1.0	1.7	3.3	**7.04E-01**	**5.00E-05**	1.00E+00	2.85E-04
Brip1_chr11	1	1	1	4	0.0	1.0	2.1	4.2	**9.62E-01**	**5.00E-05**	1.00E+00	2.85E-04
Btnl10_chr11	0	0	0	40	0.0	1.0	5.3	40.3	**6.27E-01**	**5.00E-05**	1.00E+00	2.85E-04
Bub1_chr2	1	1	1	11	-0.1	1.1	2.8	7.0	**6.43E-01**	**5.00E-05**	1.00E+00	2.92E-04
Bub1b_chr2	3	3	6	29	0.0	1.0	2.3	5.1	**9.81E-01**	**5.00E-05**	1.00E+00	2.85E-04
C1qb_chr4	65	85	69	144	0.4	1.3	1.0	2.1	**7.07E-02**	**5.00E-05**	7.84E-01	2.85E-04
C1qc_chr4	69	97	79	148	0.5	1.4	0.9	1.9	**2.01E-02**	**5.00E-05**	5.21E-01	2.85E-04
C1rl_chr6	1	1	1	2	0.0	1.0	0.8	1.7	**7.45E-01**	**5.00E-05**	1.00E+00	2.85E-04
C330027C09Rik_chr16	3	3	4	22	-0.1	1.1	2.5	5.8	**7.20E-01**	**5.00E-05**	1.00E+00	2.85E-04
C530008M17Rik_chr5	0	1	1	8	0.0	1.0	3.0	8.2	**3.44E-01**	**5.00E-05**	9.98E-01	2.85E-04
C5ar1_chr7	0	1	1	7	0.0	1.0	2.9	7.4	**3.45E-01**	**5.00E-05**	9.80E-01	2.85E-04
C5ar2_chr7	1	1	2	3	-0.1	1.0	0.6	1.5	**8.51E-01**	**3.58E-03**	1.00E+00	1.31E-02
C6_chr15	6	10	11	29	0.6	1.5	1.4	2.6	**1.26E-02**	**5.00E-05**	4.18E-01	2.85E-04
Cacna1h_chr17	2	2	4	9	-0.2	1.2	1.1	2.2	**4.05E-01**	**5.00E-05**	1.00E+00	2.85E-04
Camkk1_chr11	1	1	2	3	0.1	1.1	0.9	1.8	**8.29E-01**	**5.00E-05**	1.00E+00	2.85E-04
Camp_chr9	2	9	1	140	2.0	4.1	6.7	103.1	**2.66E-05**	**5.00E-05**	4.36E-03	2.85E-04
Car1_chr3	31	24	30	124	-0.3	1.3	2.0	4.1	**1.88E-01**	**5.00E-05**	9.45E-01	2.85E-04
Car2_chr3	13	27	21	576	1.1	2.2	4.8	26.9	**1.16E-05**	**5.00E-05**	2.11E-03	2.85E-04
Card10_chr15	1	1	2	4	-0.1	1.1	0.6	1.5	**7.28E-01**	**1.50E-04**	1.00E+00	7.89E-04
Card9_chr2	2	3	3	13	0.3	1.2	1.9	3.8	**4.91E-01**	**5.00E-05**	1.00E+00	2.85E-04
Carhsp1_chr16	12	12	20	65	0.0	1.0	1.7	3.3	**8.87E-01**	**5.00E-05**	1.00E+00	2.85E-04
Casc5_chr2	2	1	3	28	-0.4	1.3	3.1	8.4	**2.17E-01**	**5.00E-05**	9.56E-01	2.85E-04
Casp4_chr9	8	8	8	20	0.1	1.1	1.4	2.6	**7.79E-01**	**5.00E-05**	1.00E+00	2.85E-04
Ccdc18_chr5	1	0	1	4	0.0	1.0	2.1	4.2	**2.89E-01**	**5.00E-05**	9.95E-01	2.85E-04
Ccdc34_chr2	2	2	1	5	0.3	1.2	2.0	4.0	**5.25E-01**	**5.00E-05**	1.00E+00	2.85E-04
Ccl6_chr11	13	9	10	26	-0.6	1.5	1.4	2.6	**3.55E-02**	**5.00E-05**	7.70E-01	2.85E-04
Ccl9_chr11	3	2	3	5	-0.4	1.3	0.9	1.9	**2.81E-01**	**5.00E-05**	9.94E-01	2.85E-04
Ccna2_chr3	5	6	7	82	0.3	1.2	3.5	11.3	**3.49E-01**	**5.00E-05**	9.98E-01	2.85E-04
Ccnb1_chr13	4	4	5	45	0.2	1.1	3.2	9.4	**5.60E-01**	**5.00E-05**	1.00E+00	2.85E-04
Ccnb2_chr9	4	4	5	56	0.2	1.1	3.5	11.4	**5.98E-01**	**5.00E-05**	1.00E+00	2.85E-04
Ccne1_chr7	3	4	4	25	0.3	1.2	2.7	6.3	**3.73E-01**	**5.00E-05**	1.00E+00	2.85E-04
Ccnf_chr17	2	3	5	33	0.6	1.5	2.9	7.3	**9.13E-02**	**5.00E-05**	9.27E-01	2.85E-04
Ccp110_chr7	3	3	4	14	0.0	1.0	1.6	3.1	**8.60E-01**	**5.00E-05**	1.00E+00	2.85E-04
Ccr1_chr9	7	6	7	27	-0.2	1.1	1.9	3.7	**5.03E-01**	**5.00E-05**	1.00E+00	2.85E-04
Ccr2_chr9	19	20	25	64	0.1	1.0	1.4	2.6	**7.69E-01**	**5.00E-05**	1.00E+00	2.85E-04
Ccrl2_chr9	1	2	2	7	0.8	1.7	1.8	3.4	**8.02E-02**	**5.00E-05**	9.08E-01	2.85E-04
Ccrn4l_chr3	2	2	3	14	0.0	1.0	2.2	4.6	**9.10E-01**	**5.00E-05**	1.00E+00	2.85E-04
Cd14_chr18	5	5	7	12	0.2	1.2	0.8	1.7	**5.42E-01**	**5.00E-05**	1.00E+00	2.85E-04
Cd177_chr7	1	1	1	25	0.3	1.2	4.6	24.4	**1.75E-02**	**5.00E-05**	5.93E-01	2.85E-04
Cd200r4_chr16	1	1	1	3	0.3	1.2	1.5	2.8	**6.21E-01**	**5.00E-05**	1.00E+00	2.85E-04
Cd24a_chr10	133	163	160	731	0.3	1.2	2.2	4.6	**1.92E-01**	**5.00E-05**	9.86E-01	2.85E-04
Cd300lb_chr11	3	3	5	13	0.0	1.0	1.3	2.5	**9.35E-01**	**5.00E-05**	1.00E+00	2.85E-04
Cd300lf_chr11	7	8	10	30	0.2	1.2	1.6	2.9	**6.15E-01**	**5.00E-05**	1.00E+00	2.85E-04
Cd33_chr7	7	5	7	13	-0.5	1.5	1.1	2.1	**8.71E-02**	**3.47E-03**	8.71E-01	1.16E-02
Cd5l_chr3	27	33	42	186	0.3	1.2	2.2	4.5	**1.47E-01**	**5.00E-05**	9.00E-01	2.85E-04
Cdc20_chr4	3	5	6	31	0.6	1.6	2.4	5.4	**2.02E-01**	**5.00E-05**	9.87E-01	2.85E-04
Cdc25c_chr18	0	1	1	5	0.0	1.0	2.3	4.9	**7.05E-01**	**5.00E-05**	1.00E+00	2.85E-04
Cdc6_chr11	1	1	2	22	0.5	1.4	3.5	11.7	**1.61E-01**	**5.00E-05**	9.22E-01	2.85E-04
Cdca2_chr14	1	1	1	7	0.1	1.0	2.2	4.6	**7.89E-01**	**5.00E-05**	1.00E+00	2.89E-04
Cdca3_chr6	2	3	2	35	0.8	1.7	4.0	15.6	**6.01E-02**	**5.00E-05**	8.74E-01	2.85E-04
Cdca5_chr19	1	2	2	15	0.7	1.6	2.6	5.9	**1.39E-01**	**5.00E-05**	9.62E-01	2.85E-04
Cdca8_chr4	3	4	4	34	0.3	1.3	3.0	7.7	**3.96E-01**	**5.00E-05**	1.00E+00	2.85E-04
Cdk1_chr10	2	2	2	20	0.3	1.2	3.4	10.3	**4.65E-01**	**5.00E-05**	1.00E+00	2.85E-04
Cdkn2c_chr4	5	5	4	16	0.1	1.0	1.9	3.7	**8.80E-01**	**5.00E-05**	1.00E+00	2.85E-04
Cdkn2d_chr9	11	14	14	34	0.3	1.2	1.3	2.4	**2.42E-01**	**5.00E-05**	9.92E-01	2.85E-04
Cdkn3_chr14	1	1	1	13	0.0	1.0	3.7	13.4	**7.81E-01**	**5.00E-05**	1.00E+00	2.85E-04
Cdr2_chr7	13	17	26	107	0.4	1.3	2.1	4.2	**6.58E-02**	**5.00E-05**	8.76E-01	2.85E-04
Cebpb_chr2	1	2	2	5	0.5	1.4	1.4	2.6	**2.82E-01**	**5.00E-05**	9.94E-01	2.85E-04
Cebpd_chr16	1	2	2	4	0.1	1.1	0.9	1.9	**8.12E-01**	**2.76E-02**	1.00E+00	7.30E-02
Cebpe_chr14	0	0	0	7	0.0	1.0	2.7	6.7	**1.98E-01**	**5.00E-05**	1.00E+00	2.85E-04
Cenpa_chr5	6	7	8	27	0.2	1.1	1.7	3.3	**6.12E-01**	**5.00E-05**	1.00E+00	2.85E-04
Cenpe_chr3	2	2	3	24	0.0	1.0	3.0	7.9	**9.08E-01**	**5.00E-05**	1.00E+00	2.85E-04
Cenpf_chr1	1	1	2	22	0.0	1.0	3.6	12.0	**7.51E-01**	**5.00E-05**	1.00E+00	2.85E-04
Cenph_chr13	2	2	2	11	0.3	1.2	2.8	6.9	**5.31E-01**	**5.00E-05**	1.00E+00	2.85E-04
Cenpi_chrX	1	1	1	10	0.0	1.0	2.9	7.4	**9.02E-01**	**5.00E-05**	1.00E+00	2.85E-04
Cenpl_chr1	2	3	3	12	0.3	1.2	2.1	4.2	**5.59E-01**	**5.00E-05**	1.00E+00	2.92E-04
Cenpn_chr8	1	2	2	10	0.3	1.3	2.5	5.5	**4.64E-01**	**5.00E-05**	1.00E+00	2.85E-04
Cenpv_chr11	1	1	2	3	0.2	1.2	1.0	2.0	**7.24E-01**	**5.00E-05**	1.00E+00	2.85E-04
Cep76_chr18	2	3	4	19	0.2	1.1	2.4	5.3	**5.29E-01**	**5.00E-05**	1.00E+00	2.85E-04
Cercam_chr2	1	1	1	7	0.4	1.3	2.5	5.6	**8.53E-03**	**5.00E-05**	4.41E-01	2.85E-04
Ces2g_chr8	2	2	4	36	0.0	1.0	3.1	8.6	**9.53E-01**	**5.00E-05**	1.00E+00	2.85E-04
Chaf1a_chr17	2	3	4	21	0.4	1.4	2.2	4.7	**1.83E-01**	**5.00E-05**	9.86E-01	2.85E-04
Chaf1b_chr16	2	3	3	12	0.4	1.3	1.8	3.5	**3.34E-01**	**5.00E-05**	9.98E-01	2.85E-04
Chek1_chr9	1	1	1	8	-0.1	1.1	2.6	6.0	**7.19E-01**	**5.00E-05**	1.00E+00	2.85E-04
Chil1_chr1	1	1	1	10	0.0	1.0	3.0	8.1	**6.03E-01**	**5.00E-05**	1.00E+00	2.85E-04

Chil3_chr3	4	7	4	290	1.0	1.9	6.1	68.4	4.12E-03	5.00E-05	2.35E-01	2.85E-04
Chtf18_chr17	1	2	3	11	0.4	1.3	1.9	3.7	3.53E-01	5.00E-05	9.98E-01	2.85E-04
Cish_chr9	2	3	4	7	0.4	1.3	0.9	1.8	2.85E-01	5.00E-05	9.95E-01	2.85E-04
Cit_chr5	1	1	2	17	0.0	1.0	3.1	8.6	5.52E-01	5.00E-05	1.00E+00	2.85E-04
Ckap2_chr8	1	1	2	12	0.2	1.2	2.8	7.1	6.44E-01	5.00E-05	1.00E+00	2.85E-04
Ckap2l_chr2	2	2	4	23	0.2	1.2	2.7	6.3	5.41E-01	5.00E-05	1.00E+00	2.85E-04
Ckap4_chr10	5	8	11	26	0.6	1.6	1.2	2.4	1.29E-02	5.00E-05	5.25E-01	2.85E-04
Cks1b_chr3	5	6	5	19	0.3	1.2	1.9	3.6	5.27E-01	5.00E-05	1.00E+00	2.85E-04
Cks2_chr13	11	12	7	43	0.1	1.1	2.6	6.1	7.40E-01	5.00E-05	1.00E+00	2.85E-04
Clca1_chr3	31	30	48	94	0.0	1.0	0.9	1.9	9.42E-01	5.00E-05	1.00E+00	2.85E-04
Clcn2_chr16	1	1	2	8	0.0	1.0	2.3	4.8	9.55E-01	5.00E-05	1.00E+00	2.85E-04
Cldn13_chr5	1	2	1	44	0.8	1.7	5.5	43.9	1.55E-01	5.00E-05	9.13E-01	2.85E-04
Cldn15_chr5	0	1	0	2	0.0	1.0	1.0	2.0	1.08E-01	5.00E-05	9.38E-01	2.85E-04
Clec12a_chr6	13	14	11	28	0.1	1.1	1.3	2.5	5.88E-01	5.00E-05	1.00E+00	2.85E-04
Clec1b_chr6	3	4	3	9	0.6	1.5	1.8	3.4	2.08E-01	5.00E-05	9.86E-01	2.85E-04
Clec4a2_chr6	6	6	4	15	0.1	1.0	1.8	3.4	8.20E-01	5.00E-05	1.00E+00	2.85E-04
Clec4a3_chr6	17	16	15	30	-0.1	1.1	1.0	2.0	6.84E-01	5.00E-05	1.00E+00	2.85E-04
Clec4d_chr6	1	1	1	8	-0.1	1.0	2.9	7.5	9.14E-01	5.00E-05	1.00E+00	2.85E-04
Clec4e_chr6	1	0	1	5	0.0	1.0	2.4	5.4	3.84E-01	5.00E-05	1.00E+00	2.85E-04
Clec5a_chr6	1	0	1	5	0.0	1.0	2.2	4.6	2.34E-01	5.00E-05	9.59E-01	2.85E-04
Clec7a_chr6	8	6	10	27	-0.4	1.3	1.4	2.7	1.29E-01	5.00E-05	9.54E-01	2.85E-04
Clhc1_chr4	0	0	0	2	0.0	1.0	1.0	2.0	3.23E-01	5.00E-05	9.98E-01	2.85E-04
Clspn_chr4	1	1	2	17	0.2	1.1	3.1	8.8	5.99E-01	5.00E-05	1.00E+00	2.85E-04
Cmas_chr6	12	16	16	54	0.5	1.4	1.7	3.3	6.23E-02	5.00E-05	8.76E-01	2.85E-04
Cox6b2_chr7	2	2	1	3	0.1	1.1	1.3	2.5	8.90E-01	7.50E-05	1.00E+00	4.21E-04
Cpd_chr11	3	3	7	11	-0.1	1.0	0.8	1.7	8.31E-01	5.00E-05	1.00E+00	2.85E-04
Cpeb3_chr19	1	1	1	5	0.0	1.0	2.2	4.6	6.06E-01	5.00E-05	1.00E+00	2.85E-04
Cpne2_chr8	3	4	6	13	0.3	1.2	1.0	2.1	3.94E-01	5.00E-05	1.00E+00	2.85E-04
Cpox_chr16	8	11	14	162	0.4	1.3	3.5	11.4	8.65E-02	5.00E-05	8.26E-01	2.85E-04
Cpxm1_chr2	4	12	9	18	1.4	2.7	1.0	2.0	6.15E-08	5.00E-05	3.76E-05	2.85E-04
Creg1_chr1	31	33	45	107	0.1	1.1	1.2	2.4	6.31E-01	5.00E-05	1.00E+00	2.85E-04
Creld2_chr15	13	17	19	33	0.3	1.2	0.8	1.7	2.31E-01	5.00E-05	9.91E-01	2.85E-04
Csf3r_chr4	8	7	13	66	-0.2	1.1	2.4	5.2	4.78E-01	5.00E-05	1.00E+00	2.93E-04
Ctse_chr1	7	11	10	164	0.6	1.5	4.0	15.7	1.97E-02	5.00E-05	5.18E-01	2.85E-04
Ctsg_chr14	0	1	0	26	0.0	1.0	4.7	26.0	1.90E-01	5.00E-05	9.86E-01	2.85E-04
Cxcr2_chr1	5	3	7	30	-0.5	1.4	2.2	4.6	1.01E-01	5.00E-05	8.47E-01	2.85E-04
Cyp4b1_chr4	2	3	4	11	0.4	1.4	1.5	2.9	2.74E-01	5.00E-05	9.94E-01	2.85E-04
Cysltr2_chr14	0	1	0	4	0.0	1.0	2.0	3.9	1.60E-01	5.00E-05	9.78E-01	2.85E-04
D430020J02Rik_chr12	1	1	2	3	0.0	1.0	0.9	1.9	7.82E-01	5.00E-05	1.00E+00	2.82E-04
Dach1_chr14	0	0	0	2	0.0	1.0	0.9	1.9	7.80E-01	5.00E-05	1.00E+00	2.61E-04
Dapk2_chr9	4	4	6	13	0.3	1.2	1.2	2.3	4.40E-01	5.00E-05	1.00E+00	2.85E-04
Dclre1a_chr19	2	2	3	8	-0.2	1.1	1.2	2.3	6.63E-01	5.00E-05	1.00E+00	2.85E-04
Ddias_chr7	1	1	1	7	0.0	1.0	2.3	4.8	6.37E-01	5.00E-05	1.00E+00	2.85E-04
Deb1_chr9	5	5	3	7	-0.1	1.1	1.2	2.2	7.58E-01	5.00E-05	1.00E+00	2.85E-04
Dek_chr13	53	52	66	260	0.0	1.0	2.0	4.0	9.71E-01	5.00E-05	1.00E+00	2.85E-04
Dennd2c_chr3	1	1	1	6	0.0	1.0	2.4	5.3	8.75E-01	5.00E-05	1.00E+00	2.85E-04
Depdc1b_chr13	1	1	1	12	0.4	1.4	3.2	9.5	1.39E-02	5.00E-05	5.33E-01	2.85E-04
Derl3_chr10	4	5	5	15	0.4	1.3	1.7	3.2	2.77E-01	5.00E-05	9.94E-01	2.85E-04
Dfna5_chr6	0	1	1	3	0.0	1.0	1.7	3.2	4.13E-01	5.00E-05	1.00E+00	2.85E-04
Dgat2_chr7	2	2	4	7	-0.4	1.4	0.8	1.7	2.91E-01	5.00E-05	9.96E-01	2.85E-04
Dhrs11_chr11	5	9	8	76	0.9	1.8	3.2	9.2	5.74E-03	5.00E-05	3.63E-01	2.85E-04
Dhrs9_chr2	0	0	1	5	0.0	1.0	2.2	4.7	7.86E-01	5.00E-05	1.00E+00	2.85E-04
Diap3_chr14	1	1	3	20	0.4	1.3	3.0	7.8	3.32E-01	5.00E-05	9.98E-01	2.85E-04
Dlgap5_chr14	2	2	4	27	0.0	1.0	2.9	7.3	8.90E-01	5.00E-05	1.00E+00	2.85E-04
Dmtn_chr14	0	1	1	24	0.0	1.0	4.2	18.3	3.74E-01	2.34E-03	9.97E-01	7.37E-03
Dmxl2_chr9	2	2	5	8	-0.3	1.2	0.8	1.7	2.39E-01	5.00E-05	9.68E-01	2.85E-04
Dna2_chr10	3	4	6	17	0.1	1.1	1.4	2.7	5.98E-01	5.00E-05	1.00E+00	2.85E-04
Dpf3_chr12	0	0	0	3	0.0	1.0	1.7	3.3	9.36E-01	5.00E-05	1.00E+00	2.85E-04
Dscc1_chr15	1	1	1	5	0.0	1.0	2.4	5.2	6.78E-01	5.00E-05	1.00E+00	2.85E-04
Dtl_chr1	2	3	4	21	0.3	1.2	2.5	5.6	3.72E-01	5.00E-05	1.00E+00	2.85E-04
Dtwd1_chr2	3	3	3	5	0.1	1.1	0.7	1.7	8.10E-01	5.00E-05	1.00E+00	2.85E-04
Dusp8_chr7	0	0	1	4	0.0	1.0	2.2	4.5	8.33E-01	5.00E-05	1.00E+00	2.85E-04
Dyrk3_chr1	1	1	1	13	0.0	1.0	3.7	12.9	9.01E-01	5.00E-05	1.00E+00	2.85E-04
E130309D14Rik_chr11	0	0	0	12	0.0	1.0	3.5	11.6	4.53E-02	5.00E-05	1.00E+00	2.85E-04
E230029C05Rik_chr7	1	1	2	4	-0.1	1.1	1.2	2.4	3.52E-01	5.00E-05	9.98E-01	2.82E-04
E2f1_chr2	2	3	4	15	0.2	1.2	1.8	3.5	5.38E-01	5.00E-05	1.00E+00	2.85E-04
E2f2_chr4	9	12	19	94	0.5	1.4	2.3	5.0	3.34E-02	5.00E-05	7.66E-01	2.85E-04
E2f7_chr10	0	0	1	5	0.0	1.0	2.3	4.8	3.41E-01	5.00E-05	1.00E+00	2.85E-04
E2f8_chr7	1	2	3	37	0.4	1.4	3.7	13.0	2.47E-01	5.00E-05	9.92E-01	2.85E-04
Eaf2_chr16	2	2	2	5	0.1	1.1	1.4	2.6	8.54E-01	7.50E-05	1.00E+00	3.94E-04
Ear1_chr14	1	1	0	6	0.0	1.0	2.7	6.3	6.63E-01	5.00E-05	1.00E+00	2.85E-04
Ear12_chr14	13	16	9	26	0.2	1.2	1.6	3.0	4.65E-01	5.00E-05	1.00E+00	2.92E-04
Ear2_chr14	13	16	9	26	0.2	1.2	1.6	3.0	4.65E-01	5.00E-05	1.00E+00	2.85E-04
Ear6_chr14	0	0	0	7	0.0	1.0	2.8	7.0	8.84E-01	5.00E-05	1.00E+00	2.85E-04
Ear7_chr14	0	0	0	7	0.0	1.0	2.8	7.0	9.54E-01	5.00E-05	1.00E+00	2.70E-04
Ect2_chr3	2	2	2	15	0.2	1.1	2.8	6.8	7.01E-01	5.83E-05	1.00E+00	3.31E-04
Eif4ebp1_chr8	6	7	7	14	0.2	1.2	1.0	1.9	5.47E-01	5.00E-05	1.00E+00	2.85E-04
Emilin2_chr17	2	2	5	25	0.0	1.0	2.3	5.0	9.88E-01	5.00E-05	1.00E+00	2.85E-04
Epb4.2_chr2	1	3	4	118	1.0	1.9	5.0	32.6	9.29E-03	5.00E-05	3.49E-01	2.85E-04
Epdr1_chr13	1	1	2	6	0.0	1.0	1.8	3.4	9.43E-01	5.00E-05	1.00E+00	2.85E-04
Epor_chr9	2	2	2	26	0.4	1.4	3.4	10.4	3.33E-01	5.00E-05	9.98E-01	2.85E-04

Epx_chr11	0	0	0	3	0.0	1.0	1.7	3.3	**2.07E-01**	**5.00E-05**	1.00E+00	2.85E-04
Ermap_chr4	3	3	6	130	0.1	1.0	4.5	23.0	**8.52E-01**	**5.00E-05**	1.00E+00	2.85E-04
Esco2_chr14	2	1	2	27	-0.2	1.1	3.7	12.7	**7.19E-01**	**5.00E-05**	1.00E+00	2.85E-04
Espl1_chr15	1	2	3	19	0.2	1.2	2.7	6.5	**5.24E-01**	**5.00E-05**	1.00E+00	2.85E-04
Exo1_chr1	0	0	1	3	0.0	1.0	1.8	3.5	**5.54E-01**	**5.00E-05**	1.00E+00	2.85E-04
F10_chr8	0	0	1	3	0.0	1.0	1.5	2.9	**4.99E-01**	**5.00E-05**	1.00E+00	2.61E-04
F13a1_chr13	2	2	4	21	-0.1	1.0	2.4	5.3	**8.78E-01**	**5.00E-05**	1.00E+00	2.85E-04
F5_chr1	1	1	2	5	0.5	1.4	1.3	2.5	**4.43E-02**	**5.00E-05**	7.07E-01	2.85E-04
F630028O10Rik_chrX	8	6	5	17	-0.3	1.2	1.9	3.7	**2.42E-01**	**5.00E-05**	9.89E-01	2.82E-04
F830002L21Rik_chr10	0	0	0	9	0.0	1.0	3.1	8.6	**2.90E-01**	**5.00E-05**	1.00E+00	2.82E-04
Fabp4_chr3	4	3	3	8	-0.6	1.5	1.3	2.5	**2.71E-01**	**5.00E-05**	9.94E-01	2.85E-04
Fads2_chr19	3	3	7	12	0.3	1.2	0.8	1.7	**5.16E-01**	**5.00E-05**	1.00E+00	2.85E-04
Fahd1_chr17	3	3	3	13	0.2	1.1	2.1	4.2	**6.82E-01**	**5.00E-05**	1.00E+00	2.85E-04
Fam109b_chr15	1	1	2	19	-0.4	1.3	3.1	8.4	**3.89E-01**	**5.00E-05**	1.00E+00	2.85E-04
Fam117a_chr11	16	19	36	108	0.3	1.2	1.6	3.0	**2.02E-01**	**5.00E-05**	9.87E-01	2.85E-04
Fam132a_chr4	2	3	4	23	0.4	1.3	2.7	6.4	**3.98E-01**	**5.00E-05**	1.00E+00	2.85E-04
Fam132b_chr1	0	0	0	3	0.0	1.0	1.7	3.3	**8.62E-01**	**5.00E-05**	1.00E+00	2.85E-04
Fam210b_chr2	4	5	6	17	0.4	1.3	1.6	3.0	**1.70E-01**	**5.00E-05**	9.80E-01	2.85E-04
Fam213a_chr14	15	19	23	89	0.4	1.3	2.0	3.9	**1.08E-01**	**5.00E-05**	9.38E-01	2.85E-04
Fam217b_chr2	1	1	1	3	0.0	1.0	1.1	2.2	**8.54E-01**	**5.00E-05**	1.00E+00	2.85E-04
Fam46c_chr3	17	19	74	245	0.2	1.2	1.7	3.3	**3.42E-01**	**5.00E-05**	9.92E-01	2.85E-04
Fam83d_chr2	0	0	1	4	0.0	1.0	2.0	3.9	**5.72E-01**	**5.00E-05**	1.00E+00	2.85E-04
Fancd2_chr6	1	1	2	10	0.4	1.3	2.3	4.8	**2.88E-01**	**5.00E-05**	9.95E-01	2.85E-04
Fbxo17_chr7	1	1	1	2	0.0	1.0	0.7	1.7	**8.47E-01**	**5.00E-05**	1.00E+00	2.85E-04
Fbxo5_chr10	7	7	8	38	0.1	1.0	2.3	4.9	**8.42E-01**	**5.00E-05**	1.00E+00	2.85E-04
Fcgr1_chr3	2	3	3	7	0.3	1.2	1.3	2.5	**3.82E-01**	**5.00E-05**	1.00E+00	2.85E-04
Fcgr3_chr1	17	17	17	40	0.0	1.0	1.2	2.4	**8.73E-01**	**5.00E-05**	1.00E+00	2.85E-04
Fcgr4_chr1	4	6	4	28	0.6	1.5	2.9	7.4	**1.29E-01**	**5.00E-05**	9.54E-01	2.85E-04
Fcnb_chr2	0	1	0	16	0.0	1.0	4.0	16.0	**8.30E-02**	**5.00E-05**	8.18E-01	2.85E-04
Fech_chr18	14	22	32	211	0.7	1.6	2.7	6.6	**1.75E-03**	**5.00E-05**	1.80E-01	2.85E-04
Fen1_chr19	6	9	11	39	0.6	1.5	1.8	3.5	**3.68E-02**	**5.00E-05**	7.72E-01	2.85E-04
Fhdc1_chr3	1	1	1	18	0.0	1.0	3.9	15.1	**3.87E-01**	**1.12E-03**	1.00E+00	4.35E-03
Fkbp11_chr15	1	1	1	3	0.5	1.4	1.7	3.3	**3.79E-01**	**5.00E-05**	1.00E+00	2.85E-04
Fn3k_chr11	0	0	0	14	0.0	1.0	3.8	13.7	**6.95E-01**	**1.33E-04**	1.00E+00	7.20E-04
Fn3krp_chr11	3	4	6	27	0.3	1.2	2.2	4.7	**4.56E-01**	**5.00E-05**	1.00E+00	2.85E-04
Fnip2_chr3	2	2	4	13	-0.1	1.1	1.6	3.0	**6.68E-01**	**5.00E-05**	1.00E+00	2.85E-04
Fosl2_chr5	2	3	5	11	0.4	1.4	1.1	2.1	**9.90E-02**	**5.00E-05**	8.44E-01	2.85E-04
Foxm1_chr6	3	4	6	22	0.3	1.2	1.8	3.4	**3.58E-01**	**5.00E-05**	9.98E-01	2.85E-04
Fpr1_chr17	3	3	3	9	-0.1	1.1	1.4	2.7	**8.09E-01**	**5.00E-05**	1.00E+00	2.85E-04
Fpr2_chr17	2	2	2	11	0.0	1.0	2.5	5.8	**9.49E-01**	**5.00E-05**	1.00E+00	2.85E-04
Fzr1_chr10	9	12	19	63	0.5	1.4	1.7	3.3	**5.48E-02**	**5.00E-05**	8.54E-01	2.85E-04
G6pdx_chrX	12	16	21	36	0.4	1.4	0.8	1.7	**2.11E-01**	**2.85E-03**	9.88E-01	1.07E-02
Gadd45a_chr6	6	7	6	22	0.4	1.3	2.0	3.9	**2.19E-01**	**5.00E-05**	9.90E-01	2.85E-04
Galnt3_chr2	3	3	5	10	0.2	1.2	1.0	2.0	**4.74E-01**	**5.00E-05**	1.00E+00	2.85E-04
Garem_chr18	0	0	1	6	0.0	1.0	2.6	6.2	**7.63E-01**	**5.00E-05**	1.00E+00	2.85E-04
Gas2_chr7	1	1	1	2	0.0	1.0	0.7	1.6	**7.71E-01**	**1.65E-03**	1.00E+00	6.61E-03
Gas2l3_chr10	1	1	1	4	0.0	1.0	1.6	3.0	**6.56E-01**	**5.00E-05**	1.00E+00	2.72E-04
Gata1_chrX	1	3	3	34	0.8	1.7	3.6	12.5	**7.74E-02**	**5.00E-05**	8.05E-01	2.85E-04
Gatm_chr2	22	23	31	50	0.1	1.0	0.7	1.6	**8.13E-01**	**5.00E-05**	1.00E+00	2.85E-04
Gca_chr2	3	3	4	9	0.0	1.0	1.4	2.6	**9.89E-01**	**5.00E-05**	1.00E+00	2.85E-04
Gclm_chr3	7	11	13	89	0.6	1.5	2.8	7.0	**4.66E-02**	**5.00E-05**	8.39E-01	2.85E-04
Gda_chr19	5	6	12	91	0.3	1.2	3.0	7.8	**2.14E-01**	**5.00E-05**	9.89E-01	2.85E-04
Gdpd1_chr11	2	2	2	4	0.3	1.2	0.8	1.7	**5.34E-01**	**5.00E-05**	1.00E+00	2.85E-04
Gen1_chr12	1	1	3	10	-0.4	1.3	2.0	3.9	**3.86E-01**	**5.00E-05**	1.00E+00	2.85E-04
Gfap_chr11	0	0	0	5	0.0	1.0	2.4	5.4	**7.29E-01**	**5.00E-05**	1.00E+00	2.85E-04
Gfi1b_chr2	1	1	1	14	0.2	1.2	3.0	8.1	**5.50E-01**	**5.00E-05**	1.00E+00	2.92E-04
Gla_chrX	1	1	1	2	0.0	1.0	0.7	1.6	**9.46E-01**	**5.00E-05**	1.00E+00	2.85E-04
Glipr2_chr4	12	13	14	25	0.1	1.1	0.8	1.7	**5.79E-01**	**5.00E-05**	1.00E+00	2.85E-04
Glrx_chr13	15	17	15	31	0.2	1.1	1.1	2.1	**4.63E-01**	**5.00E-05**	1.00E+00	2.85E-04
Glrx5_chr12	9	14	11	47	0.6	1.6	2.1	4.4	**3.72E-02**	**5.00E-05**	7.78E-01	2.85E-04
Gm4841_chr18	0	0	1	5	0.0	1.0	2.4	5.2	**6.28E-01**	**5.00E-05**	1.00E+00	2.85E-04
Gm5150_chr3	4	5	5	13	0.2	1.1	1.5	2.8	**7.07E-01**	**5.00E-05**	1.00E+00	2.85E-04
Gm5483_chr16	1	1	0	5	0.0	1.0	2.4	5.4	**8.45E-01**	**5.00E-05**	1.00E+00	2.85E-04
Gm9733_chr3	4	4	3	8	0.1	1.1	1.2	2.4	**8.42E-01**	**5.00E-05**	1.00E+00	2.85E-04
Gmnn_chr13	9	10	9	40	0.0	1.0	2.1	4.3	**9.87E-01**	**5.00E-05**	1.00E+00	2.85E-04
Gp49a_chr10	2	1	2	13	-0.4	1.3	2.7	6.5	**4.32E-01**	**5.00E-05**	1.00E+00	2.85E-04
Gp5_chr16	1	3	3	5	1.1	2.1	0.9	1.9	**8.14E-03**	**5.00E-05**	4.32E-01	2.85E-04
Gp9_chr6	2	2	2	6	0.3	1.2	1.8	3.4	**5.95E-01**	**5.00E-05**	1.00E+00	2.85E-04
Gpc1_chr1	2	3	5	9	0.5	1.4	0.7	1.6	**1.48E-01**	**5.00E-05**	9.68E-01	2.85E-04
Gpr141_chr13	7	5	10	25	-0.4	1.3	1.4	2.6	**1.07E-01**	**5.00E-05**	9.38E-01	2.85E-04
Gpr160_chr3	2	1	2	4	-0.1	1.1	0.9	1.9	**8.73E-01**	**6.25E-04**	1.00E+00	2.75E-03
Gpr97_chr8	1	1	1	5	0.0	1.0	2.1	4.3	**9.49E-01**	**5.00E-05**	1.00E+00	2.85E-04
Gpsm2_chr3	1	1	2	21	0.3	1.2	3.4	10.8	**6.93E-01**	**5.00E-05**	1.00E+00	2.85E-04
Gpx1_chr9	106	141	120	360	0.4	1.3	1.6	3.0	**4.91E-02**	**5.00E-05**	8.46E-01	2.85E-04
Gpx3_chr11	27	28	32	56	0.1	1.1	0.8	1.8	**7.39E-01**	**5.00E-05**	1.00E+00	2.85E-04
Grina_chr15	21	30	34	127	0.5	1.4	1.9	3.7	**1.91E-02**	**5.00E-05**	6.13E-01	2.85E-04
Gsr_chr8	12	11	22	57	-0.1	1.1	1.4	2.6	**6.74E-01**	**5.00E-05**	1.00E+00	2.85E-04
Gsta3_chr1	4	4	4	6	0.0	1.0	0.6	1.5	**9.08E-01**	**2.59E-03**	1.00E+00	9.95E-03
Gstm5_chr3	3	3	3	11	-0.1	1.0	1.9	3.8	**9.02E-01**	**5.00E-05**	1.00E+00	2.85E-04
Gtse1_chr15	1	1	2	11	0.4	1.3	2.7	6.4	**9.00E-02**	**5.00E-05**	9.27E-01	2.85E-04
Gypa_chr8	5	10	5	301	0.9	1.9	5.8	55.0	**2.06E-03**	**5.00E-05**	1.42E-01	2.85E-04

Gypc_chr18	13	16	19	69	0.3	1.2	1.8	3.6	**1.82E-01**	**5.00E-05**	9.86E-01	2.85E-04
Gzmb_chr14	1	2	1	5	0.8	1.8	2.0	4.1	**1.02E-01**	**5.00E-05**	9.38E-01	2.85E-04
H2-Q10_chr17	1	1	1	9	0.2	1.1	2.7	6.3	**7.65E-01**	**5.00E-05**	1.00E+00	2.85E-04
H2afx_chr9	5	8	12	36	0.6	1.5	1.6	3.1	**4.92E-02**	**5.00E-05**	8.46E-01	2.85E-04
H2afz_chr3	99	105	105	310	0.1	1.1	1.6	3.0	**6.67E-01**	**5.00E-05**	1.00E+00	2.85E-04
Hagh_chr17	11	13	14	56	0.2	1.2	2.0	4.1	**4.37E-01**	**5.00E-05**	1.00E+00	2.85E-04
Hbq1b_chr11	1	1	1	12	0.2	1.2	3.6	11.7	**1.40E-01**	**5.00E-05**	9.63E-01	2.85E-04
Hdc_chr2	1	1	2	17	0.3	1.2	3.4	10.3	**5.55E-01**	**5.00E-05**	1.00E+00	2.85E-04
Hemgn_chr4	1	3	3	160	1.2	2.4	5.9	59.4	**3.65E-03**	**5.00E-05**	2.17E-01	2.85E-04
Hist2h2bb_chr3	1	1	0	4	0.0	1.0	1.9	3.7	**6.21E-01**	**5.00E-05**	1.00E+00	2.85E-04
Hist3h2ba_chr11	1	1	1	2	0.1	1.1	0.7	1.6	**6.97E-01**	**3.50E-04**	1.00E+00	1.69E-03
Hk3_chr13	5	5	8	24	0.0	1.0	1.6	2.9	**8.87E-01**	**5.00E-05**	1.00E+00	2.99E-04
Hmgb2_chr8	37	40	39	247	0.1	1.1	2.7	6.3	**7.08E-01**	**5.00E-05**	1.00E+00	2.85E-04
Hmgb3_chrX	6	8	8	46	0.2	1.2	2.6	6.0	**4.18E-01**	**5.00E-05**	1.00E+00	2.85E-04
Hmgn2_chr4	71	92	82	220	0.4	1.3	1.4	2.7	**6.96E-02**	**5.00E-05**	8.82E-01	2.85E-04
Hmmr_chr11	2	2	3	31	-0.1	1.1	3.4	10.3	**7.79E-01**	**5.00E-05**	1.00E+00	2.85E-04
Hnrnpll_chr17	8	7	11	20	-0.1	1.1	0.9	1.8	**7.76E-01**	**5.00E-05**	1.00E+00	2.85E-04
Hp_chr8	3	3	4	47	-0.1	1.1	3.6	12.1	**8.61E-01**	**5.00E-05**	1.00E+00	2.85E-04
Hpn_chr7	1	1	1	4	0.0	1.0	1.8	3.6	**5.25E-01**	**5.00E-05**	1.00E+00	2.85E-04
Hsd11b1_chr1	13	14	3	8	0.0	1.0	1.6	3.0	**7.09E-01**	**1.40E-03**	1.00E+00	6.00E-03
Iba57_chr11	2	2	4	11	0.2	1.2	1.7	3.2	**4.56E-01**	**5.00E-05**	1.00E+00	2.85E-04
Icam4_chr9	0	0	0	8	0.0	1.0	3.0	8.0	**7.97E-01**	**5.00E-05**	1.00E+00	2.85E-04
Ier3_chr17	1	1	1	2	0.1	1.0	1.0	1.9	**6.14E-01**	**4.50E-04**	1.00E+00	2.12E-03
Ifi204_chr1	15	8	17	31	-0.8	1.8	0.9	1.8	**1.09E-03**	**5.00E-05**	9.17E-02	2.85E-04
Ifi44_chr3	1	1	1	10	0.4	1.3	3.3	9.6	**1.93E-01**	**5.00E-05**	9.87E-01	2.85E-04
Ifitm1_chr7	17	12	1	9	-0.5	1.4	3.2	9.5	**1.42E-01**	**1.50E-04**	9.67E-01	8.29E-04
Ifitm2_chr7	41	41	34	58	0.0	1.0	0.8	1.7	**9.60E-01**	**5.00E-05**	1.00E+00	2.85E-04
Ifitm3_chr7	45	59	40	88	0.4	1.3	1.1	2.2	**9.48E-02**	**5.00E-05**	9.27E-01	2.85E-04
Ifitm6_chr7	7	11	5	38	0.6	1.5	3.0	8.0	**1.34E-01**	**5.00E-05**	9.56E-01	2.85E-04
Ifrd2_chr9	6	9	12	54	0.5	1.4	2.2	4.5	**9.47E-02**	**5.00E-05**	9.27E-01	2.85E-04
Igj_chr5	305	359	246	862	0.2	1.2	1.8	3.5	**4.19E-01**	**5.00E-05**	1.00E+00	2.85E-04
Igsf6_chr7	19	18	25	50	-0.1	1.0	1.0	2.0	**7.93E-01**	**5.00E-05**	1.00E+00	2.85E-04
Il15ra_chr2	3	3	4	6	-0.1	1.1	0.7	1.6	**7.56E-01**	**5.75E-04**	1.00E+00	2.51E-03
Il18bp_chr7	7	8	9	15	0.2	1.1	0.7	1.6	**6.12E-01**	**5.00E-05**	1.00E+00	2.85E-04
Il18rap_chr1	4	4	7	17	0.2	1.1	1.3	2.5	**6.30E-01**	**5.00E-05**	1.00E+00	2.85E-04
Il1b_chr2	11	14	13	42	0.3	1.2	1.7	3.2	**2.53E-01**	**5.00E-05**	9.70E-01	2.85E-04
Il1f9_chr2	1	1	1	8	0.0	1.0	2.9	7.3	**9.18E-01**	**5.00E-05**	1.00E+00	2.85E-04
Il1r2_chr1	1	1	1	6	0.6	1.5	2.6	5.9	**1.01E-01**	**5.00E-05**	9.37E-01	2.85E-04
Il1rl1_chr1	1	1	1	4	0.0	1.0	2.2	4.5	**9.66E-01**	**5.00E-05**	1.00E+00	2.85E-04
Il1rn_chr2	1	0	1	4	0.0	1.0	1.6	3.0	**4.25E-01**	**5.00E-05**	1.00E+00	2.49E-04
Incenp_chr19	7	9	13	47	0.3	1.3	1.9	3.7	**1.85E-01**	**5.00E-05**	9.86E-01	2.85E-04
Iqgap3_chr3	0	1	1	6	0.0	1.0	2.4	5.3	**8.44E-01**	**5.00E-05**	1.00E+00	2.85E-04
Isca1_chr13	31	40	54	170	0.4	1.3	1.7	3.2	**8.55E-02**	**5.00E-05**	9.18E-01	2.85E-04
Isg15_chr4	6	9	4	47	0.6	1.5	3.5	10.9	**1.10E-01**	**5.00E-05**	9.38E-01	2.85E-04
Isg20_chr7	17	24	16	81	0.4	1.4	2.4	5.2	**1.86E-01**	**5.00E-05**	9.73E-01	2.89E-04
Itga2b_chr11	5	9	10	21	1.0	2.0	1.1	2.1	**1.37E-04**	**5.00E-05**	1.84E-02	2.85E-04
Itgad_chr7	20	22	38	61	0.2	1.1	0.7	1.6	**4.55E-01**	**5.00E-05**	1.00E+00	2.85E-04
Itgam_chr7	4	5	7	26	0.5	1.4	1.9	3.7	**1.81E-01**	**5.00E-05**	9.50E-01	2.92E-04
Itgb2l_chr16	0	0	0	4	0.0	1.0	2.0	3.9	**2.12E-01**	**5.00E-05**	1.00E+00	2.85E-04
Kcnj2_chr11	1	1	2	4	0.1	1.0	1.0	2.0	**8.87E-01**	**5.00E-05**	1.00E+00	2.85E-04
Kel_chr6	1	1	1	65	0.3	1.2	5.7	50.7	**2.63E-01**	**5.00E-05**	9.74E-01	2.85E-04
Kif11_chr19	3	4	6	62	0.1	1.0	3.4	10.3	**8.29E-01**	**5.00E-05**	1.00E+00	2.85E-04
Kif14_chr1	0	0	1	8	0.0	1.0	3.0	7.8	**6.10E-01**	**5.00E-05**	1.00E+00	2.85E-04
Kif15_chr9	2	2	4	22	0.1	1.0	2.7	6.4	**8.40E-01**	**5.00E-05**	1.00E+00	2.85E-04
Kif18a_chr2	2	1	2	20	-0.4	1.3	3.1	8.3	**3.34E-01**	**5.00E-05**	9.98E-01	2.85E-04
Kif18b_chr11	1	1	2	20	0.1	1.1	3.6	11.7	**2.31E-01**	**5.00E-05**	9.91E-01	2.85E-04
Kif22_chr7	2	3	4	32	0.5	1.4	3.0	8.0	**1.86E-01**	**5.00E-05**	9.86E-01	2.85E-04
Kif23_chr9	4	4	6	27	0.0	1.0	2.2	4.4	**9.75E-01**	**5.00E-05**	1.00E+00	2.85E-04
Kif24_chr4	1	1	1	5	0.0	1.0	2.1	4.3	**8.02E-01**	**5.00E-05**	1.00E+00	2.85E-04
Kif2c_chr4	1	1	2	12	0.3	1.2	2.7	6.6	**4.86E-01**	**5.00E-05**	1.00E+00	2.85E-04
Kif4_chrX	1	1	2	19	0.2	1.2	3.1	8.4	**5.19E-01**	**5.00E-05**	1.00E+00	2.85E-04
Kifc1_chr17	2	2	3	23	0.4	1.4	2.8	7.0	**2.73E-01**	**5.00E-05**	9.94E-01	2.85E-04
Kifc5b_chr17	1	2	3	9	0.2	1.2	1.8	3.5	**5.97E-01**	**5.00E-05**	1.00E+00	2.85E-04
Klf1_chr8	1	2	2	56	0.5	1.4	4.5	23.3	**3.59E-01**	**5.00E-05**	9.94E-01	2.85E-04
Klf5_chr14	0	0	1	2	0.0	1.0	1.1	2.1	**7.31E-01**	**5.00E-05**	1.00E+00	2.85E-04
Klra2_chr6	4	4	4	16	0.1	1.1	2.0	4.0	**8.36E-01**	**5.00E-05**	1.00E+00	2.85E-04
Knstrn_chr2	2	3	3	13	0.1	1.1	2.2	4.5	**7.52E-01**	**5.00E-05**	1.00E+00	2.85E-04
Kntc1_chr5	1	1	1	14	0.0	1.0	3.3	9.6	**3.71E-01**	**5.00E-05**	1.00E+00	2.85E-04
Kpna2_chr11	23	28	30	86	0.3	1.2	1.5	2.8	**2.35E-01**	**5.00E-05**	9.91E-01	2.85E-04
Larp1b_chr3	6	6	7	14	0.1	1.1	1.0	2.0	**7.88E-01**	**5.00E-05**	1.00E+00	2.85E-04
Lbp_chr2	0	0	1	3	0.0	1.0	1.7	3.2	**6.64E-01**	**5.00E-05**	1.00E+00	2.85E-04
Lcn2_chr2	1	3	1	74	1.8	3.4	6.2	73.7	**5.28E-04**	**5.00E-05**	8.17E-02	2.85E-04
Lgals3_chr14	11	15	10	28	0.4	1.3	1.6	2.9	**2.24E-01**	**5.00E-05**	9.53E-01	3.24E-04
Lig1_chr7	6	9	11	42	0.6	1.5	1.9	3.7	**3.11E-02**	**5.00E-05**	7.48E-01	2.85E-04
Lilrb4_chr10	12	8	14	36	-0.7	1.6	1.4	2.6	**2.07E-02**	**5.00E-05**	6.41E-01	2.85E-04
Lmna_chr3	3	4	9	32	0.3	1.2	1.8	3.6	**5.02E-01**	**5.00E-05**	1.00E+00	2.85E-04
Lmnb1_chr18	12	18	20	58	0.5	1.5	1.5	2.9	**1.45E-02**	**5.00E-05**	5.46E-01	2.85E-04
LOC100038947_chr3	6	4	5	14	-0.6	1.5	1.5	2.8	**1.17E-01**	**5.00E-05**	9.46E-01	2.85E-04
Lrg1_chr17	3	5	4	29	0.8	1.7	2.8	6.9	**4.34E-02**	**5.00E-05**	8.14E-01	2.85E-04
Lrr1_chr12	0	0	0	3	0.0	1.0	1.5	2.8	**4.69E-01**	**5.00E-05**	1.00E+00	2.85E-04
Lrrc29_chr8	1	1	1	3	0.0	1.0	1.5	2.8	**9.04E-01**	**5.00E-05**	1.00E+00	2.85E-04

Ltb4r1_chr14	0	1	1	4	0.0	1.0	1.8	3.6	**3.80E-01**	**5.00E-05**	1.00E+00	2.85E-04
Ltf_chr9	1	5	2	136	2.2	4.6	6.4	81.7	**2.54E-09**	**5.00E-05**	1.28E-06	2.85E-04
Ly6c2_chr15	16	27	12	86	0.8	1.7	2.8	7.1	**4.01E-03**	**5.00E-05**	3.11E-01	2.85E-04
Ly6i_chr15	0	0	0	2	0.0	1.0	0.8	1.7	**7.16E-01**	**5.00E-05**	1.00E+00	2.85E-04
Mad2l1_chr6	9	9	10	40	0.0	1.0	2.0	4.1	**9.45E-01**	**5.00E-05**	1.00E+00	2.85E-04
Mapk13_chr17	0	1	1	4	0.0	1.0	2.0	3.9	**4.32E-01**	**5.00E-05**	1.00E+00	2.85E-04
March3_chr18	2	2	3	16	0.5	1.4	2.3	4.9	**2.28E-01**	**5.00E-05**	9.91E-01	2.85E-04
March8_chr6	5	5	11	63	0.0	1.0	2.6	5.9	**8.78E-01**	**5.00E-05**	1.00E+00	2.85E-04
Mastl_chr2	1	0	1	5	0.0	1.0	2.2	4.7	**4.36E-01**	**5.00E-05**	1.00E+00	2.85E-04
Matn2_chr15	1	2	2	5	1.0	2.0	1.1	2.2	**6.53E-03**	**5.00E-05**	3.81E-01	2.85E-04
Mboat2_chr12	1	0	1	6	0.0	1.0	2.6	5.9	**4.47E-01**	**5.00E-05**	1.00E+00	2.85E-04
Mcemp1_chr8	4	5	4	13	0.2	1.1	1.6	3.1	**6.84E-01**	**5.00E-05**	1.00E+00	2.85E-04
Mcm10_chr2	1	1	2	14	0.4	1.3	2.7	6.6	**3.66E-01**	**5.00E-05**	9.97E-01	2.85E-04
Mcm2_chr6	9	12	19	68	0.4	1.4	1.8	3.5	**5.15E-02**	**5.00E-05**	8.48E-01	2.85E-04
Mcm5_chr8	10	15	19	58	0.5	1.4	1.6	3.0	**1.74E-02**	**5.00E-05**	5.92E-01	2.85E-04
Mcm7_chr5	15	20	25	80	0.4	1.3	1.7	3.2	**7.95E-02**	**5.00E-05**	9.08E-01	2.85E-04
Mcph1_chr8	2	2	3	8	0.1	1.0	1.4	2.6	**8.69E-01**	**5.00E-05**	1.00E+00	2.85E-04
Megf9_chr4	2	2	4	10	0.1	1.1	1.4	2.6	**8.29E-01**	**5.00E-05**	1.00E+00	2.85E-04
Melk_chr4	1	1	2	7	0.0	1.0	2.2	4.6	**9.43E-01**	**5.00E-05**	1.00E+00	2.85E-04
Memo1_chr17	14	14	19	76	0.0	1.0	2.0	4.0	**9.54E-01**	**5.00E-05**	1.00E+00	2.85E-04
Metap2_chr10	16	17	19	87	0.1	1.1	2.2	4.6	**6.50E-01**	**5.00E-05**	1.00E+00	2.85E-04
Mfsd2b_chr12	3	4	6	40	0.4	1.3	2.6	6.1	**2.37E-01**	**5.00E-05**	9.68E-01	2.85E-04
Mfsd9_chr1	1	1	1	3	0.0	1.0	1.3	2.4	**7.01E-01**	**5.00E-05**	1.00E+00	2.85E-04
Mgst1_chr6	16	15	14	40	-0.1	1.1	1.5	2.8	**7.22E-01**	**5.00E-05**	1.00E+00	2.85E-04
Mgst2_chr3	3	2	2	5	-0.2	1.2	1.2	2.3	**6.72E-01**	**5.00E-05**	1.00E+00	2.85E-04
Mgst3_chr1	2	3	2	36	0.5	1.4	4.3	19.2	**3.98E-01**	**5.00E-05**	1.00E+00	2.85E-04
Micall2_chr5	2	2	3	12	0.4	1.3	1.8	3.5	**2.51E-01**	**5.00E-05**	9.92E-01	2.85E-04
Minpp1_chr19	8	9	15	43	0.3	1.2	1.6	2.9	**3.04E-01**	**5.00E-05**	9.96E-01	2.85E-04
Mir22hg_chr11	5	5	6	11	0.1	1.1	0.8	1.8	**8.08E-01**	**5.00E-05**	1.00E+00	2.82E-04
Mis18bp1_chr12	2	1	3	18	-0.2	1.2	2.9	7.3	**5.22E-01**	**5.00E-05**	1.00E+00	2.85E-04
Mki67_chr7	8	9	16	228	0.2	1.2	3.8	14.1	**3.04E-01**	**5.00E-05**	9.86E-01	2.85E-04
Mkrn1_chr6	35	58	72	180	0.7	1.6	1.3	2.5	**6.42E-04**	**5.00E-05**	9.50E-02	2.85E-04
Mlkl_chr8	2	2	3	7	0.0	1.0	1.2	2.4	**9.73E-01**	**5.00E-05**	1.00E+00	2.85E-04
Mmp19_chr10	1	1	1	2	0.0	1.0	0.9	1.8	**6.89E-01**	**1.15E-03**	1.00E+00	4.86E-03
Mmp25_chr17	0	0	1	6	0.0	1.0	2.6	6.1	**3.86E-01**	**5.00E-05**	1.00E+00	2.85E-04
Mmp3_chr9	1	1	1	2	0.4	1.3	0.7	1.6	**3.72E-01**	**2.00E-03**	1.00E+00	7.82E-03
Mmp8_chr9	1	1	1	31	0.0	1.0	4.7	26.5	**6.74E-01**	**5.00E-05**	1.00E+00	2.85E-04
Mmp9_chr2	2	3	5	36	0.5	1.4	2.7	6.7	**1.48E-01**	**5.00E-05**	9.69E-01	2.85E-04
Mms22l_chr4	3	3	4	10	0.0	1.0	1.2	2.4	**9.84E-01**	**5.00E-05**	1.00E+00	2.85E-04
Mnda_chr1	2	2	3	9	0.0	1.0	1.7	3.3	**9.92E-01**	**5.00E-05**	1.00E+00	2.85E-04
Mns1_chr9	1	2	2	26	0.7	1.6	3.7	12.6	**3.03E-01**	**5.00E-05**	9.96E-01	2.85E-04
Mocos_chr18	1	1	1	3	0.0	1.0	1.1	2.1	**9.52E-01**	**5.00E-05**	1.00E+00	2.85E-04
Mpo_chr11	0	2	1	65	1.0	2.0	5.9	61.4	**3.90E-05**	**5.00E-05**	6.01E-03	2.85E-04
Mpp1_chrX	17	21	25	62	0.3	1.3	1.3	2.5	**2.85E-01**	**5.00E-05**	9.95E-01	2.85E-04
Mpp2_chr11	1	1	2	9	0.0	1.0	2.5	5.6	**5.57E-01**	**5.00E-05**	1.00E+00	2.85E-04
Ms4a3_chr19	0	0	0	12	0.0	1.0	3.6	12.2	**8.83E-02**	**5.00E-05**	1.00E+00	2.85E-04
Ms4a4d_chr19	3	4	3	10	0.6	1.5	1.8	3.5	**1.51E-01**	**5.00E-05**	9.71E-01	2.85E-04
Ms4a6d_chr19	7	4	7	17	-0.6	1.5	1.3	2.5	**1.08E-01**	**5.00E-05**	8.52E-01	2.85E-04
Ms4a8a_chr19	0	1	0	2	0.0	1.0	0.6	1.5	**1.06E-01**	**5.00E-05**	9.38E-01	2.85E-04
Msantd3_chr4	1	1	1	2	0.0	1.0	0.9	1.8	**8.43E-01**	**5.00E-05**	1.00E+00	2.70E-04
Msrb1_chr17	18	21	18	52	0.2	1.2	1.6	2.9	**4.47E-01**	**5.00E-05**	1.00E+00	2.85E-04
Mt1_chr8	6	7	6	15	0.1	1.1	1.4	2.7	**8.67E-01**	**5.00E-05**	1.00E+00	2.85E-04
Mt2_chr8	3	3	2	9	-0.1	1.1	2.2	4.4	**8.03E-01**	**5.00E-05**	1.00E+00	2.85E-04
Mtfp1_chr11	1	1	2	4	0.3	1.2	1.4	2.7	**6.16E-01**	**5.00E-05**	1.00E+00	2.85E-04
Mtfr2_chr10	1	1	1	6	0.0	1.0	2.6	6.0	**8.50E-01**	**5.00E-05**	1.00E+00	2.85E-04
Mthfd2_chr6	8	11	12	27	0.4	1.4	1.2	2.2	**8.38E-02**	**5.00E-05**	9.17E-01	2.85E-04
Mtus1_chr8	4	4	7	11	0.2	1.2	0.7	1.6	**4.46E-01**	**1.00E-04**	1.00E+00	4.95E-04
Mvb12b_chr2	3	3	7	13	0.0	1.0	0.9	1.8	**9.41E-01**	**5.00E-05**	1.00E+00	2.85E-04
Mxd1_chr6	7	8	14	56	0.1	1.1	2.0	4.0	**5.34E-01**	**5.00E-05**	1.00E+00	2.85E-04
Mybl2_chr2	1	2	3	22	0.2	1.2	3.0	8.1	**5.77E-01**	**5.00E-05**	1.00E+00	2.85E-04
Myh10_chr11	2	2	4	18	0.2	1.2	2.2	4.6	**4.38E-01**	**5.00E-05**	1.00E+00	2.85E-04
Mylk3_chr8	5	6	9	19	0.4	1.3	1.0	2.0	**1.22E-01**	**5.00E-05**	9.50E-01	2.85E-04
Myo1d_chr11	2	2	5	10	0.1	1.1	0.8	1.8	**7.00E-01**	**5.00E-05**	1.00E+00	2.85E-04
Nanp_chr2	7	8	8	18	0.3	1.2	1.2	2.3	**3.79E-01**	**5.00E-05**	1.00E+00	2.85E-04
Naprt_chr15	1	1	1	5	0.2	1.1	1.9	3.7	**2.40E-01**	**5.00E-05**	9.92E-01	2.85E-04
Ncapd2_chr6	5	10	11	66	0.9	1.9	2.6	6.0	**4.69E-05**	**5.00E-05**	1.08E-02	2.85E-04
Ncapd3_chr9	8	7	13	32	-0.1	1.1	1.3	2.4	**6.07E-01**	**5.00E-05**	1.00E+00	2.85E-04
Ncapg_chr5	2	2	4	33	0.0	1.0	3.2	9.2	**9.71E-01**	**5.00E-05**	1.00E+00	2.85E-04
Ncapg2_chr12	4	3	7	36	-0.3	1.2	2.4	5.4	**2.15E-01**	**5.00E-05**	9.89E-01	2.85E-04
Ncaph_chr2	2	3	4	22	0.5	1.4	2.6	6.2	**1.85E-01**	**5.00E-05**	9.86E-01	2.85E-04
Ndc80_chr17	4	4	5	19	0.1	1.1	1.9	3.8	**6.92E-01**	**5.00E-05**	1.00E+00	2.85E-04
Neil3_chr8	1	1	1	21	0.2	1.1	3.9	14.7	**7.12E-01**	**5.00E-05**	1.00E+00	2.85E-04
Nek2_chr1	2	2	3	19	0.4	1.3	2.8	6.7	**3.53E-01**	**5.00E-05**	9.98E-01	2.85E-04
Neto2_chr8	1	1	1	2	0.0	1.0	0.8	1.8	**4.15E-01**	**5.00E-05**	1.00E+00	2.85E-04
Nfe2_chr15	2	4	4	44	0.6	1.5	3.5	11.2	**1.23E-01**	**5.00E-05**	9.50E-01	2.85E-04
Nfil3_chr13	1	1	1	3	0.6	1.5	1.3	2.4	**9.28E-02**	**5.00E-05**	9.27E-01	2.85E-04
Ngp_chr9	4	16	4	325	2.1	4.2	6.4	82.4	**2.64E-10**	**5.00E-05**	1.73E-07	2.85E-04
Nhsl2_chrX	1	1	2	4	0.0	1.0	0.9	1.9	**8.52E-01**	**5.00E-05**	1.00E+00	2.85E-04
Ninl_chr2	1	1	2	6	0.0	1.0	1.9	3.7	**7.94E-01**	**5.00E-05**	1.00E+00	2.85E-04
Nipa1_chr7	2	2	3	12	0.1	1.1	2.2	4.5	**8.26E-01**	**5.00E-05**	1.00E+00	2.85E-04
Nlrp12_chr7	0	0	1	4	0.0	1.0	2.1	4.4	**8.30E-01**	**5.00E-05**	1.00E+00	2.85E-04

Nlrx1_chr9	1	3	4	7	0.8	1.8	1.0	1.9	**5.51E-02**	**1.25E-04**	8.15E-01	6.73E-04
Nme4_chr17	2	2	2	4	-0.1	1.0	1.0	2.0	**9.07E-01**	**5.00E-05**	1.00E+00	2.85E-04
Nmnat3_chr9	1	1	2	9	0.1	1.1	2.2	4.6	**8.45E-01**	**5.00E-05**	1.00E+00	2.85E-04
Nqo1_chr8	1	1	1	5	0.2	1.2	2.2	4.6	**5.16E-01**	**5.00E-05**	1.00E+00	2.85E-04
Nrip3_chr7	0	0	0	3	0.0	1.0	1.3	2.5	**7.70E-01**	**5.00E-05**	1.00E+00	2.85E-04
Nsl1_chr1	3	3	4	10	0.1	1.1	1.4	2.7	**7.65E-01**	**5.00E-05**	1.00E+00	2.85E-04
Nudt12_chr17	1	0	1	2	0.0	1.0	1.1	2.2	**7.07E-01**	**5.00E-05**	1.00E+00	2.85E-04
Nudt4_chr10	16	15	23	69	0.0	1.0	1.5	2.9	**8.54E-01**	**5.00E-05**	1.00E+00	2.85E-04
Nuf2_chr1	2	2	2	20	0.3	1.2	3.0	8.1	**4.40E-01**	**5.00E-05**	1.00E+00	2.85E-04
Nxpe2_chr9	2	6	3	65	1.7	3.3	4.6	25.0	**9.84E-09**	**5.00E-05**	7.84E-06	2.85E-04
Nxpe5_chr5	0	1	1	6	0.0	1.0	2.7	6.4	**6.82E-02**	**5.00E-05**	8.77E-01	2.85E-04
Oaf_chr9	1	1	2	5	0.0	1.0	1.7	3.3	**9.01E-01**	**5.00E-05**	1.00E+00	2.85E-04
Oas1g_chr5	0	0	0	3	0.0	1.0	1.4	2.7	**9.58E-02**	**5.00E-05**	1.00E+00	2.85E-04
Oas3_chr5	1	2	2	30	0.7	1.6	4.0	15.5	**1.00E-02**	**5.00E-05**	4.64E-01	2.85E-04
Oasl2_chr5	2	3	3	15	0.7	1.7	2.3	5.0	**3.66E-02**	**5.00E-05**	7.72E-01	2.85E-04
Odc1_chr12	26	34	41	158	0.4	1.3	2.0	3.9	**6.33E-02**	**5.00E-05**	8.76E-01	2.85E-04
Olfm4_chr14	0	0	0	2	0.0	1.0	1.0	1.9	**1.43E-01**	**5.00E-05**	1.00E+00	2.85E-04
Oosp1_chr19	2	2	1	4	0.2	1.1	2.1	4.3	**7.39E-01**	**5.00E-05**	1.00E+00	2.85E-04
Optn_chr2	5	5	8	23	0.0	1.0	1.5	2.9	**8.68E-01**	**5.00E-05**	1.00E+00	2.85E-04
Orc1_chr4	0	1	1	10	0.0	1.0	3.3	9.9	**7.72E-01**	**5.00E-05**	1.00E+00	2.85E-04
Orm1_chr4	0	0	0	2	0.0	1.0	1.2	2.4	**5.70E-01**	**1.00E-04**	1.00E+00	5.44E-04
Osbpl1a_chr18	2	2	2	5	0.1	1.1	1.1	2.1	**8.62E-01**	**5.00E-05**	1.00E+00	2.85E-04
Otub2_chr12	2	2	3	10	0.3	1.2	1.8	3.5	**5.22E-01**	**5.00E-05**	1.00E+00	2.85E-04
P2ry1_chr3	1	1	2	5	0.3	1.2	1.6	3.0	**3.25E-01**	**5.00E-05**	9.98E-01	2.85E-04
Padi4_chr4	0	0	0	6	0.0	1.0	2.7	6.3	**9.65E-03**	**5.00E-05**	4.58E-01	2.85E-04
Paqr9_chr9	5	7	12	39	0.4	1.3	1.7	3.3	**1.82E-01**	**5.00E-05**	9.86E-01	2.85E-04
Parpbp_chr10	1	1	1	7	0.0	1.0	2.8	7.0	**9.95E-01**	**5.00E-05**	1.00E+00	2.85E-04
Parvb_chr15	6	8	14	35	0.5	1.4	1.3	2.5	**4.69E-02**	**5.00E-05**	8.39E-01	2.85E-04
Pask_chr1	0	0	1	5	0.0	1.0	2.4	5.3	**8.44E-01**	**5.00E-05**	1.00E+00	2.85E-04
Pbk_chr14	2	2	2	18	0.0	1.0	3.2	9.4	**9.84E-01**	**5.00E-05**	1.00E+00	2.85E-04
Pck2_chr14	8	10	15	30	0.4	1.3	1.0	2.0	**1.10E-01**	**5.00E-05**	9.38E-01	2.85E-04
Pcx_chr19	1	1	2	9	0.1	1.1	1.9	3.8	**4.33E-01**	**5.00E-05**	1.00E+00	2.85E-04
Pcyt1a_chr16	7	7	12	34	0.2	1.2	1.5	2.8	**3.82E-01**	**5.00E-05**	1.00E+00	2.85E-04
Pcyt1b_chrX	0	1	1	8	0.0	1.0	2.9	7.5	**2.54E-01**	**2.34E-03**	9.70E-01	9.00E-03
Pde7b_chr10	0	0	1	3	0.0	1.0	1.4	2.6	**9.68E-01**	**5.00E-05**	1.00E+00	2.85E-04
Pdgfc_chr3	1	1	1	3	0.0	1.0	1.2	2.3	**9.41E-01**	**5.00E-05**	1.00E+00	2.85E-04
Pdzk1ip1_chr4	1	1	1	11	0.4	1.3	3.5	11.3	**3.20E-01**	**5.63E-04**	1.00E+00	2.51E-03
Pf4_chr5	16	22	12	25	0.5	1.4	1.1	2.1	**1.32E-01**	**5.00E-05**	9.56E-01	2.85E-04
Pglyrp1_chr7	8	11	6	26	0.5	1.4	2.2	4.6	**1.79E-01**	**5.00E-05**	9.84E-01	2.85E-04
Phyhip_chr14	0	0	0	10	0.0	1.0	3.3	9.7	**2.02E-01**	**5.00E-05**	1.00E+00	2.85E-04
Pi16_chr17	1	1	2	10	0.0	1.0	2.5	5.7	**9.65E-01**	**5.00E-05**	1.00E+00	2.85E-04
Pi4k2b_chr5	3	3	4	17	-0.1	1.1	2.1	4.2	**7.43E-01**	**5.00E-05**	1.00E+00	2.85E-04
Pif1_chr9	1	1	1	8	0.0	1.0	3.0	7.9	**6.55E-01**	**5.00E-05**	1.00E+00	2.85E-04
Pigq_chr17	14	17	28	118	0.3	1.3	2.1	4.2	**1.16E-01**	**5.00E-05**	9.45E-01	2.85E-04
Pik3r6_chr11	1	1	2	4	-0.1	1.1	1.0	2.0	**6.47E-01**	**7.50E-05**	1.00E+00	4.25E-04
Pilra_chr5	7	7	9	19	0.0	1.0	1.1	2.1	**9.25E-01**	**5.00E-05**	1.00E+00	2.85E-04
Pilrb1_chr5	7	8	8	17	0.2	1.2	1.1	2.2	**5.28E-01**	**5.00E-05**	1.00E+00	2.85E-04
Pilrb2_chr5	5	5	6	13	0.1	1.0	1.1	2.2	**8.68E-01**	**5.00E-05**	1.00E+00	2.85E-04
Pip5k1b_chr19	1	2	2	12	0.4	1.3	2.6	6.2	**4.72E-01**	**5.00E-05**	1.00E+00	2.85E-04
Pkhd1l1_chr15	0	0	0	11	0.0	1.0	3.4	10.6	**2.57E-02**	**5.00E-05**	1.00E+00	2.85E-04
Pklr_chr3	1	1	1	12	0.3	1.3	2.8	6.8	**4.74E-01**	**8.21E-03**	1.00E+00	2.40E-02
Pla2g4c_chr7	0	0	0	4	0.0	1.0	2.0	4.1	**9.40E-01**	**5.00E-05**	1.00E+00	2.85E-04
Plek2_chr12	0	0	0	5	0.0	1.0	2.3	5.0	**5.70E-01**	**5.00E-05**	1.00E+00	2.85E-04
Plk1_chr7	1	3	3	23	0.8	1.7	2.9	7.5	**5.32E-02**	**5.00E-05**	8.48E-01	2.85E-04
Plk4_chr3	4	4	6	24	-0.1	1.1	2.0	3.9	**7.69E-01**	**5.00E-05**	1.00E+00	2.85E-04
Pls1_chr9	1	1	2	4	0.3	1.3	1.2	2.2	**1.60E-01**	**5.00E-05**	9.78E-01	2.85E-04
Plscr1_chr9	4	4	5	11	0.0	1.0	1.1	2.1	**8.81E-01**	**5.00E-05**	1.00E+00	2.85E-04
Pmf1_chr3	5	8	7	16	0.5	1.4	1.2	2.3	**1.80E-01**	**5.00E-05**	9.85E-01	2.85E-04
Pnp_chr14	8	14	8	41	0.8	1.7	2.3	4.9	**1.17E-03**	**5.00E-05**	1.39E-01	2.85E-04
Pnp2_chr14	0	1	0	9	0.0	1.0	3.2	9.4	**2.99E-01**	**5.00E-05**	9.96E-01	2.85E-04
Pnpo_chr11	8	14	14	42	0.7	1.6	1.5	2.9	**4.66E-03**	**5.00E-05**	3.39E-01	2.85E-04
Poc1a_chr9	1	1	2	5	0.1	1.1	1.5	2.9	**7.12E-01**	**5.00E-05**	1.00E+00	2.85E-04
Pole_chr5	2	3	4	15	0.3	1.2	1.8	3.5	**2.80E-01**	**5.00E-05**	9.94E-01	2.85E-04
Pole3_chr4	8	8	11	22	0.0	1.0	1.0	2.0	**9.16E-01**	**5.00E-05**	1.00E+00	2.85E-04
Polq_chr16	1	1	2	8	0.0	1.0	2.0	4.1	**9.58E-01**	**5.00E-05**	1.00E+00	2.85E-04
Pon3_chr6	5	4	7	15	-0.2	1.2	1.0	2.1	**4.93E-01**	**5.00E-05**	1.00E+00	2.85E-04
Ppapdc1b_chr8	3	5	5	12	0.4	1.4	1.4	2.6	**2.30E-01**	**5.00E-05**	9.91E-01	2.85E-04
Ppbp_chr5	46	68	49	112	0.5	1.5	1.2	2.3	**1.32E-02**	**5.00E-05**	5.25E-01	2.85E-04
Ppox_chr1	10	12	14	46	0.3	1.2	1.7	3.2	**2.67E-01**	**5.00E-05**	9.94E-01	2.85E-04
Ppp1r15a_chr7	8	9	13	81	0.3	1.2	2.7	6.3	**2.65E-01**	**5.00E-05**	9.94E-01	2.85E-04
Ppp1r3b_chr8	1	2	2	4	0.3	1.2	0.7	1.6	**4.35E-01**	**5.00E-05**	1.00E+00	2.85E-04
Ppp1r3d_chr2	1	1	1	4	0.0	1.0	1.9	3.9	**6.36E-01**	**5.00E-05**	1.00E+00	2.85E-04
Pram1_chr17	2	3	4	20	0.6	1.5	2.4	5.2	**1.28E-01**	**5.00E-05**	9.50E-01	2.85E-04
Prc1_chr7	3	3	4	41	0.2	1.2	3.2	9.1	**5.14E-01**	**5.00E-05**	1.00E+00	2.85E-04
Prdx2_chr8	41	59	43	227	0.5	1.5	2.4	5.2	**1.40E-02**	**5.00E-05**	5.34E-01	2.85E-04
Prdx4_chrX	11	10	9	27	-0.1	1.1	1.5	2.8	**7.38E-01**	**5.00E-05**	1.00E+00	2.85E-04
Prdx5_chr19	32	36	31	64	0.1	1.1	1.0	2.1	**5.55E-01**	**5.00E-05**	1.00E+00	2.85E-04
Prg2_chr2	1	9	1	51	2.6	6.0	5.2	36.9	**4.89E-08**	**5.00E-05**	1.76E-05	2.85E-04
Prg3_chr2	1	1	1	4	0.3	1.2	2.1	4.3	**5.69E-01**	**5.00E-05**	1.00E+00	2.85E-04
Prim1_chr10	7	7	7	25	0.0	1.0	1.9	3.7	**9.73E-01**	**5.00E-05**	1.00E+00	2.85E-04
Prim2_chr1	4	5	7	17	0.3	1.2	1.3	2.4	**3.83E-01**	**5.00E-05**	1.00E+00	2.85E-04

Prkar2b_chr12	6	7	9	39	0.2	1.1	2.1	4.4	**4.58E-01**	**5.00E-05**	1.00E+00	2.85E-04
Prokr1_chr6	0	0	0	2	0.0	1.0	1.1	2.1	**8.67E-01**	**5.00E-05**	1.00E+00	2.85E-04
Prom1_chr5	0	1	1	4	0.0	1.0	2.0	4.1	**1.02E-01**	**5.00E-05**	9.20E-01	2.49E-04
Prr11_chr11	1	1	2	12	0.2	1.2	2.8	6.9	**5.95E-01**	**5.00E-05**	1.00E+00	2.85E-04
Prss34_chr17	0	0	0	2	0.0	1.0	1.2	2.3	**3.71E-01**	**5.00E-05**	1.00E+00	2.85E-04
Ptdss2_chr7	3	4	6	37	0.2	1.2	2.6	6.0	**5.24E-01**	**5.00E-05**	1.00E+00	2.85E-04
Ptgr1_chr4	1	1	2	3	-0.2	1.1	1.1	2.1	**7.29E-01**	**5.00E-05**	1.00E+00	2.85E-04
Ptpla_chr2	1	1	1	3	-0.2	1.1	1.4	2.7	**7.57E-01**	**5.00E-05**	1.00E+00	2.85E-04
Pxmp2_chr5	1	1	1	2	0.0	1.0	1.2	2.3	**9.99E-01**	**5.00E-05**	1.00E+00	2.85E-04
Pygl_chr12	7	9	12	37	0.4	1.3	1.7	3.2	**9.91E-02**	**5.00E-05**	9.35E-01	2.85E-04
Rab15_chr12	1	0	1	2	0.0	1.0	1.3	2.4	**6.64E-01**	**5.00E-05**	1.00E+00	2.85E-04
Rab27a_chr9	7	8	11	17	0.2	1.1	0.6	1.5	**4.79E-01**	**1.00E-04**	1.00E+00	5.44E-04
Rab3il1_chr19	8	9	16	58	0.2	1.2	1.9	3.8	**3.53E-01**	**5.00E-05**	9.98E-01	2.85E-04
Rab44_chr17	1	1	1	14	0.0	1.0	3.3	10.1	**8.56E-01**	**5.00E-05**	1.00E+00	2.85E-04
Rad51_chr2	2	2	3	14	0.3	1.2	2.3	5.0	**5.19E-01**	**5.00E-05**	1.00E+00	2.85E-04
Rad51ap1_chr6	1	2	2	14	0.3	1.2	2.9	7.6	**5.84E-01**	**5.00E-05**	1.00E+00	2.85E-04
Ranbp10_chr8	12	13	23	98	0.1	1.1	2.1	4.2	**5.11E-01**	**5.00E-05**	1.00E+00	2.85E-04
Rec8_chr14	0	0	0	5	0.0	1.0	2.4	5.1	**4.01E-03**	**1.00E-04**	3.11E-01	5.44E-04
Recql4_chr15	1	1	2	9	0.1	1.1	2.2	4.5	**7.69E-01**	**5.00E-05**	1.00E+00	2.85E-04
Redrum_chr18	0	0	0	7	0.0	1.0	2.7	6.7	**1.65E-01**	**5.00E-05**	1.00E+00	2.82E-04
Retnlg_chr16	8	5	4	52	-0.7	1.6	3.6	12.0	**1.12E-01**	**5.00E-05**	9.39E-01	2.85E-04
Rfx2_chr17	1	1	3	12	0.4	1.3	2.2	4.5	**3.83E-01**	**5.00E-05**	1.00E+00	2.85E-04
Rgcc_chr14	2	2	1	12	0.1	1.1	3.1	8.7	**8.78E-01**	**5.00E-05**	1.00E+00	2.85E-04
Rgs1_chr1	14	11	13	20	-0.3	1.3	0.7	1.6	**2.14E-01**	**5.00E-05**	9.88E-01	2.85E-04
Rhag_chr17	1	2	2	82	0.6	1.5	5.7	51.7	**2.11E-01**	**5.00E-05**	9.53E-01	2.85E-04
Rhd_chr4	1	3	2	79	1.3	2.5	5.6	48.2	**1.11E-02**	**5.00E-05**	3.86E-01	2.85E-04
Rhou_chr8	0	0	0	2	0.0	1.0	1.2	2.4	**3.50E-01**	**5.00E-05**	1.00E+00	2.85E-04
Rnaseh2b_chr14	6	8	7	22	0.3	1.2	1.6	3.1	**3.10E-01**	**5.00E-05**	9.97E-01	2.85E-04
Rnasel_chr1	13	12	21	35	-0.1	1.1	0.7	1.6	**7.07E-01**	**5.00E-05**	1.00E+00	2.85E-04
Rnd1_chr15	1	1	1	2	0.0	1.0	0.6	1.6	**9.51E-01**	**5.00E-05**	1.00E+00	2.85E-04
Rnf149_chr1	13	15	20	37	0.1	1.1	0.9	1.9	**6.25E-01**	**5.00E-05**	1.00E+00	2.85E-04
Rrm1_chr7	14	15	23	86	0.2	1.1	1.9	3.8	**4.05E-01**	**5.00E-05**	1.00E+00	2.85E-04
Rrm2_chr12	6	10	10	140	0.7	1.7	3.8	14.3	**6.40E-03**	**5.00E-05**	2.87E-01	2.85E-04
Rsad2_chr12	14	16	26	116	0.3	1.2	2.1	4.4	**2.45E-01**	**5.00E-05**	9.69E-01	2.85E-04
Rundc3a_chr11	1	1	1	2	0.0	1.0	0.9	1.9	**7.11E-01**	**7.50E-05**	1.00E+00	4.25E-04
S100a8_chr3	48	70	24	1,172	0.6	1.5	5.6	49.4	**2.72E-02**	**5.00E-05**	5.97E-01	2.85E-04
S100a9_chr3	41	63	26	1,322	0.6	1.5	5.7	50.9	**1.20E-02**	**5.00E-05**	4.04E-01	2.85E-04
Samd14_chr11	2	3	5	34	0.2	1.2	2.7	6.3	**5.21E-01**	**5.00E-05**	1.00E+00	2.85E-04
Sapcd2_chr2	0	0	0	2	0.0	1.0	1.2	2.3	**7.17E-01**	**5.00E-05**	1.00E+00	2.85E-04
Scrn3_chr2	3	3	4	17	-0.2	1.1	2.1	4.2	**5.42E-01**	**5.00E-05**	1.00E+00	2.85E-04
Sdsl_chr5	0	0	0	2	0.0	1.0	1.0	2.0	**9.12E-01**	**5.00E-05**	1.00E+00	2.85E-04
Sec14l2_chr11	0	0	0	9	0.0	1.0	3.1	8.6	**1.47E-01**	**5.00E-05**	9.68E-01	2.85E-04
Sema4a_chr3	6	7	4	11	0.0	1.0	1.5	2.8	**4.02E-01**	**5.00E-05**	1.00E+00	2.99E-04
Sept5_chr16	1	1	1	5	0.0	1.0	2.2	4.6	**8.27E-01**	**5.00E-05**	1.00E+00	2.85E-04
Serpina3g_chr12	46	48	68	157	0.0	1.0	1.2	2.3	**8.24E-01**	**5.00E-05**	1.00E+00	2.85E-04
Sertad3_chr7	4	6	6	13	0.4	1.3	1.1	2.1	**2.80E-01**	**5.00E-05**	9.94E-01	2.85E-04
Sfxn5_chr6	2	2	4	6	0.2	1.1	0.8	1.8	**5.87E-01**	**5.00E-05**	1.00E+00	2.85E-04
Sgms2_chr3	1	1	1	4	0.0	1.0	1.6	3.0	**9.28E-01**	**5.00E-05**	1.00E+00	2.85E-04
Sgol1_chr17	1	1	1	15	0.0	1.0	3.6	11.8	**8.25E-01**	**5.00E-05**	1.00E+00	2.85E-04
Sgol2_chr1	1	1	1	6	0.0	1.0	2.4	5.3	**6.46E-01**	**5.00E-05**	1.00E+00	2.90E-04
Sh3tc2_chr18	1	1	3	20	-0.2	1.2	2.9	7.2	**5.78E-01**	**5.00E-05**	1.00E+00	2.85E-04
Sh3yl1_chr12	0	1	1	4	0.0	1.0	2.0	3.9	**3.48E-01**	**5.00E-05**	9.98E-01	2.85E-04
Shcbp1_chr8	2	2	2	16	-0.1	1.1	2.9	7.2	**7.60E-01**	**5.00E-05**	1.00E+00	2.85E-04
Siah1b_chrX	1	2	2	5	0.2	1.1	1.2	2.3	**7.49E-01**	**5.00E-05**	1.00E+00	2.85E-04
Siglece_chr7	8	12	14	42	0.6	1.5	1.5	2.9	**3.43E-02**	**5.00E-05**	6.53E-01	2.85E-04
Sirpb1b_chr3	4	3	4	13	-0.4	1.3	1.6	3.1	**3.37E-01**	**5.00E-05**	9.98E-01	2.85E-04
Ska1_chr18	0	0	0	5	0.0	1.0	2.3	4.9	**6.77E-01**	**5.00E-05**	1.00E+00	2.85E-04
Ska3_chr14	1	1	1	7	0.0	1.0	2.5	5.7	**4.30E-01**	**5.00E-05**	1.00E+00	2.85E-04
Slc16a10_chr10	4	5	8	43	0.2	1.1	2.5	5.6	**5.69E-01**	**5.00E-05**	1.00E+00	2.85E-04
Slc16a3_chr11	2	2	2	6	0.4	1.3	1.2	2.2	**4.88E-01**	**3.53E-03**	1.00E+00	1.15E-02
Slc22a23_chr13	2	2	4	13	0.1	1.1	1.9	3.7	**7.36E-01**	**5.00E-05**	1.00E+00	2.85E-04
Slc22a4_chr11	1	0	1	11	0.0	1.0	3.4	10.6	**2.69E-01**	**5.00E-05**	9.94E-01	2.85E-04
Slc25a21_chr12	1	0	1	9	0.0	1.0	3.2	9.2	**7.97E-01**	**5.00E-05**	1.00E+00	2.85E-04
Slc25a37_chr14	37	48	55	319	0.4	1.3	2.5	5.8	**9.45E-02**	**5.00E-05**	9.27E-01	2.85E-04
Slc25a38_chr9	8	9	12	41	0.2	1.2	1.7	3.3	**3.93E-01**	**5.00E-05**	1.00E+00	2.85E-04
Slc25a39_chr11	15	27	30	63	0.8	1.7	1.1	2.1	**5.22E-04**	**5.00E-05**	8.17E-02	2.85E-04
Slc2a4_chr11	0	0	0	5	0.0	1.0	2.4	5.3	**8.95E-01**	**5.00E-05**	1.00E+00	2.85E-04
Slc38a5_chrX	0	1	1	20	0.0	1.0	4.1	17.2	**1.24E-01**	**5.00E-05**	8.74E-01	2.85E-04
Slc43a3_chr2	6	10	11	74	0.7	1.6	2.7	6.5	**9.16E-03**	**5.00E-05**	4.45E-01	2.85E-04
Slc4a1_chr11	8	14	27	806	0.8	1.8	4.9	29.3	**1.35E-03**	**5.00E-05**	1.09E-01	2.85E-04
Slc6a20a_chr9	1	1	2	6	0.0	1.0	1.7	3.2	**9.54E-01**	**5.00E-05**	1.00E+00	2.85E-04
Slc6a9_chr4	1	1	2	32	0.2	1.1	4.4	20.6	**1.40E-01**	**5.00E-05**	9.64E-01	2.85E-04
Slc7a5_chr8	6	8	15	61	0.5	1.4	2.0	4.0	**6.68E-02**	**5.00E-05**	8.76E-01	2.85E-04
Slco4c1_chr1	0	0	0	2	0.0	1.0	0.9	1.9	**8.78E-01**	**5.00E-05**	1.00E+00	2.85E-04
Slfn14_chr11	0	1	1	33	0.0	1.0	5.0	32.5	**9.51E-02**	**5.00E-05**	9.28E-01	2.85E-04
Slfn4_chr11	1	2	2	47	0.5	1.4	5.0	31.5	**1.93E-01**	**5.00E-05**	9.87E-01	2.85E-04
Slpi_chr2	23	47	19	107	1.0	2.1	2.5	5.8	**1.41E-05**	**5.00E-05**	3.69E-03	2.85E-04
Smc2_chr4	8	8	14	68	0.0	1.0	2.3	5.0	**8.54E-01**	**5.00E-05**	1.00E+00	2.85E-04
Smim3_chr18	3	5	5	8	0.5	1.4	0.6	1.5	**1.42E-01**	**1.00E-04**	9.65E-01	5.44E-04
Snhg4_chr18	4	4	3	5	-0.1	1.1	0.7	1.6	**7.38E-01**	**4.00E-04**	1.00E+00	1.89E-03
Soat2_chr15	1	1	1	4	0.0	1.0	2.1	4.2	**9.40E-01**	**5.00E-05**	1.00E+00	2.85E-04

Socs3_chr11	6	6	11	23	0.1	1.1	1.1	2.2	**6.24E-01**	**5.00E-05**	1.00E+00	2.85E-04
Sort1_chr3	6	7	14	22	0.1	1.1	0.7	1.6	**5.31E-01**	**5.00E-05**	1.00E+00	2.85E-04
Sowaha_chr11	0	0	0	17	0.0	1.0	4.1	16.9	**2.76E-01**	**5.00E-05**	1.00E+00	2.85E-04
Sox6_chr7	0	0	0	12	0.0	1.0	3.6	11.9	**8.17E-01**	**1.91E-02**	1.00E+00	4.83E-02
Spag5_chr11	2	2	3	27	0.4	1.3	3.2	9.3	**2.32E-01**	**5.00E-05**	9.91E-01	2.85E-04
Spc24_chr9	2	2	3	11	0.0	1.0	2.0	4.0	**9.54E-01**	**5.00E-05**	1.00E+00	2.85E-04
Spc25_chr2	3	3	2	23	0.1	1.1	3.1	8.5	**8.06E-01**	**5.00E-05**	1.00E+00	2.93E-04
Spdl1_chr11	2	2	3	10	0.2	1.1	1.8	3.5	**6.08E-01**	**5.00E-05**	1.00E+00	2.85E-04
Specc1_chr11	3	5	11	49	0.6	1.6	2.2	4.5	**7.81E-03**	**5.00E-05**	4.27E-01	2.85E-04
Spire1_chr18	2	2	4	19	0.1	1.1	2.2	4.6	**8.10E-01**	**5.00E-05**	1.00E+00	2.90E-04
Spon1_chr7	1	1	2	5	0.3	1.3	1.1	2.1	**2.12E-01**	**5.00E-05**	9.88E-01	2.85E-04
Spta1_chr1	2	2	7	76	0.0	1.0	3.5	11.3	**9.08E-01**	**5.00E-05**	1.00E+00	2.85E-04
Sptb_chr12	1	2	5	97	0.4	1.3	4.3	20.0	**1.41E-01**	**5.00E-05**	8.93E-01	2.85E-04
Ssx2ip_chr3	1	2	2	9	0.2	1.1	2.3	5.0	**8.04E-01**	**5.00E-05**	1.00E+00	2.92E-04
St7_chr6	2	2	3	8	-0.2	1.2	1.3	2.4	**6.21E-01**	**5.00E-05**	1.00E+00	2.85E-04
Stard10_chr7	8	11	13	29	0.4	1.3	1.2	2.3	**2.43E-01**	**5.00E-05**	9.92E-01	2.85E-04
Steap3_chr1	2	3	5	23	0.4	1.3	2.3	5.1	**2.61E-01**	**5.00E-05**	9.94E-01	2.85E-04
Steap4_chr5	1	1	2	4	0.0	1.0	1.2	2.3	**9.82E-01**	**5.00E-05**	1.00E+00	2.85E-04
Stfa2l1_chr16	1	1	0	5	0.0	1.0	2.4	5.1	**9.72E-01**	**3.50E-04**	1.00E+00	1.69E-03
Stil_chr4	1	1	1	10	0.0	1.0	3.2	9.1	**7.80E-01**	**5.00E-05**	1.00E+00	2.85E-04
Stmn1_chr4	17	24	23	97	0.5	1.4	2.1	4.3	**5.92E-02**	**5.00E-05**	7.61E-01	2.85E-04
Stom_chr2	16	19	25	86	0.2	1.2	1.8	3.4	**2.77E-01**	**5.00E-05**	9.94E-01	2.85E-04
Stx2_chr5	7	7	13	39	0.0	1.0	1.6	2.9	**9.78E-01**	**5.00E-05**	1.00E+00	2.85E-04
Svip_chr7	2	2	3	11	-0.2	1.1	2.1	4.4	**6.10E-01**	**5.00E-05**	1.00E+00	2.85E-04
Syngr1_chr15	0	0	0	2	0.0	1.0	1.2	2.3	**8.02E-01**	**3.88E-03**	1.00E+00	1.35E-02
Tacc3_chr5	5	6	8	34	0.2	1.2	2.1	4.3	**3.93E-01**	**5.00E-05**	1.00E+00	2.85E-04
Tal1_chr4	2	3	5	66	0.2	1.1	3.9	14.5	**5.46E-01**	**5.00E-05**	1.00E+00	2.85E-04
Tarm1_chr7	0	0	0	2	0.0	1.0	0.8	1.8	**7.27E-01**	**5.00E-05**	1.00E+00	2.85E-04
Tarsl2_chr7	2	2	4	10	-0.1	1.0	1.3	2.5	**8.49E-01**	**5.00E-05**	1.00E+00	2.85E-04
Tbc1d2_chr4	0	0	1	2	0.0	1.0	0.7	1.6	**8.80E-01**	**5.00E-05**	1.00E+00	2.85E-04
Tbc1d24_chr17	1	1	2	4	-0.3	1.2	0.9	1.9	**3.18E-01**	**1.83E-03**	9.96E-01	6.77E-03
Tceal8_chrX	3	3	3	5	-0.1	1.1	1.0	2.0	**7.70E-01**	**5.00E-05**	1.00E+00	2.85E-04
Tfdp1_chr8	17	18	29	75	0.1	1.1	1.4	2.6	**6.85E-01**	**5.00E-05**	1.00E+00	2.85E-04
Tfec_chr6	4	3	4	9	-0.4	1.3	1.1	2.2	**2.87E-01**	**5.00E-05**	9.95E-01	2.85E-04
Tfr2_chr5	1	1	1	11	0.0	1.0	2.9	7.5	**6.35E-01**	**5.00E-05**	1.00E+00	2.85E-04
Tfrc_chr16	13	14	18	325	0.1	1.1	4.2	18.5	**6.65E-01**	**5.00E-05**	1.00E+00	2.85E-04
Thbs1_chr2	6	10	14	32	0.8	1.7	1.2	2.2	**6.74E-04**	**5.00E-05**	6.64E-02	2.85E-04
Ticrr_chr7	1	1	1	7	0.0	1.0	2.5	5.5	**6.95E-01**	**5.00E-05**	1.00E+00	2.85E-04
Tigd3_chr19	0	1	1	2	0.0	1.0	1.2	2.4	**5.19E-01**	**5.00E-05**	1.00E+00	2.85E-04
Tigit_chr16	2	3	2	5	0.6	1.6	0.9	1.9	**1.94E-01**	**5.00E-05**	9.87E-01	2.85E-04
Tipin_chr9	9	10	9	29	0.2	1.1	1.7	3.2	**5.59E-01**	**5.00E-05**	1.00E+00	2.85E-04
Tk1_chr11	10	10	12	38	0.0	1.0	1.7	3.2	**9.14E-01**	**5.00E-05**	1.00E+00	2.85E-04
Tlcd1_chr11	1	1	1	8	0.0	1.0	2.7	6.7	**8.73E-01**	**5.00E-05**	1.00E+00	2.85E-04
Tlr13_chrX	6	5	10	21	-0.3	1.2	1.1	2.1	**2.23E-01**	**5.00E-05**	9.91E-01	2.85E-04
Tlr8_chrX	4	3	7	13	-0.5	1.4	1.0	2.0	**1.06E-01**	**5.00E-05**	8.51E-01	2.85E-04
Tmcc2_chr1	3	5	8	181	0.6	1.5	4.5	23.2	**3.45E-02**	**5.00E-05**	6.53E-01	2.85E-04
Tmem120b_chr5	1	1	2	9	0.0	1.0	2.2	4.4	**9.87E-01**	**5.00E-05**	1.00E+00	2.85E-04
Tmem14c_chr13	30	34	28	81	0.2	1.1	1.6	2.9	**4.29E-01**	**5.00E-05**	1.00E+00	2.85E-04
Tmem216_chr19	2	3	2	3	0.4	1.3	0.6	1.5	**4.32E-01**	**9.75E-03**	1.00E+00	3.06E-02
Tmem255a_chrX	1	1	2	3	0.6	1.5	1.0	2.0	**1.08E-01**	**5.00E-05**	9.38E-01	2.85E-04
Tmem40_chr6	1	2	1	4	0.6	1.6	1.6	3.1	**2.75E-01**	**5.00E-05**	9.87E-01	2.85E-04
Tmem56_chr3	0	0	0	11	0.0	1.0	3.5	11.1	**7.68E-01**	**5.00E-05**	1.00E+00	2.85E-04
Tnfaip2_chr12	8	9	16	57	0.1	1.1	1.9	3.7	**5.43E-01**	**5.00E-05**	1.00E+00	2.85E-04
Tnfrsf14_chr4	17	18	39	91	0.1	1.1	1.2	2.3	**7.54E-01**	**5.00E-05**	1.00E+00	2.85E-04
Tnfrsf17_chr16	1	1	1	2	0.0	1.0	1.3	2.4	**5.36E-01**	**5.00E-05**	1.00E+00	2.85E-04
Tnfsf14_chr17	2	3	3	8	0.5	1.5	1.3	2.4	**1.61E-01**	**5.00E-05**	9.78E-01	2.85E-04
Tom1l1_chr11	1	1	2	13	0.1	1.1	3.1	8.3	**8.39E-01**	**5.00E-05**	1.00E+00	2.85E-04
Top2a_chr11	9	11	17	127	0.3	1.3	2.9	7.5	**1.23E-01**	**5.00E-05**	8.73E-01	2.85E-04
Traip_chr9	1	1	1	6	0.5	1.4	2.1	4.2	**2.04E-01**	**5.00E-05**	9.87E-01	2.85E-04
Trak2_chr1	20	20	39	121	0.0	1.0	1.6	3.1	**9.05E-01**	**5.00E-05**	1.00E+00	2.85E-04
Trem1_chr17	2	1	3	5	-0.4	1.3	0.8	1.8	**3.52E-01**	**5.00E-05**	9.98E-01	2.85E-04
Trem3_chr17	1	1	1	11	0.0	1.0	3.4	10.6	**8.86E-01**	**5.00E-05**	1.00E+00	2.85E-04
Treml1_chr17	2	4	2	7	1.2	2.3	1.6	3.1	**6.21E-03**	**5.00E-05**	3.73E-01	2.85E-04
Trim10_chr17	4	7	8	137	0.8	1.7	4.1	16.6	**9.53E-03**	**5.00E-05**	3.54E-01	2.85E-04
Trim58_chr11	0	0	1	19	0.0	1.0	4.3	19.4	**5.70E-01**	**5.00E-05**	1.00E+00	2.85E-04
Trip13_chr13	1	2	2	6	0.1	1.1	1.6	3.0	**7.35E-01**	**5.00E-05**	1.00E+00	2.85E-04
Troap_chr15	0	0	1	5	0.0	1.0	2.4	5.2	**7.88E-01**	**5.00E-05**	1.00E+00	2.85E-04
Tspan33_chr6	5	5	10	89	0.1	1.1	3.2	9.1	**7.20E-01**	**5.00E-05**	1.00E+00	2.85E-04
Tspo_chr15	22	27	20	42	0.3	1.2	1.1	2.2	**2.21E-01**	**5.00E-05**	9.90E-01	2.85E-04
Tspo2_chr17	0	1	0	28	0.3	1.3	4.8	27.9	**2.05E-03**	**5.00E-05**	1.98E-01	2.85E-04
Tst_chr15	2	3	3	5	0.6	1.6	0.9	1.9	**2.02E-01**	**1.00E-04**	9.87E-01	5.44E-04
Ttk_chr9	1	1	1	11	0.0	1.0	3.2	9.5	**9.45E-01**	**5.00E-05**	1.00E+00	2.85E-04
Tuba4a_chr1	23	34	37	96	0.6	1.5	1.4	2.6	**1.99E-02**	**5.00E-05**	6.31E-01	2.85E-04
Tuba8_chr6	1	1	1	3	0.1	1.1	1.8	3.4	**1.04E-01**	**5.00E-05**	9.38E-01	2.85E-04
Tubb1_chr2	8	11	18	38	0.6	1.5	1.1	2.1	**4.77E-02**	**5.00E-05**	7.23E-01	2.85E-04
Tubb4b_chr2	41	58	58	161	0.5	1.4	1.5	2.8	**1.59E-02**	**5.00E-05**	5.75E-01	2.85E-04
Tusc1_chr4	1	1	1	2	0.0	1.0	1.3	2.5	**9.96E-01**	**5.00E-05**	1.00E+00	2.85E-04
Txn1_chr4	57	55	34	80	0.0	1.0	1.3	2.4	**8.76E-01**	**5.00E-05**	1.00E+00	2.85E-04
Tyms_chr5	3	3	3	13	-0.1	1.1	1.9	3.8	**7.41E-01**	**5.00E-05**	1.00E+00	2.85E-04
Ubac1_chr2	5	6	8	47	0.4	1.3	2.6	6.1	**1.49E-01**	**5.00E-05**	9.69E-01	2.85E-04
Ube2c_chr2	6	9	8	65	0.6	1.5	3.0	8.1	**1.03E-01**	**5.00E-05**	9.38E-01	2.85E-04

Ube2l6_chr2	27	51	42	175	0.9	1.9	2.1	4.2	1.44E-05	5.00E-05	3.70E-03	2.85E-04
Ube2o_chr11	10	17	32	124	0.7	1.7	1.9	3.8	5.12E-04	5.00E-05	5.54E-02	2.85E-04
Ube2s_chr7	14	17	18	49	0.2	1.2	1.5	2.8	4.31E-01	5.00E-05	1.00E+00	2.85E-04
Ube2t_chr1	2	2	2	9	0.1	1.1	2.4	5.3	8.53E-01	5.00E-05	1.00E+00	2.85E-04
Ufsp1_chr5	1	1	1	4	0.3	1.3	2.0	3.9	5.84E-01	5.00E-05	1.00E+00	2.85E-04
Ugt1a7c_chr1	2	2	3	6	-0.1	1.0	1.1	2.2	8.70E-01	5.00E-05	1.00E+00	2.85E-04
Uhrf1bp1_chr17	2	2	4	8	0.1	1.0	1.0	1.9	8.55E-01	5.00E-05	1.00E+00	2.85E-04
Upp1_chr11	1	1	1	2	0.0	1.0	1.2	2.3	6.28E-01	5.00E-05	1.00E+00	2.85E-04
Urod_chr4	10	13	12	78	0.5	1.4	2.7	6.5	9.21E-02	5.00E-05	9.27E-01	2.85E-04
Uros_chr7	6	6	6	39	0.2	1.1	2.6	6.0	5.78E-01	5.00E-05	1.00E+00	2.85E-04
Usp46_chr5	4	4	8	21	0.0	1.0	1.5	2.8	8.91E-01	5.00E-05	1.00E+00	2.85E-04
Vcam1_chr3	169	149	245	391	-0.2	1.1	0.7	1.6	4.94E-01	2.10E-03	1.00E+00	8.18E-03
Vcan_chr13	0	0	1	3	0.0	1.0	1.7	3.3	6.13E-01	5.00E-05	1.00E+00	2.61E-04
Vmp1_chr11	14	13	15	33	-0.1	1.0	1.1	2.2	8.20E-01	5.00E-05	1.00E+00	2.85E-04
Vopp1_chr6	11	14	17	44	0.3	1.2	1.4	2.6	2.04E-01	5.00E-05	9.87E-01	2.85E-04
Wbscr27_chr5	1	1	2	4	-0.2	1.2	1.4	2.6	3.99E-01	5.00E-05	1.00E+00	2.85E-04
Wdhd1_chr14	4	5	6	27	0.3	1.2	2.1	4.2	2.42E-01	5.00E-05	9.92E-01	2.85E-04
Wdr34_chr2	1	1	2	4	0.0	1.0	1.0	2.0	9.58E-01	5.00E-05	1.00E+00	2.85E-04
Wdr62_chr7	1	1	3	7	0.0	1.0	1.4	2.7	9.91E-01	5.00E-05	1.00E+00	2.85E-04
Wfdc17_chr11	7	7	4	41	0.0	1.0	3.3	9.5	9.57E-01	5.00E-05	1.00E+00	2.85E-04
Wfdc21_chr11	2	2	1	26	0.3	1.3	4.7	26.1	6.13E-01	5.00E-05	1.00E+00	2.85E-04
Wipi1_chr11	3	3	5	15	0.1	1.1	1.5	2.8	8.00E-01	5.00E-05	1.00E+00	2.85E-04
Xbp1_chr11	48	60	75	169	0.3	1.2	1.2	2.2	1.26E-01	5.00E-05	9.51E-01	2.85E-04
Xdh_chr17	9	8	20	39	-0.2	1.1	1.0	2.0	4.56E-01	5.00E-05	1.00E+00	2.85E-04
Xk_chrX	2	3	4	14	0.3	1.3	1.8	3.4	2.71E-01	5.00E-05	9.94E-01	2.85E-04
Xkr5_chr8	0	0	0	2	0.0	1.0	0.8	1.7	5.75E-01	5.00E-05	1.00E+00	2.61E-04
Xpo7_chr14	5	6	9	53	0.2	1.2	2.5	5.6	3.19E-01	5.00E-05	9.97E-01	2.85E-04
Ybx3_chr6	11	15	24	68	0.4	1.4	1.5	2.8	2.45E-01	5.00E-05	8.88E-01	3.08E-04
Ypel4_chr2	0	0	0	33	0.0	1.0	5.1	33.3	3.03E-01	5.00E-05	1.00E+00	2.85E-04
Zbtbd6_chr14	0	0	0	2	0.0	1.0	1.1	2.2	6.51E-01	5.00E-05	1.00E+00	2.85E-04
Zfand4_chr6	1	1	1	4	0.0	1.0	1.3	2.4	5.56E-01	5.00E-05	1.00E+00	2.85E-04
Zfpm1_chr8	5	6	14	67	0.3	1.2	2.2	4.7	2.55E-01	5.00E-05	9.92E-01	2.85E-04
Zwilch_chr9	2	2	3	12	-0.1	1.0	2.1	4.2	8.75E-01	5.00E-05	1.00E+00	2.85E-04
0610009B22Rik_chr11	5	5	4	7	0.1	1.1	0.9	1.8	8.47E-01	5.00E-05	1.00E+00	2.85E-04
1110004E09Rik_chr16	3	5	4	6	0.4	1.4	0.6	1.5	2.59E-01	1.25E-03	9.93E-01	5.20E-03
1110008F13Rik_chr2	6	7	6	9	0.3	1.3	0.6	1.6	4.44E-01	3.04E-02	1.00E+00	7.90E-02
1110059G10Rik_chr9	3	3	2	4	0.1	1.1	0.7	1.6	7.44E-01	3.00E-04	1.00E+00	1.47E-03
1500011K16Rik_chr2	8	8	5	8	0.0	1.0	0.6	1.5	9.83E-01	1.15E-03	1.00E+00	4.79E-03
1600002H07Rik_chr17	2	3	3	6	0.1	1.1	0.9	1.9	7.19E-01	5.00E-05	1.00E+00	2.85E-04
1600010M07Rik_chr7	5	6	3	7	0.1	1.0	1.1	2.1	8.89E-01	5.00E-05	1.00E+00	2.82E-04
1700052K11Rik_chr11	1	2	2	2	0.4	1.3	0.7	1.6	3.41E-01	4.00E-04	9.97E-01	1.89E-03
1810022K09Rik_chr3	39	33	16	32	-0.2	1.2	1.0	1.9	4.65E-01	5.00E-05	1.00E+00	2.85E-04
1810032O08Rik_chr11	4	7	4	9	0.7	1.6	1.1	2.1	1.74E-01	2.00E-03	9.20E-01	7.31E-03
1810037I17Rik_chr3	17	24	13	36	0.5	1.4	1.5	2.8	3.90E-02	5.00E-05	7.91E-01	2.85E-04
1810058I24Rik_chr6	18	25	17	27	0.5	1.4	0.7	1.6	5.47E-02	5.00E-05	8.47E-01	2.82E-04
2010107E04Rik_chr12	61	62	34	57	0.0	1.0	0.8	1.7	9.96E-01	5.00E-05	1.00E+00	2.85E-04
2210408F21Rik_chr6	1	1	1	2	0.0	1.0	0.8	1.7	9.44E-01	6.35E-03	1.00E+00	1.97E-02
2410127L17Rik_chr19	8	8	10	21	0.1	1.1	1.1	2.1	7.19E-01	5.00E-05	1.00E+00	2.85E-04
2500004C02Rik_chr2	2	1	1	2	-0.3	1.2	0.7	1.7	5.41E-01	5.00E-04	1.00E+00	2.30E-03
2610301B20Rik_chr4	4	4	5	8	0.0	1.0	0.6	1.6	8.85E-01	1.00E-04	1.00E+00	5.44E-04
2610318N02Rik_chr16	1	1	1	2	0.0	1.0	0.9	1.9	8.69E-01	5.00E-05	1.00E+00	2.85E-04
2700029M09Rik_chr8	12	15	14	25	0.3	1.2	0.9	1.9	2.42E-01	5.00E-05	9.92E-01	2.85E-04
2700097O09Rik_chr12	2	2	1	3	-0.1	1.1	1.1	2.1	8.69E-01	3.15E-02	1.00E+00	6.43E-02
2700099C18Rik_chr17	1	2	2	4	0.2	1.2	1.4	2.7	7.04E-01	5.00E-05	1.00E+00	2.82E-04
2810408I11Rik_chr1	1	1	0	3	0.0	1.0	1.3	2.5	9.95E-01	5.00E-05	1.00E+00	2.82E-04
2900076A07Rik_chr7	2	1	1	2	-0.2	1.2	0.6	1.5	7.05E-01	7.30E-03	1.00E+00	2.37E-02
3110002H16Rik_chr18	13	15	19	30	0.2	1.2	0.6	1.6	5.50E-01	1.67E-02	1.00E+00	4.80E-02
4930427A07Rik_chr12	3	5	6	13	0.7	1.6	1.1	2.2	1.78E-02	5.00E-05	6.00E-01	2.85E-04
4930430F08Rik_chr10	3	3	4	22	0.0	1.0	2.4	5.4	9.44E-01	5.00E-05	1.00E+00	2.85E-04
5830415F09Rik_chr4	4	5	6	13	0.2	1.2	1.0	2.0	5.12E-01	5.00E-05	1.00E+00	2.85E-04
6430706D22Rik_chr1	4	12	7	49	1.5	2.7	2.8	7.0	2.75E-05	5.00E-05	6.38E-03	2.82E-04
6720489N17Rik_chr13	2	2	2	6	-0.3	1.3	1.2	2.3	3.87E-01	5.00E-05	1.00E+00	2.85E-04
8430419L09Rik_chr6	6	10	13	27	0.7	1.6	1.0	2.0	3.91E-03	5.00E-05	3.11E-01	2.85E-04
9030025P20Rik_chr17	1	1	1	2	0.0	1.0	0.7	1.6	9.33E-01	4.90E-03	1.00E+00	1.71E-02
9230114K14Rik_chr5	1	0	1	2	0.0	1.0	1.0	2.1	8.15E-01	5.00E-05	1.00E+00	2.82E-04
9330159M07Rik_chr9	0	0	0	2	0.0	1.0	0.8	1.7	6.99E-01	2.82E-03	1.00E+00	1.05E-02
9330175E14Rik_chr8	3	3	5	8	0.0	1.0	0.6	1.6	9.78E-01	1.00E-04	1.00E+00	5.40E-04
9430037G07Rik_chr9	0	0	0	2	0.0	1.0	1.3	2.5	3.40E-01	5.00E-05	1.00E+00	2.82E-04
A130077B15Rik_chr10	6	4	7	11	-0.3	1.3	0.7	1.6	2.43E-01	5.00E-05	9.89E-01	2.82E-04
A430005L14Rik_chr4	7	8	8	15	0.3	1.2	0.9	1.8	4.61E-01	5.00E-05	1.00E+00	2.85E-04
A430033K04Rik_chr5	2	2	3	4	0.4	1.4	0.8	1.7	2.17E-01	5.00E-05	9.89E-01	2.85E-04
A630019I02Rik_chr13	1	2	1	2	0.6	1.5	0.9	1.9	3.31E-02	3.70E-03	7.51E-01	1.33E-02
A630089N07Rik_chr16	2	2	3	6	-0.2	1.1	0.8	1.8	6.79E-01	5.00E-05	1.00E+00	2.82E-04
A730008H23Rik_chr1	4	7	11	40	0.6	1.5	1.8	3.6	2.49E-01	5.00E-05	9.92E-01	2.85E-04
A730036I17Rik_chr2	0	0	0	3	0.0	1.0	1.7	3.2	8.26E-01	5.00E-05	1.00E+00	2.82E-04
AA986860_chr1	0	0	1	2	0.0	1.0	0.7	1.6	7.52E-01	5.00E-05	1.00E+00	2.85E-04
Abca13_chr11	0	0	0	2	0.0	1.0	1.2	2.3	3.91E-01	5.00E-05	1.00E+00	2.85E-04
Abcb9_chr5	1	1	2	4	0.2	1.2	0.9	1.8	5.56E-01	5.00E-05	1.00E+00	2.85E-04
Abcc3_chr11	7	16	15	34	1.2	2.3	1.1	2.2	3.64E-08	5.00E-05	1.36E-05	2.85E-04
Abhd4_chr14	7	9	8	11	0.3	1.3	0.6	1.5	1.90E-01	4.17E-02	9.87E-01	1.04E-01
Abi3_chr11	9	13	0	5	0.5	1.4	2.4	5.2	7.67E-02	2.46E-02	8.98E-01	6.89E-02

Abracl_chr10	44	44	35	57	0.0	1.0	0.7	1.6	**9.87E-01**	**5.00E-05**	1.00E+00	2.85E-04
Acadl_chr1	16	25	23	35	0.6	1.6	0.6	1.5	**4.78E-03**	**5.00E-05**	3.40E-01	2.85E-04
Acer3_chr7	9	7	11	21	-0.2	1.2	1.0	1.9	**3.50E-01**	**5.00E-05**	9.98E-01	2.85E-04
Acyp1_chr12	9	9	5	8	0.0	1.0	0.6	1.6	**8.99E-01**	**1.90E-03**	1.00E+00	7.48E-03
Adam10_chr9	32	34	57	85	0.1	1.1	0.6	1.5	**6.76E-01**	**4.50E-04**	1.00E+00	2.12E-03
Adam8_chr7	7	8	14	21	0.1	1.1	0.6	1.5	**6.05E-01**	**1.00E-04**	1.00E+00	5.44E-04
Adamts5_chr16	2	2	4	5	0.1	1.1	0.6	1.5	**7.94E-01**	**5.00E-05**	1.00E+00	2.85E-04
Adcy4_chr14	1	2	3	5	1.0	2.0	0.8	1.8	**9.70E-03**	**5.00E-05**	4.58E-01	2.85E-04
Adcy6_chr15	7	6	15	26	-0.1	1.1	0.9	1.8	**5.15E-01**	**5.00E-05**	1.00E+00	2.85E-04
Add1_chr5	25	32	5	50	0.3	1.2	3.3	9.7	**5.04E-01**	**5.00E-05**	9.69E-01	3.08E-04
Adipor1_chr1	38	51	82	161	0.4	1.3	1.0	2.0	**5.16E-02**	**5.00E-05**	8.48E-01	2.85E-04
Adrb2_chr18	12	15	18	28	0.3	1.3	0.7	1.6	**1.64E-01**	**5.00E-05**	9.80E-01	2.85E-04
AF251705_chr11	12	13	10	20	0.1	1.1	1.0	2.0	**6.12E-01**	**5.00E-05**	1.00E+00	2.85E-04
Afmid_chr11	6	7	9	13	0.1	1.1	0.6	1.5	**6.59E-01**	**1.64E-02**	1.00E+00	4.73E-02
Agap1_chr1	2	2	5	10	0.1	1.1	0.9	1.8	**6.23E-01**	**5.00E-05**	1.00E+00	2.85E-04
Agfg2_chr5	3	4	6	15	0.3	1.2	1.2	2.4	**5.28E-01**	**1.36E-04**	1.00E+00	7.21E-04
Agpat4_chr17	4	5	6	11	0.2	1.2	0.9	1.8	**4.81E-01**	**5.00E-05**	1.00E+00	2.85E-04
Agtr1a_chr13	8	8	13	21	-0.1	1.1	0.6	1.5	**6.87E-01**	**5.00E-05**	1.00E+00	2.85E-04
Ahi1_chr10	1	1	2	4	0.2	1.1	0.9	1.9	**6.60E-01**	**5.00E-05**	1.00E+00	2.85E-04
AI662270_chr11	55	65	43	101	0.2	1.2	1.2	2.3	**2.64E-01**	**5.00E-05**	9.91E-01	2.82E-04
Aimp1_chr3	25	24	27	43	-0.1	1.0	0.7	1.6	**7.69E-01**	**5.00E-05**	1.00E+00	2.85E-04
Akap7_chr10	2	3	3	7	0.5	1.4	1.0	2.0	**1.16E-01**	**5.00E-05**	9.45E-01	2.85E-04
Akip1_chr7	4	5	4	6	0.4	1.3	0.8	1.8	**3.39E-01**	**5.00E-05**	9.98E-01	2.85E-04
Aldh18a1_chr19	4	6	10	15	0.4	1.3	0.6	1.5	**3.66E-01**	**3.78E-02**	9.02E-01	8.12E-02
Aldh1a7_chr19	2	1	2	4	-0.1	1.1	1.2	2.3	**7.94E-01**	**5.00E-05**	1.00E+00	2.85E-04
Aldh3b1_chr19	8	8	11	18	0.1	1.1	0.6	1.5	**7.72E-01**	**1.00E-04**	1.00E+00	5.44E-04
Alg6_chr4	3	3	3	5	0.0	1.0	0.6	1.5	**9.70E-01**	**1.00E-04**	1.00E+00	5.44E-04
Alms1_chr6	1	1	2	5	-0.2	1.2	1.0	2.1	**4.93E-01**	**5.00E-05**	1.00E+00	2.85E-04
Alox12_chr11	3	6	7	11	0.8	1.8	0.7	1.7	**4.75E-03**	**5.00E-05**	3.40E-01	2.85E-04
Als2cr12_chr1	1	1	1	2	0.0	1.0	0.8	1.7	**7.95E-01**	**5.00E-05**	1.00E+00	2.85E-04
Alyref_chr11	17	20	24	46	0.3	1.2	0.9	1.9	**2.66E-01**	**5.00E-05**	9.94E-01	2.85E-04
Amigo3_chr9	3	2	6	16	-0.6	1.5	1.3	2.5	**4.36E-01**	**3.67E-02**	1.00E+00	9.25E-02
Ammecr1_chrX	3	3	7	20	0.0	1.0	1.6	3.0	**9.07E-01**	**5.00E-05**	1.00E+00	2.85E-04
Amy2a5_chr3	0	0	0	79	0.0	1.0	6.3	79.1	**7.90E-01**	**5.00E-05**	1.00E+00	2.85E-04
Ang_chr14	6	10	7	10	0.7	1.6	0.6	1.5	**3.33E-02**	**8.50E-04**	7.65E-01	3.58E-03
Ank_chr15	7	8	15	31	0.3	1.2	1.1	2.1	**2.79E-01**	**5.00E-05**	9.94E-01	2.85E-04
Ank1_chr8	1	1	1	40	0.3	1.2	4.2	18.2	**2.26E-02**	**4.08E-03**	5.47E-01	1.34E-02
Ankrd2_chr19	1	1	1	2	-0.1	1.0	0.7	1.7	**9.11E-01**	**5.10E-03**	1.00E+00	1.77E-02
Anln_chr9	1	1	2	20	-0.1	1.0	3.3	9.6	**9.49E-01**	**5.00E-05**	1.00E+00	2.85E-04
Anp32b_chr4	69	102	85	177	0.6	1.5	1.1	2.1	**7.01E-03**	**5.00E-05**	3.94E-01	2.85E-04
Anxa3_chr5	5	5	7	13	-0.1	1.1	0.9	1.8	**6.71E-01**	**5.00E-05**	1.00E+00	2.85E-04
Aoc2_chr11	3	3	5	11	-0.1	1.1	1.1	2.1	**7.29E-01**	**5.00E-05**	1.00E+00	2.85E-04
Ap1s1_chr5	12	14	15	24	0.2	1.1	0.7	1.7	**5.60E-01**	**5.00E-05**	1.00E+00	2.85E-04
Ap1s2_chrX	7	6	9	14	-0.2	1.1	0.6	1.5	**4.31E-01**	**1.00E-04**	1.00E+00	5.44E-04
Ap2a2_chr7	11	13	24	40	0.2	1.2	0.7	1.6	**2.94E-01**	**5.00E-05**	9.96E-01	2.85E-04
Apeh_chr9	20	26	38	61	0.4	1.3	0.7	1.6	**7.71E-02**	**5.00E-05**	9.03E-01	2.85E-04
Apip_chr2	8	7	7	12	-0.2	1.2	0.9	1.8	**5.27E-01**	**5.00E-05**	1.00E+00	2.85E-04
Apitd1_chr4	2	6	2	7	1.8	3.4	2.0	3.9	**1.20E-04**	**5.00E-05**	2.47E-02	2.85E-04
Aplf_chr6	2	2	2	5	0.3	1.2	1.1	2.1	**5.45E-01**	**1.50E-04**	1.00E+00	7.99E-04
Apobec1_chr6	1	6	1	9	2.5	5.8	2.8	7.1	**4.46E-03**	**5.00E-05**	3.77E-01	3.24E-04
Apobr_chr7	9	10	13	21	0.1	1.1	0.7	1.6	**6.00E-01**	**5.00E-05**	1.00E+00	2.85E-04
Apol10b_chr15	1	2	2	9	0.8	1.7	2.5	5.5	**6.61E-02**	**5.00E-05**	8.76E-01	2.85E-04
Apol7c_chr15	0	17	0	10	4.1	16.8	3.3	9.5	**1.00E-20**	**5.00E-05**	1.00E-20	2.85E-04
Apol7e_chr15	0	2	0	10	1.3	2.4	3.4	10.3	**1.28E-08**	**5.00E-05**	9.63E-06	2.85E-04
Apoo_chrX	2	2	1	3	0.3	1.2	1.3	2.5	**6.89E-01**	**3.50E-04**	1.00E+00	1.69E-03
Arap3_chr18	3	3	6	9	0.3	1.2	0.8	1.8	**4.04E-01**	**3.24E-03**	9.90E-01	1.16E-02
Arf5_chr6	20	29	33	71	0.5	1.5	1.1	2.2	**3.18E-02**	**5.00E-05**	7.58E-01	2.85E-04
Arg2_chr12	0	0	0	3	0.0	1.0	1.3	2.5	**8.97E-01**	**1.38E-02**	1.00E+00	4.10E-02
Arhgap11a_chr2	7	8	12	27	0.2	1.1	1.2	2.3	**4.45E-01**	**5.00E-05**	1.00E+00	2.85E-04
Arhgap19_chr19	7	9	12	39	0.3	1.2	1.7	3.3	**2.25E-01**	**5.00E-05**	9.87E-01	2.85E-04
Arhgap23_chr11	6	6	16	29	0.0	1.0	0.9	1.8	**9.73E-01**	**5.00E-05**	1.00E+00	2.85E-04
Arhgap33_chr7	2	2	4	11	0.1	1.0	1.3	2.5	**8.71E-01**	**5.00E-05**	1.00E+00	2.85E-04
Arhgef12_chr9	8	8	17	29	0.1	1.1	0.7	1.7	**7.35E-01**	**5.00E-05**	1.00E+00	2.85E-04
Arl4a_chr12	4	4	4	13	0.0	1.0	1.6	2.9	**8.77E-01**	**5.00E-05**	1.00E+00	2.85E-04
Arl5a_chr2	15	23	27	41	0.6	1.5	0.6	1.6	**2.61E-03**	**2.50E-04**	2.36E-01	1.25E-03
Arl6ip6_chr2	9	10	11	20	0.1	1.1	0.8	1.8	**6.32E-01**	**5.00E-05**	1.00E+00	2.85E-04
Arrb1_chr7	13	14	29	62	0.0	1.0	1.1	2.2	**9.40E-01**	**1.87E-03**	1.00E+00	6.95E-03
Asap3_chr4	1	1	1	2	0.1	1.1	0.9	1.8	**1.87E-02**	**5.00E-05**	6.08E-01	2.85E-04
Asb1_chr1	5	5	6	19	0.0	1.0	1.7	3.3	**8.52E-01**	**5.13E-03**	1.00E+00	1.62E-02
Aspa_chr11	1	1	1	2	-0.1	1.0	0.7	1.7	**1.88E-01**	**1.65E-03**	9.86E-01	6.61E-03
Atad2_chr15	10	10	16	41	0.1	1.1	1.3	2.5	**6.70E-01**	**5.00E-05**	1.00E+00	2.85E-04
Atat1_chr17	2	3	3	5	0.2	1.1	0.7	1.7	**7.17E-01**	**9.78E-03**	1.00E+00	2.85E-02
Atg4a_chr3	8	9	10	31	0.1	1.1	1.6	3.0	**5.78E-01**	**5.00E-05**	1.00E+00	2.85E-04
Atg4d_chr9	5	6	9	20	0.2	1.2	1.1	2.1	**6.46E-01**	**4.00E-04**	1.00E+00	1.91E-03
Atg9a_chr1	6	7	14	24	0.2	1.2	0.8	1.8	**3.05E-01**	**5.00E-05**	9.96E-01	2.85E-04
Atp1a3_chr7	2	3	7	12	0.3	1.2	0.8	1.8	**4.18E-01**	**5.00E-05**	1.00E+00	2.85E-04
Atp1b2_chr11	3	4	5	13	0.7	1.7	1.4	2.6	**2.01E-02**	**5.00E-05**	6.33E-01	2.85E-04
Atp5f1_chr3	58	62	57	96	0.1	1.1	0.7	1.7	**7.52E-01**	**3.00E-04**	1.00E+00	1.47E-03
Atp5g1_chr11	13	16	2	7	0.3	1.2	1.5	2.9	**4.63E-01**	**6.00E-04**	1.00E+00	2.86E-03
Atp5g3_chr2	58	76	49	74	0.4	1.3	0.6	1.5	**7.19E-02**	**5.00E-05**	8.92E-01	2.85E-04
Atp5j_chr16	40	43	31	60	0.1	1.1	1.0	1.9	**8.01E-01**	**6.80E-03**	1.00E+00	2.25E-02

Atp5j2_chr5	54	54	31	64	0.0	1.0	1.1	2.1	**9.82E-01**	**5.00E-05**	1.00E+00	2.85E-04
Atp5k_chr5	56	58	30	56	0.1	1.0	0.9	1.8	**8.30E-01**	**5.00E-05**	1.00E+00	2.85E-04
Atp5l_chr9	90	84	50	97	-0.1	1.1	1.0	1.9	**6.40E-01**	**5.00E-05**	1.00E+00	2.85E-04
Atp6v0a1_chr11	7	10	15	25	0.4	1.4	0.8	1.7	**1.71E-01**	**2.00E-03**	9.42E-01	7.93E-03
Atp6v0e_chr17	54	58	52	81	0.1	1.1	0.6	1.6	**6.10E-01**	**5.00E-05**	1.00E+00	2.85E-04
AU021092_chr16	3	6	4	14	1.0	2.1	1.7	3.2	**4.96E-03**	**5.00E-05**	2.56E-01	2.85E-04
AW112010_chr19	46	57	28	99	0.3	1.2	1.8	3.6	**1.98E-01**	**5.00E-05**	9.87E-01	2.85E-04
Azin1_chr15	17	19	6	22	0.2	1.1	1.8	3.4	**5.04E-01**	**5.00E-05**	1.00E+00	3.24E-04
B2m_chr2	1,043	1,243	743	1,258	0.3	1.2	0.8	1.7	**4.45E-01**	**5.00E-05**	1.00E+00	2.85E-04
B3gnt3_chr8	0	1	0	4	0.0	1.0	1.9	3.7	**1.46E-04**	**5.00E-05**	2.93E-02	2.85E-04
B4galt3_chr1	7	11	11	17	0.6	1.5	0.6	1.5	**2.41E-02**	**2.00E-04**	6.72E-01	1.02E-03
Baiap3_chr17	1	1	2	4	0.3	1.2	0.9	1.9	**5.14E-01**	**5.00E-05**	1.00E+00	2.85E-04
Batf2_chr19	1	1	1	3	0.0	1.0	1.2	2.3	**4.86E-01**	**5.00E-05**	1.00E+00	2.85E-04
Batf3_chr1	2	4	3	4	0.6	1.5	0.6	1.5	**2.37E-01**	**6.55E-03**	9.92E-01	2.19E-02
Bbc3_chr7	2	2	3	6	-0.1	1.1	0.8	1.8	**8.21E-01**	**5.00E-05**	1.00E+00	2.85E-04
BC018473_chr11	0	26	0	69	4.7	26.3	6.1	68.6	**2.22E-16**	**5.00E-05**	3.64E-13	2.82E-04
BC021614_chr19	1	2	2	3	0.3	1.2	0.7	1.6	**6.85E-01**	**9.70E-03**	1.00E+00	3.05E-02
BC030307_chr10	0	1	1	2	0.0	1.0	0.7	1.7	**8.95E-01**	**1.00E-04**	1.00E+00	4.76E-04
BC055324_chr1	2	2	3	6	0.2	1.2	0.9	1.9	**7.37E-01**	**3.29E-02**	1.00E+00	8.45E-02
BC147527_chr13	8	8	10	16	0.1	1.1	0.6	1.5	**7.50E-01**	**5.00E-05**	1.00E+00	2.85E-04
Bcap29_chr12	16	17	13	19	0.0	1.0	0.6	1.5	**8.46E-01**	**1.57E-02**	1.00E+00	4.03E-02
Bcl2a1d_chr9	7	7	6	15	0.1	1.1	1.4	2.7	**7.46E-01**	**5.00E-05**	1.00E+00	2.85E-04
Bcorl1_chrX	1	2	3	6	0.5	1.5	0.9	1.9	**9.72E-02**	**5.00E-05**	9.33E-01	2.85E-04
Bend4_chr5	1	1	1	3	0.0	1.0	1.2	2.3	**3.98E-01**	**5.00E-05**	1.00E+00	2.85E-04
Bet1_chr6	11	12	10	16	0.1	1.1	0.6	1.5	**6.92E-01**	**1.50E-04**	1.00E+00	7.89E-04
Bex6_chr16	3	4	4	9	0.3	1.2	1.1	2.1	**4.76E-01**	**5.00E-05**	1.00E+00	2.85E-04
Blvra_chr2	12	13	12	21	0.1	1.1	0.7	1.7	**6.36E-01**	**5.00E-05**	1.00E+00	2.85E-04
Bnip3l_chr14	57	59	97	213	0.0	1.0	1.1	2.2	**8.25E-01**	**5.00E-05**	1.00E+00	2.85E-04
Bola3_chr6	9	10	8	23	0.2	1.1	1.5	2.8	**6.29E-01**	**5.00E-05**	1.00E+00	2.85E-04
Brpf3_chr17	7	7	15	36	0.1	1.1	1.3	2.4	**6.62E-01**	**5.00E-05**	1.00E+00	2.85E-04
Bsdc1_chr4	15	20	31	77	0.4	1.3	1.3	2.4	**9.86E-02**	**5.00E-05**	9.35E-01	2.85E-04
Bsn_chr9	0	1	1	2	0.0	1.0	1.2	2.3	**9.84E-03**	**5.00E-05**	4.59E-01	2.85E-04
Bst2_chr8	28	36	24	38	0.4	1.3	0.7	1.6	**1.45E-01**	**5.00E-05**	9.68E-01	2.85E-04
Btnl4_chr17	1	1	1	5	0.0	1.0	2.0	4.0	**8.39E-01**	**5.00E-05**	1.00E+00	2.85E-04
Btnl6_chr17	1	1	2	8	0.1	1.1	2.3	4.9	**8.02E-01**	**5.00E-05**	1.00E+00	2.85E-04
Bzrap1_chr11	1	2	2	5	0.7	1.7	1.3	2.5	**1.82E-02**	**5.00E-05**	6.01E-01	2.85E-04
C130050O18Rik_chr5	1	1	2	5	0.3	1.2	1.4	2.6	**7.66E-01**	**2.64E-02**	1.00E+00	7.05E-02
C130083M11Rik_chr5	0	0	1	2	0.0	1.0	0.7	1.6	**9.71E-01**	**5.00E-05**	1.00E+00	2.82E-04
C1d_chr11	10	9	8	15	-0.1	1.1	1.0	2.0	**5.75E-01**	**5.00E-05**	1.00E+00	2.85E-04
C1galt1c1_chrX	9	9	8	17	-0.1	1.0	1.1	2.1	**8.47E-01**	**5.00E-05**	1.00E+00	2.85E-04
C330018D20Rik_chr18	5	5	5	9	0.0	1.0	0.9	1.8	**9.68E-01**	**5.00E-05**	1.00E+00	2.85E-04
Cacna1g_chr11	0	0	0	4	0.0	1.0	1.8	3.6	**3.75E-01**	**5.00E-05**	1.00E+00	2.61E-04
Cacybp_chr1	21	22	24	42	0.1	1.1	0.8	1.7	**6.69E-01**	**5.00E-05**	1.00E+00	2.85E-04
Cadm3_chr1	1	2	2	5	1.2	2.2	1.5	2.7	**1.23E-03**	**5.00E-05**	1.42E-01	2.85E-04
Calm2_chr17	128	138	130	209	0.1	1.1	0.7	1.6	**6.02E-01**	**5.00E-05**	1.00E+00	2.85E-04
Camk2b_chr11	1	2	1	2	0.8	1.8	0.7	1.6	**6.88E-02**	**1.63E-03**	8.23E-01	6.60E-03
Capn11_chr17	0	0	0	2	0.0	1.0	1.1	2.1	**9.81E-01**	**5.00E-05**	1.00E+00	2.85E-04
Capn5_chr7	2	3	5	11	0.2	1.1	1.1	2.1	**5.17E-01**	**5.00E-05**	1.00E+00	2.85E-04
Cars_chr7	6	7	7	14	0.1	1.1	1.0	2.0	**7.03E-01**	**4.52E-03**	1.00E+00	1.45E-02
Casp12_chr9	3	2	3	5	-0.2	1.1	0.7	1.6	**6.10E-01**	**5.00E-05**	1.00E+00	2.85E-04
Casp3_chr8	12	12	16	33	0.0	1.0	1.0	2.0	**9.52E-01**	**5.00E-05**	1.00E+00	2.85E-04
Cass4_chr2	1	1	2	4	0.2	1.1	0.9	1.9	**3.86E-01**	**5.00E-05**	1.00E+00	2.85E-04
Cat_chr2	30	43	48	73	0.5	1.4	0.6	1.5	**1.37E-02**	**5.00E-05**	5.30E-01	2.85E-04
Cbr4_chr8	4	4	3	5	0.0	1.0	0.6	1.5	**9.90E-01**	**1.10E-03**	1.00E+00	4.65E-03
Cbwd1_chr19	3	3	3	6	0.2	1.1	0.8	1.8	**6.99E-01**	**1.25E-04**	1.00E+00	6.83E-04
Cbx3_chr6	60	67	69	110	0.2	1.1	0.7	1.6	**3.97E-01**	**5.00E-05**	1.00E+00	2.85E-04
Ccdc23_chr4	9	12	7	15	0.3	1.2	1.0	2.0	**3.65E-01**	**5.00E-05**	1.00E+00	2.85E-04
Ccdc57_chr11	0	0	1	2	0.0	1.0	0.7	1.6	**8.98E-01**	**5.00E-05**	1.00E+00	2.85E-04
Ccdc62_chr5	1	1	1	2	0.0	1.0	0.7	1.6	**5.37E-01**	**5.00E-05**	1.00E+00	2.85E-04
Ccdc71l_chr12	10	11	15	26	0.1	1.1	0.8	1.7	**5.51E-01**	**5.00E-05**	1.00E+00	2.85E-04
Cchcr1_chr17	2	2	3	8	0.4	1.3	1.5	2.8	**3.09E-01**	**5.00E-05**	9.97E-01	2.85E-04
Ccnd3_chr17	3	10	14	64	1.6	3.0	2.2	4.7	**7.01E-03**	**5.00E-05**	4.19E-01	2.99E-04
Ccne2_chr4	1	0	1	11	0.0	1.0	3.2	9.4	**8.44E-01**	**1.52E-02**	1.00E+00	3.99E-02
Ccnyl1_chr1	3	4	5	9	0.2	1.2	1.0	2.0	**4.57E-01**	**5.00E-05**	1.00E+00	2.85E-04
Ccsap_chr8	1	2	3	4	0.1	1.1	0.6	1.5	**7.48E-01**	**5.50E-04**	1.00E+00	2.52E-03
Cd101_chr3	2	2	3	8	0.4	1.3	1.4	2.6	**3.23E-01**	**5.00E-05**	9.90E-01	2.85E-04
Cd1d2_chr3	1	1	1	6	0.1	1.1	2.5	5.7	**2.75E-01**	**5.00E-05**	9.92E-01	2.85E-04
Cd200r1_chr16	4	4	6	10	0.0	1.0	0.9	1.8	**9.70E-01**	**5.00E-05**	1.00E+00	2.85E-04
Cd209c_chr8	2	3	3	7	0.5	1.4	1.1	2.1	**2.00E-01**	**5.00E-05**	9.87E-01	2.85E-04
Cd244_chr1	7	7	10	23	0.1	1.0	1.2	2.2	**7.75E-01**	**5.00E-05**	1.00E+00	2.85E-04
Cd300a_chr11	10	11	14	24	0.2	1.2	0.8	1.7	**2.90E-01**	**5.00E-05**	9.96E-01	2.85E-04
Cd302_chr2	12	12	11	17	0.0	1.0	0.7	1.6	**9.33E-01**	**5.00E-05**	1.00E+00	2.85E-04
Cd47_chr16	35	39	64	98	0.2	1.1	0.6	1.5	**4.55E-01**	**1.00E-04**	1.00E+00	5.44E-04
Cd68_chr11	14	25	21	35	0.9	1.8	0.7	1.7	**7.03E-04**	**5.00E-05**	1.01E-01	2.85E-04
Cdc123_chr2	17	21	19	30	0.2	1.2	0.6	1.5	**3.05E-01**	**5.00E-05**	9.96E-01	2.85E-04
Cdc25a_chr9	4	5	7	12	0.4	1.3	0.8	1.7	**1.67E-01**	**5.00E-05**	9.80E-01	2.85E-04
Cdc25b_chr2	10	14	22	46	0.5	1.4	1.1	2.1	**4.10E-01**	**2.70E-02**	9.95E-01	7.14E-02
Cdc34_chr10	10	12	13	21	0.3	1.2	0.6	1.5	**3.50E-01**	**1.50E-04**	9.98E-01	7.89E-04
Cdc45_chr16	2	3	3	16	0.4	1.3	2.4	5.2	**3.44E-01**	**5.00E-05**	1.00E+00	2.85E-04
Cdc7_chr5	6	7	9	14	0.1	1.0	0.6	1.5	**7.98E-01**	**5.00E-05**	1.00E+00	2.85E-04
Cdca4_chr12	12	13	16	26	0.2	1.1	0.7	1.6	**3.96E-01**	**5.00E-05**	1.00E+00	2.85E-04

Cdca7_chr2	5	7	9	19	0.5	1.4	1.1	2.2	**1.05E-01**	**5.00E-05**	9.38E-01	2.85E-04
Cdca7l_chr12	4	5	7	11	0.2	1.2	0.6	1.5	**5.15E-01**	**1.00E-04**	1.00E+00	5.44E-04
Cdpf1_chr15	3	4	3	6	0.4	1.3	0.9	1.8	**5.29E-01**	**8.75E-05**	1.00E+00	4.94E-04
Cdt1_chr8	7	11	15	27	0.6	1.5	0.8	1.8	**2.23E-02**	**5.00E-05**	6.61E-01	2.85E-04
Ceacam16_chr7	3	5	4	14	1.0	1.9	1.6	3.1	**8.36E-03**	**5.00E-05**	3.39E-01	2.85E-04
Cecr2_chr6	3	7	6	9	1.1	2.2	0.6	1.5	**7.62E-07**	**5.00E-05**	3.53E-04	2.85E-04
Celsr1_chr15	1	1	2	4	0.0	1.0	0.9	1.8	**2.18E-01**	**5.00E-05**	9.89E-01	2.85E-04
Cenpc1_chr5	7	7	10	18	0.1	1.0	0.8	1.7	**8.34E-01**	**5.00E-05**	1.00E+00	2.85E-04
Cenpk_chr13	1	1	1	8	0.0	1.0	2.9	7.7	**7.22E-01**	**5.00E-05**	1.00E+00	2.90E-04
Cenpm_chr15	1	1	1	3	0.0	1.0	1.7	3.2	**6.65E-01**	**5.00E-05**	1.00E+00	2.61E-04
Cenpp_chr13	1	1	1	11	-0.2	1.2	3.3	10.1	**8.17E-01**	**5.00E-05**	1.00E+00	2.85E-04
Cenpq_chr17	9	9	10	21	-0.1	1.1	1.1	2.1	**7.89E-01**	**5.00E-05**	1.00E+00	2.85E-04
Cenpt_chr8	3	4	5	8	0.3	1.2	0.7	1.7	**4.15E-01**	**5.00E-05**	1.00E+00	2.85E-04
Cenpu_chr8	1	1	1	3	0.0	1.0	1.8	3.4	**8.80E-01**	**5.90E-03**	1.00E+00	2.00E-02
Cenpw_chr10	1	1	1	4	0.0	1.0	2.0	3.9	**5.75E-01**	**5.00E-05**	1.00E+00	2.85E-04
Cep128_chr12	3	3	5	11	0.1	1.0	1.1	2.2	**8.07E-01**	**5.00E-05**	1.00E+00	2.85E-04
Cep290_chr10	1	1	2	10	0.1	1.1	2.4	5.1	**7.23E-01**	**5.00E-05**	1.00E+00	2.85E-04
Cep55_chr19	2	2	2	5	0.1	1.1	1.1	2.2	**7.69E-01**	**5.00E-05**	1.00E+00	2.82E-04
Cep70_chr9	4	4	5	11	-0.1	1.1	1.0	2.0	**7.15E-01**	**5.00E-05**	1.00E+00	2.85E-04
Cep72_chr13	2	2	2	4	-0.1	1.1	0.6	1.5	**8.28E-01**	**2.50E-04**	1.00E+00	1.25E-03
Cep85_chr4	4	4	7	12	0.0	1.0	0.8	1.7	**9.76E-01**	**5.00E-05**	1.00E+00	2.85E-04
Cetn3_chr13	29	29	22	41	0.0	1.0	0.9	1.8	**9.14E-01**	**5.00E-05**	1.00E+00	2.85E-04
Cgrrf1_chr14	5	5	6	10	-0.1	1.1	0.8	1.7	**7.91E-01**	**5.00E-05**	1.00E+00	2.85E-04
Chac1_chr2	0	0	0	2	0.0	1.0	0.7	1.7	**5.91E-01**	**5.00E-05**	1.00E+00	2.85E-04
Chac2_chr11	3	3	3	21	0.1	1.1	3.1	8.4	**8.22E-01**	**5.00E-05**	1.00E+00	2.85E-04
Chchd1_chr14	18	18	13	28	0.0	1.0	1.1	2.1	**9.16E-01**	**5.00E-05**	1.00E+00	2.85E-04
Chek2_chr5	4	4	6	13	0.1	1.1	1.2	2.2	**7.99E-01**	**5.00E-05**	1.00E+00	2.85E-04
Chst1_chr2	3	6	8	13	0.8	1.7	0.7	1.6	**6.14E-03**	**5.00E-05**	3.72E-01	2.85E-04
Cir1_chr2	17	16	16	31	-0.2	1.1	1.0	1.9	**4.95E-01**	**5.00E-05**	1.00E+00	2.85E-04
Cited4_chr4	0	0	0	2	0.0	1.0	1.2	2.4	**3.83E-01**	**5.00E-05**	1.00E+00	2.85E-04
Clcn3_chr8	4	4	2	17	0.2	1.1	3.3	9.7	**7.32E-01**	**5.00E-05**	1.00E+00	3.01E-04
Clec4a1_chr6	11	12	12	21	0.2	1.1	0.8	1.8	**4.88E-01**	**5.00E-05**	1.00E+00	2.85E-04
Clec4a4_chr6	3	5	3	6	0.8	1.8	1.1	2.2	**4.60E-02**	**5.00E-05**	8.37E-01	2.85E-04
Clec4b1_chr6	2	2	1	3	-0.3	1.2	1.4	2.6	**6.92E-01**	**1.00E-04**	1.00E+00	5.57E-04
Clec4n_chr6	36	29	38	78	-0.3	1.2	1.0	2.0	**4.05E-01**	**2.29E-02**	9.91E-01	5.46E-02
Cln8_chr8	4	4	8	17	0.0	1.0	1.2	2.2	**9.67E-01**	**5.00E-05**	1.00E+00	2.85E-04
Clybl_chr14	3	4	3	6	0.2	1.1	0.7	1.7	**7.14E-01**	**1.50E-04**	1.00E+00	7.89E-04
Cmbl_chr15	2	3	2	5	0.5	1.4	1.1	2.2	**3.16E-01**	**5.00E-05**	9.97E-01	2.85E-04
Cmc2_chr8	2	3	2	5	0.6	1.5	1.1	2.2	**1.77E-01**	**5.00E-05**	9.84E-01	2.85E-04
Cmpk2_chr12	3	5	6	28	0.5	1.4	2.2	4.4	**6.40E-02**	**5.00E-05**	8.76E-01	2.85E-04
Cnnm2_chr19	1	1	2	7	0.0	1.0	1.5	2.9	**8.35E-01**	**5.00E-05**	1.00E+00	3.08E-04
Cnpy2_chr10	12	12	12	19	0.1	1.1	0.6	1.5	**7.62E-01**	**1.50E-04**	1.00E+00	7.89E-04
Coa6_chr8	7	6	5	8	-0.3	1.3	0.7	1.6	**4.20E-01**	**6.00E-04**	1.00E+00	2.73E-03
Commd3_chr2	22	21	17	29	-0.1	1.0	0.8	1.7	**7.95E-01**	**5.00E-05**	1.00E+00	2.85E-04
Cops2_chr2	19	18	23	42	-0.1	1.1	0.9	1.8	**6.55E-01**	**5.00E-05**	1.00E+00	2.85E-04
Cops5_chr1	19	20	21	34	0.1	1.1	0.7	1.6	**6.62E-01**	**5.00E-05**	1.00E+00	2.85E-04
Coq7_chr7	3	4	3	5	0.2	1.2	0.7	1.6	**6.04E-01**	**8.00E-04**	1.00E+00	3.53E-03
Coro2b_chr9	1	1	1	2	0.0	1.0	0.7	1.6	**1.94E-01**	**3.00E-04**	9.87E-01	1.47E-03
Cox11_chr11	3	3	4	6	-0.1	1.0	0.7	1.7	**8.47E-01**	**1.53E-02**	1.00E+00	4.48E-02
Cox17_chr16	28	35	21	34	0.3	1.3	0.7	1.6	**2.22E-01**	**5.00E-05**	9.91E-01	2.85E-04
Cox5a_chr9	28	38	21	34	0.4	1.4	0.7	1.6	**7.60E-02**	**1.00E-04**	9.03E-01	5.44E-04
Cox6c_chr15	78	75	45	102	-0.1	1.0	1.2	2.3	**8.07E-01**	**5.00E-05**	1.00E+00	2.85E-04
Cox7a2_chr9	28	26	15	35	-0.1	1.0	1.2	2.3	**8.20E-01**	**5.00E-05**	1.00E+00	2.85E-04
Cox7b_chrX	35	30	17	40	-0.2	1.1	1.2	2.3	**4.23E-01**	**5.00E-05**	1.00E+00	2.85E-04
Cox7c_chr13	70	73	43	80	0.1	1.0	0.9	1.9	**7.82E-01**	**5.00E-05**	1.00E+00	2.85E-04
Cpeb4_chr11	7	7	16	42	-0.2	1.1	1.4	2.6	**5.71E-01**	**5.00E-05**	1.00E+00	2.85E-04
Cpq_chr15	12	14	16	27	0.2	1.1	0.7	1.6	**5.54E-01**	**5.00E-05**	1.00E+00	2.85E-04
Crat_chr2	4	5	8	15	0.2	1.1	0.9	1.9	**5.72E-01**	**5.00E-05**	1.00E+00	2.85E-04
Creb3l1_chr2	1	2	2	3	1.1	2.2	0.6	1.6	**1.87E-03**	**7.50E-04**	1.88E-01	3.33E-03
Crls1_chr2	5	5	4	6	0.0	1.0	0.7	1.6	**9.37E-01**	**3.63E-02**	1.00E+00	8.07E-02
Csf2ra_chr19	12	16	20	36	0.4	1.3	0.8	1.8	**8.57E-02**	**5.00E-05**	9.18E-01	2.85E-04
Csf2rb_chr15	15	16	31	57	0.1	1.1	0.9	1.8	**6.04E-01**	**5.00E-05**	1.00E+00	2.85E-04
Ctla2a_chr13	17	19	7	20	0.2	1.1	1.4	2.7	**5.15E-01**	**6.26E-03**	1.00E+00	1.92E-02
Ctla2b_chr13	4	5	4	14	0.1	1.1	1.7	3.3	**7.96E-01**	**5.00E-05**	1.00E+00	2.85E-04
Ctnnd2_chr15	0	1	0	3	0.0	1.0	1.8	3.5	**8.42E-10**	**5.00E-05**	1.00E-06	2.85E-04
Ctrc_chr4	2	1	1	40	-0.8	1.7	5.0	31.9	**1.49E-01**	**5.00E-05**	9.03E-01	2.85E-04
Ctsb_chr14	106	147	184	318	0.5	1.4	0.8	1.7	**9.12E-02**	**4.00E-04**	9.27E-01	1.91E-03
Ctsd_chr7	113	140	186	351	0.3	1.2	0.9	1.9	**1.76E-01**	**5.00E-05**	9.84E-01	2.85E-04
Ctsh_chr9	51	60	58	87	0.2	1.2	0.6	1.5	**2.44E-01**	**2.00E-04**	9.92E-01	1.02E-03
Cttnbp2_chr6	1	1	1	2	0.0	1.0	0.6	1.6	**5.63E-01**	**3.50E-04**	1.00E+00	1.69E-03
Cul4a_chr8	15	16	27	64	0.1	1.1	1.3	2.4	**5.33E-01**	**5.00E-05**	1.00E+00	2.85E-04
Cuzd1_chr7	0	0	0	3	0.0	1.0	1.7	3.1	**3.39E-01**	**5.00E-05**	1.00E+00	2.85E-04
Cyb5a_chr18	42	47	34	72	0.2	1.1	1.1	2.1	**4.74E-01**	**5.00E-05**	1.00E+00	2.85E-04
Cycs_chr6	14	14	11	23	0.0	1.0	1.1	2.1	**9.93E-01**	**5.00E-05**	1.00E+00	2.85E-04
Cygb_chr11	3	12	5	17	1.9	3.7	1.7	3.2	**4.11E-11**	**5.00E-05**	3.59E-08	2.85E-04
Cyp4b1-ps2_chr4	0	1	0	6	0.0	1.0	2.6	6.2	**3.33E-01**	**5.00E-05**	9.97E-01	2.82E-04
Cyp4f16_chr17	10	20	15	27	1.0	2.0	0.8	1.7	**2.71E-05**	**5.00E-05**	6.68E-03	2.85E-04
Cysltr1_chrX	1	1	1	2	0.0	1.0	1.1	2.1	**8.88E-01**	**5.00E-05**	1.00E+00	2.85E-04
D030056L22Rik_chr19	5	7	7	17	0.3	1.3	1.3	2.4	**2.72E-01**	**5.00E-05**	9.94E-01	2.85E-04
D17Wsu92e_chr17	16	19	32	47	0.2	1.2	0.6	1.5	**4.34E-01**	**2.18E-02**	9.98E-01	5.52E-02
Daam1_chr12	4	4	8	14	-0.1	1.0	0.8	1.7	**7.06E-01**	**1.64E-02**	1.00E+00	3.87E-02

Dbf4_chr5	5	5	7	21	0.0	1.0	1.7	3.2	**9.48E-01**	**5.00E-05**	1.00E+00	2.85E-04
Dcaf12_chr4	23	31	44	71	0.4	1.4	0.7	1.6	**3.44E-02**	**5.00E-05**	7.66E-01	2.85E-04
Dcaf6_chr1	8	9	14	30	0.1	1.1	1.1	2.1	**6.80E-01**	**5.00E-05**	1.00E+00	2.85E-04
Dck_chr5	14	17	22	60	0.3	1.2	1.4	2.7	**2.01E-01**	**5.00E-05**	9.87E-01	2.85E-04
Dclk2_chr3	4	5	0	4	0.2	1.2	1.9	3.8	**4.90E-01**	**1.66E-02**	1.00E+00	5.10E-02
Dclre1b_chr3	4	4	6	12	0.0	1.0	0.8	1.8	**9.31E-01**	**5.00E-05**	1.00E+00	2.85E-04
Dctpp1_chr7	5	6	5	9	0.2	1.1	0.7	1.6	**6.93E-01**	**7.50E-04**	1.00E+00	3.33E-03
Dcun1d5_chr9	23	23	23	36	0.0	1.0	0.6	1.5	**9.72E-01**	**1.50E-04**	1.00E+00	7.89E-04
Ddx60_chr8	3	3	5	11	0.1	1.1	1.2	2.4	**7.25E-01**	**5.00E-05**	1.00E+00	2.85E-04
Def8_chr8	3	3	3	7	0.3	1.2	1.1	2.1	**4.49E-01**	**1.44E-02**	1.00E+00	3.95E-02
Dennd4a_chr9	19	25	35	57	0.4	1.3	0.7	1.6	**7.44E-02**	**5.00E-05**	7.99E-01	2.85E-04
Depdc1a_chr3	1	1	1	18	-0.1	1.1	3.4	10.5	**6.75E-01**	**5.00E-05**	1.00E+00	2.92E-04
Dgkg_chr16	0	0	1	2	0.0	1.0	0.8	1.7	**6.52E-01**	**5.00E-05**	1.00E+00	2.85E-04
Dhfr_chr13	1	1	1	6	-0.1	1.1	2.2	4.5	**8.36E-01**	**5.00E-05**	1.00E+00	2.85E-04
Dhrs13_chr11	1	1	1	2	0.0	1.0	0.9	1.9	**1.85E-01**	**5.00E-05**	9.86E-01	2.85E-04
Dhrs3_chr4	3	8	5	10	1.1	2.1	0.9	1.9	**6.08E-02**	**3.59E-02**	4.31E-01	7.96E-02
Dhx58_chr11	5	7	8	20	0.4	1.3	1.2	2.4	**1.82E-01**	**5.00E-05**	9.85E-01	2.85E-04
Disc1_chr8	1	1	2	3	0.0	1.0	0.8	1.7	**5.94E-01**	**5.00E-05**	1.00E+00	2.85E-04
Dmbt1_chr7	0	0	0	11	0.0	1.0	3.4	10.8	**6.09E-01**	**5.00E-05**	1.00E+00	2.85E-04
Dmwd_chr7	3	4	7	11	0.3	1.2	0.6	1.6	**3.98E-01**	**5.00E-05**	1.00E+00	2.85E-04
Dnaaf2_chr12	3	3	4	7	0.2	1.1	0.8	1.7	**6.14E-01**	**1.30E-03**	1.00E+00	5.38E-03
Dnaaf3_chr7	3	4	4	6	0.7	1.7	0.6	1.5	**3.18E-02**	**1.50E-04**	7.58E-01	7.89E-04
Dnaja4_chr9	2	3	4	13	0.5	1.4	1.5	2.9	**1.22E-01**	**5.00E-05**	9.50E-01	2.85E-04
Dnajb13_chr7	1	1	1	2	0.0	1.0	1.0	2.1	**5.79E-01**	**5.00E-05**	1.00E+00	2.85E-04
Dnajb2_chr1	4	5	4	16	0.4	1.3	2.1	4.4	**3.88E-01**	**5.00E-05**	9.95E-01	2.97E-04
Dnajb3_chr1	0	0	0	2	0.0	1.0	0.8	1.7	**9.00E-01**	**3.21E-02**	1.00E+00	8.28E-02
Dnajb4_chr3	10	12	13	26	0.2	1.1	1.0	2.0	**4.11E-01**	**5.00E-05**	1.00E+00	2.85E-04
Dnajc15_chr14	10	12	8	16	0.3	1.2	1.0	1.9	**3.95E-01**	**5.00E-05**	1.00E+00	2.85E-04
Dnase1l1_chrX	6	6	7	10	0.1	1.0	0.6	1.5	**8.54E-01**	**5.50E-04**	1.00E+00	2.52E-03
Dnmt1_chr9	13	16	27	43	0.3	1.2	0.7	1.6	**3.43E-01**	**5.79E-03**	9.86E-01	1.96E-02
Dnph1_chr17	1	1	1	3	0.0	1.0	1.5	2.9	**8.43E-01**	**5.00E-05**	1.00E+00	2.85E-04
Dock4_chr12	3	3	6	9	0.1	1.1	0.6	1.5	**5.71E-01**	**5.00E-05**	1.00E+00	2.85E-04
Dpy30_chr17	12	14	9	15	0.3	1.2	0.7	1.6	**4.32E-01**	**5.00E-05**	1.00E+00	2.85E-04
Dsn1_chr2	4	4	6	14	0.1	1.1	1.3	2.5	**6.58E-01**	**5.00E-05**	1.00E+00	2.85E-04
Dtymk_chr1	13	15	17	28	0.2	1.1	0.7	1.6	**6.36E-01**	**3.58E-03**	1.00E+00	1.21E-02
Dut_chr2	5	5	3	9	0.2	1.1	1.6	3.1	**5.95E-01**	**5.00E-05**	1.00E+00	2.97E-04
Dynlt1a_chr17	3	2	2	4	-0.3	1.2	0.9	1.8	**5.75E-01**	**5.00E-04**	1.00E+00	2.32E-03
Dysf_chr6	3	4	7	12	0.5	1.5	0.7	1.7	**3.02E-02**	**5.00E-05**	7.32E-01	2.85E-04
E230016M11Rik_chr6	1	1	1	2	0.0	1.0	0.9	1.8	**9.26E-01**	**1.11E-02**	1.00E+00	3.39E-02
E2f4_chr8	28	35	54	111	0.3	1.3	1.0	2.1	**1.11E-01**	**5.00E-05**	9.39E-01	2.85E-04
Eef1e1_chr13	12	14	13	23	0.2	1.1	0.9	1.8	**4.77E-01**	**5.00E-05**	1.00E+00	2.85E-04
Eef2k_chr7	4	5	8	15	0.4	1.3	0.9	1.8	**3.03E-01**	**1.03E-03**	9.67E-01	4.23E-03
Efcab11_chr12	0	0	0	2	0.0	1.0	0.6	1.5	**7.06E-01**	**5.00E-05**	1.00E+00	2.85E-04
Ehbp1l1_chr19	9	12	18	37	0.4	1.4	1.1	2.1	**3.57E-01**	**2.74E-03**	9.89E-01	1.00E-02
Eif2ak1_chr5	16	22	29	76	0.5	1.4	1.4	2.6	**5.52E-02**	**5.00E-05**	8.54E-01	2.85E-04
Eif2ak2_chr17	4	5	6	23	0.1	1.1	2.0	3.9	**7.00E-01**	**5.00E-05**	1.00E+00	2.85E-04
Eif2s1_chr12	18	18	22	35	0.0	1.0	0.7	1.6	**9.03E-01**	**5.00E-05**	1.00E+00	2.85E-04
Eif2s2_chr2	32	32	29	56	0.0	1.0	1.0	1.9	**9.97E-01**	**5.00E-05**	1.00E+00	2.85E-04
Eif3j1_chr2	21	23	25	41	0.1	1.1	0.7	1.7	**6.86E-01**	**4.90E-03**	1.00E+00	1.75E-02
Eif3j2_chr2	21	23	25	41	0.1	1.1	0.7	1.7	**6.86E-01**	**4.90E-03**	1.00E+00	1.75E-02
Eif4e_chr3	19	19	22	38	0.0	1.0	0.8	1.7	**8.72E-01**	**5.00E-05**	1.00E+00	2.85E-04
Ell2_chr13	11	13	17	30	0.3	1.2	0.8	1.7	**2.51E-01**	**5.00E-05**	9.92E-01	2.85E-04
Emc2_chr15	23	23	20	33	0.0	1.0	0.7	1.6	**9.53E-01**	**5.00E-05**	1.00E+00	2.85E-04
Eme1_chr11	1	1	2	9	0.2	1.2	2.5	5.7	**7.25E-01**	**8.50E-04**	1.00E+00	3.72E-03
Emr1_chr17	21	33	40	64	0.6	1.5	0.7	1.6	**4.78E-03**	**5.00E-05**	2.52E-01	2.85E-04
Endod1_chr9	6	6	11	26	0.0	1.0	1.2	2.3	**8.39E-01**	**5.00E-05**	1.00E+00	2.85E-04
Enkd1_chr8	1	1	1	3	0.0	1.0	1.4	2.6	**6.83E-01**	**5.00E-05**	1.00E+00	2.85E-04
Eno1b_chr18	8	26	17	27	1.6	3.1	0.7	1.7	**3.63E-11**	**5.00E-05**	8.70E-08	2.97E-04
Epb4.1_chr4	9	16	34	126	0.9	1.8	2.1	4.4	**2.33E-01**	**8.64E-04**	6.46E-01	3.58E-03
Epb4.1l3_chr17	5	7	10	17	0.3	1.3	0.7	1.7	**1.94E-01**	**5.00E-05**	9.48E-01	2.85E-04
Ercc6l_chrX	2	2	3	10	0.0	1.0	1.7	3.2	**8.86E-01**	**5.00E-05**	1.00E+00	2.85E-04
Ergic2_chr6	11	10	14	23	-0.3	1.2	0.9	1.8	**6.56E-01**	**1.25E-02**	1.00E+00	3.64E-02
Erh_chr12	35	40	31	58	0.2	1.2	0.9	1.9	**3.84E-01**	**5.00E-05**	1.00E+00	2.85E-04
Eri1_chr8	9	10	14	23	0.0	1.0	0.7	1.6	**9.54E-01**	**5.00E-05**	1.00E+00	2.85E-04
Erp27_chr6	1	1	1	2	0.0	1.0	1.0	1.9	**5.06E-01**	**5.00E-05**	1.00E+00	2.85E-04
Esd_chr14	13	18	12	31	0.5	1.4	1.3	2.5	**4.19E-02**	**5.00E-05**	8.13E-01	2.85E-04
Etfb_chr7	23	26	23	38	0.2	1.1	0.7	1.6	**4.35E-01**	**5.00E-05**	1.00E+00	2.85E-04
Ethe1_chr7	3	4	3	6	0.3	1.2	0.9	1.8	**4.21E-01**	**5.00E-05**	1.00E+00	2.85E-04
Evi5_chr5	5	4	8	20	-0.2	1.1	1.2	2.3	**4.48E-01**	**5.00E-05**	1.00E+00	2.85E-04
Exosc8_chr3	14	16	13	21	0.2	1.2	0.7	1.6	**4.39E-01**	**5.00E-05**	1.00E+00	2.85E-04
Ezh2_chr6	9	10	12	36	0.1	1.1	1.6	2.9	**6.09E-01**	**5.00E-05**	1.00E+00	2.85E-04
F8_chrX	2	1	3	4	-0.4	1.3	0.7	1.6	**3.02E-01**	**5.00E-05**	9.86E-01	2.85E-04
F830016B08Rik_chr18	1	1	3	8	-0.5	1.5	1.5	2.9	**6.19E-02**	**5.00E-05**	7.70E-01	2.85E-04
Fam126a_chr5	10	11	17	32	0.1	1.1	0.9	1.8	**6.19E-01**	**5.00E-05**	1.00E+00	2.85E-04
Fam212a_chr9	2	2	2	6	0.2	1.2	1.3	2.5	**6.15E-01**	**5.00E-05**	1.00E+00	2.85E-04
Fam214b_chr4	4	5	5	18	0.3	1.3	1.7	3.3	**4.45E-01**	**5.00E-05**	9.98E-01	3.07E-04
Fam216a_chr5	3	4	3	6	0.3	1.2	0.7	1.7	**5.67E-01**	**3.50E-04**	1.00E+00	1.69E-03
Fam220a_chr5	11	17	2	6	0.5	1.4	1.5	2.9	**1.41E-01**	**1.30E-02**	7.40E-01	4.33E-02
Fam53b_chr7	10	11	11	35	0.2	1.1	1.7	3.2	**4.61E-01**	**5.00E-05**	1.00E+00	2.99E-04
Fam64a_chr11	1	1	1	3	0.0	1.0	1.6	3.0	**8.30E-01**	**5.00E-05**	1.00E+00	2.85E-04
Fam96a_chr9	17	20	17	26	0.3	1.2	0.6	1.5	**2.21E-01**	**2.50E-04**	9.90E-01	1.25E-03

Fanca_chr8	2	2	3	13	0.0	1.0	2.0	3.9	**9.76E-01**	**5.00E-05**	1.00E+00	2.85E-04
Fancb_chrX	2	2	3	5	-0.1	1.1	0.6	1.5	**7.64E-01**	**7.75E-04**	1.00E+00	3.31E-03
Fanci_chr7	1	1	2	6	-0.1	1.0	1.7	3.3	**9.41E-01**	**7.55E-03**	1.00E+00	2.46E-02
Fancl_chr11	4	5	5	8	0.1	1.1	0.7	1.7	**8.10E-01**	**1.91E-02**	1.00E+00	5.39E-02
Fbxo10_chr4	1	1	3	5	0.1	1.1	0.7	1.6	**7.57E-01**	**5.00E-05**	1.00E+00	2.85E-04
Fbxo30_chr10	4	3	6	27	-0.2	1.1	2.2	4.7	**5.09E-01**	**5.00E-05**	1.00E+00	2.85E-04
Fbxo34_chr14	4	5	2	5	0.4	1.3	1.6	3.1	**2.01E-01**	**3.31E-02**	9.74E-01	9.02E-02
Fbxo42_chr4	5	7	12	20	0.3	1.2	0.7	1.6	**2.32E-01**	**5.00E-05**	9.91E-01	2.85E-04
Fbxo48_chr11	2	2	2	6	-0.1	1.1	1.5	2.8	**8.68E-01**	**5.00E-05**	1.00E+00	2.85E-04
Fbxo6_chr4	3	4	2	5	0.5	1.4	1.7	3.3	**4.59E-01**	**3.00E-04**	9.94E-01	1.67E-03
Fbxo7_chr10	8	10	12	27	0.2	1.2	1.2	2.2	**3.67E-01**	**5.00E-05**	9.99E-01	2.85E-04
Fbxo9_chr9	9	10	14	26	0.1	1.1	0.9	1.9	**5.25E-01**	**1.21E-03**	1.00E+00	4.78E-03
Fcer1g_chr1	37	56	25	72	0.6	1.5	1.5	2.9	**1.37E-02**	**5.00E-05**	5.30E-01	2.85E-04
Fcf1_chr12	24	25	16	28	0.0	1.0	0.8	1.7	**9.16E-01**	**5.00E-05**	1.00E+00	2.85E-04
Fcna_chr2	62	88	83	126	0.5	1.4	0.6	1.5	**1.79E-02**	**5.00E-05**	4.97E-01	2.85E-04
Fes_chr7	13	17	25	39	0.3	1.2	0.7	1.6	**1.58E-01**	**5.00E-05**	9.76E-01	2.85E-04
Fgl2_chr5	24	22	39	63	-0.1	1.1	0.7	1.6	**4.99E-01**	**5.00E-05**	1.00E+00	2.85E-04
Fgr_chr4	17	22	32	50	0.3	1.3	0.6	1.6	**1.01E-01**	**5.00E-05**	9.37E-01	2.85E-04
Fignl1_chr11	3	4	4	18	0.2	1.1	2.4	5.3	**6.54E-01**	**5.00E-05**	1.00E+00	2.93E-04
Fopnl_chr16	14	14	14	23	0.0	1.0	0.8	1.7	**9.50E-01**	**5.00E-05**	1.00E+00	2.85E-04
Foxd2os_chr4	1	1	1	2	0.0	1.0	0.9	1.9	**7.70E-01**	**5.00E-05**	1.00E+00	2.82E-04
Foxo3_chr10	8	9	28	59	0.1	1.1	1.1	2.1	**6.85E-01**	**5.00E-05**	1.00E+00	2.85E-04
Frmd4a_chr2	2	3	5	18	0.2	1.2	2.0	4.0	**5.18E-01**	**5.00E-05**	1.00E+00	2.97E-04
Fsd1l_chr4	0	0	1	2	0.0	1.0	0.8	1.7	**3.62E-01**	**5.00E-05**	9.98E-01	2.85E-04
Ftsj1_chrX	2	2	3	5	0.2	1.2	0.9	1.8	**5.66E-01**	**5.00E-05**	1.00E+00	2.85E-04
Fundc2_chrX	8	8	9	16	0.0	1.0	0.8	1.8	**9.97E-01**	**5.00E-05**	1.00E+00	2.85E-04
Fuom_chr7	1	1	1	2	-0.2	1.2	0.8	1.7	**4.24E-01**	**9.15E-03**	1.00E+00	2.90E-02
Fut1_chr7	0	0	0	3	0.0	1.0	1.5	2.9	**5.47E-01**	**5.00E-05**	1.00E+00	2.85E-04
Fxn_chr19	3	3	3	7	0.2	1.2	1.1	2.1	**6.07E-01**	**5.00E-05**	1.00E+00	2.85E-04
G2e3_chr12	7	5	10	15	-0.4	1.3	0.6	1.5	**8.41E-02**	**2.00E-04**	8.62E-01	1.05E-03
G6b_chr17_v1	1	2	2	4	0.8	1.8	1.1	2.1	**1.22E-01**	**5.00E-05**	9.12E-01	2.85E-04
Gale_chr4	2	2	2	4	0.4	1.4	0.8	1.8	**3.48E-01**	**5.00E-05**	9.98E-01	2.85E-04
Gas2l1_chr11	2	3	5	9	0.5	1.4	0.7	1.6	**2.96E-01**	**1.64E-02**	9.93E-01	4.43E-02
Gas5_chr1_v1	33	35	30	45	0.1	1.1	0.6	1.5	**7.27E-01**	**5.00E-05**	1.00E+00	2.82E-04
Gbgt1_chr2	1	1	3	5	0.1	1.1	0.9	1.8	**8.30E-01**	**5.00E-05**	1.00E+00	2.85E-04
Gbp10_chr5	0	0	1	4	0.0	1.0	2.0	3.9	**7.98E-01**	**5.00E-05**	1.00E+00	2.85E-04
Gbp2_chr3	13	11	19	33	-0.2	1.1	0.8	1.7	**4.18E-01**	**5.00E-05**	1.00E+00	2.85E-04
Gbp2b_chr3	0	4	0	31	1.9	3.8	4.9	30.8	**6.77E-14**	**5.00E-05**	6.83E-11	2.85E-04
Gbp6_chr5	4	3	5	15	-0.1	1.0	1.6	2.9	**8.23E-01**	**5.00E-05**	1.00E+00	2.85E-04
Gbp7_chr3	14	12	19	40	-0.2	1.2	1.1	2.1	**2.74E-01**	**5.00E-05**	9.93E-01	2.85E-04
Gbp8_chr5	18	18	23	46	-0.1	1.0	1.0	2.0	**8.05E-01**	**5.00E-05**	1.00E+00	2.85E-04
Gch1_chr14	3	3	4	13	0.1	1.0	1.7	3.2	**8.35E-01**	**5.00E-05**	1.00E+00	2.85E-04
Gclc_chr9	16	16	27	53	0.0	1.0	1.0	2.0	**9.70E-01**	**5.00E-05**	1.00E+00	2.85E-04
Gcnt2_chr13	2	2	4	16	0.0	1.0	1.9	3.8	**9.13E-01**	**5.00E-05**	1.00E+00	2.85E-04
Gdpd2_chrX	22	29	34	61	0.4	1.3	0.8	1.8	**6.23E-02**	**5.00E-05**	7.70E-01	2.85E-04
Gemin6_chr17	4	4	4	8	0.2	1.1	1.1	2.1	**6.72E-01**	**5.00E-05**	1.00E+00	2.85E-04
Ggh_chr4	6	3	7	18	-0.8	1.7	1.4	2.7	**4.18E-02**	**5.00E-05**	8.13E-01	2.85E-04
Gid8_chr2	13	15	21	41	0.2	1.1	1.0	2.0	**4.30E-01**	**5.00E-05**	1.00E+00	2.85E-04
Gins1_chr2	2	2	1	7	0.3	1.2	2.3	4.9	**6.25E-01**	**2.33E-04**	1.00E+00	1.17E-03
Gins3_chr8	3	3	4	8	0.1	1.1	1.0	2.1	**8.13E-01**	**5.00E-05**	1.00E+00	2.85E-04
Gm10872_chr15	0	0	0	2	0.0	1.0	0.9	1.9	**6.72E-01**	**5.00E-05**	1.00E+00	2.82E-04
Gm11127_chr17	1	1	2	3	0.1	1.1	0.7	1.6	**8.69E-01**	**9.05E-03**	1.00E+00	2.87E-02
Gm12185_chr11	1	1	1	3	0.0	1.0	1.4	2.6	**6.18E-01**	**5.00E-05**	1.00E+00	2.85E-04
Gm12250_chr11	5	5	8	25	0.1	1.1	1.6	3.1	**6.42E-01**	**5.00E-05**	1.00E+00	2.85E-04
Gm13154_chr4	0	1	0	2	0.0	1.0	0.7	1.6	**2.05E-04**	**5.00E-05**	3.84E-02	2.85E-04
Gm14005_chr2	3	3	2	5	0.0	1.0	1.0	2.1	**9.76E-01**	**1.19E-03**	1.00E+00	5.13E-03
Gm14446_chr19	2	3	2	10	0.6	1.5	2.5	5.6	**1.80E-01**	**5.00E-05**	9.70E-01	2.90E-04
Gm15800_chr5	7	6	19	41	-0.3	1.2	1.1	2.2	**2.17E-01**	**5.00E-05**	9.56E-01	2.85E-04
Gm1976_chr17	2	1	2	4	-0.6	1.6	1.1	2.1	**2.59E-01**	**5.00E-05**	9.97E-01	2.82E-04
Gm2382_chr9	9	9	7	11	0.0	1.0	0.6	1.6	**9.40E-01**	**4.00E-04**	1.00E+00	1.91E-03
Gm3604_chr13	2	1	2	5	-0.7	1.6	1.0	2.0	**9.90E-02**	**5.00E-05**	9.35E-01	2.85E-04
Gm3893_chr4	1	0	2	3	0.0	1.0	0.7	1.6	**3.36E-01**	**4.13E-02**	9.97E-01	1.02E-01
Gm4070_chr7	2	1	1	9	-0.2	1.2	2.8	6.8	**1.00E+00**	**5.00E-05**	1.00E+00	2.92E-04
Gm4349_chr3	0	0	0	2	0.0	1.0	0.8	1.7	**9.69E-01**	**5.00E-05**	1.00E+00	2.82E-04
Gm4951_chr18	3	3	4	14	0.0	1.0	1.8	3.5	**9.49E-01**	**5.00E-05**	1.00E+00	2.85E-04
Gm4956_chr1	1	5	1	10	2.2	4.7	3.3	9.7	**1.45E-06**	**5.00E-05**	6.10E-04	2.82E-04
Gm5086_chr13	1	1	1	2	0.4	1.4	0.9	1.9	**2.49E-01**	**4.50E-04**	9.90E-01	2.10E-03
Gm5088_chr14	0	0	0	2	0.0	1.0	0.9	1.9	**7.50E-01**	**5.00E-05**	1.00E+00	2.82E-04
Gm5431_chr11	1	1	2	3	0.4	1.3	0.8	1.7	**3.55E-01**	**2.50E-04**	9.98E-01	1.25E-03
Gm561_chr2	7	7	4	7	0.0	1.0	0.6	1.6	**9.91E-01**	**4.65E-03**	1.00E+00	1.63E-02
Gm5643_chrX	1	1	1	2	0.0	1.0	0.6	1.5	**6.20E-01**	**1.90E-03**	1.00E+00	7.83E-03
Gm6548_chr17	3	4	4	19	0.4	1.4	2.4	5.3	**2.12E-01**	**5.00E-05**	9.84E-01	2.82E-04
Gm6682_chr12	1	1	3	4	-0.2	1.1	0.6	1.5	**7.24E-01**	**2.55E-03**	1.00E+00	9.61E-03
Gm7367_chr11	16	20	24	39	0.3	1.3	0.7	1.6	**1.88E-01**	**5.00E-05**	9.82E-01	2.82E-04
Gm7609_chr1	9	11	12	23	0.3	1.2	0.9	1.8	**2.76E-01**	**5.00E-05**	9.94E-01	2.85E-04
Gm7694_chr1	2	2	4	8	0.4	1.3	1.0	2.0	**2.34E-01**	**5.00E-05**	9.91E-01	2.85E-04
Gm8369_chr19	4	7	3	6	0.8	1.7	0.9	1.8	**2.22E-02**	**5.00E-05**	5.44E-01	2.85E-04
Gm9199_chr14	0	0	0	2	0.0	1.0	0.8	1.8	**7.86E-02**	**5.00E-05**	8.96E-01	2.82E-04
Gm9320_chr17	5	5	3	8	-0.1	1.1	1.5	2.9	**8.42E-01**	**5.00E-05**	1.00E+00	2.82E-04
Gm9895_chr19	0	0	0	2	0.0	1.0	1.0	2.0	**5.84E-01**	**5.00E-05**	1.00E+00	2.82E-04
Gm996_chr2	1	1	1	3	0.0	1.0	1.0	2.0	**6.25E-01**	**5.00E-05**	1.00E+00	2.85E-04

Gnaz_chr10	1	1	2	3	0.0	1.0	0.7	1.6	**8.73E-01**	**5.00E-04**	1.00E+00	2.32E-03
Gng11_chr6	12	13	8	16	0.1	1.1	1.0	1.9	**7.44E-01**	**5.00E-05**	1.00E+00	2.85E-04
Gp1ba_chr11	2	3	3	5	0.6	1.5	0.7	1.6	**9.66E-02**	**1.00E-04**	9.32E-01	5.44E-04
Gp6_chr7	1	2	2	5	0.7	1.6	1.3	2.5	**2.36E-01**	**5.00E-05**	9.91E-01	2.85E-04
Gpaa1_chr15	5	7	8	13	0.4	1.4	0.7	1.7	**1.33E-01**	**5.00E-05**	9.56E-01	2.85E-04
Gpd1_chr15	1	2	2	4	0.3	1.2	0.8	1.8	**5.23E-01**	**5.00E-05**	1.00E+00	2.85E-04
Gpr128_chr16	0	0	0	2	0.0	1.0	0.8	1.7	**4.36E-01**	**5.00E-05**	1.00E+00	2.85E-04
Gpr146_chr5	8	8	0	11	0.0	1.0	3.5	11.4	**9.71E-01**	**1.37E-02**	1.00E+00	4.24E-02
Gpr35_chr1	4	5	8	13	0.2	1.2	0.6	1.5	**4.65E-01**	**7.50E-05**	1.00E+00	4.08E-04
Gpr56_chr8	3	6	8	13	0.9	1.9	0.7	1.6	**1.52E-03**	**7.50E-05**	1.62E-01	4.21E-04
Gpr82_chrX	1	1	1	3	0.3	1.2	1.6	3.0	**7.00E-01**	**5.05E-03**	1.00E+00	1.75E-02
Gpr88_chr3	1	2	2	3	1.0	2.0	1.0	2.0	**1.99E-03**	**5.00E-05**	1.95E-01	2.85E-04
Gsg2_chr11	2	2	3	11	0.1	1.1	1.7	3.2	**8.47E-01**	**5.00E-05**	1.00E+00	2.85E-04
Gtf2a2_chr9	19	21	13	21	0.2	1.1	0.7	1.6	**5.17E-01**	**5.00E-05**	1.00E+00	2.85E-04
Gtf2b_chr3	19	20	23	38	0.1	1.0	0.7	1.7	**7.90E-01**	**5.00E-05**	1.00E+00	2.85E-04
Gucd1_chr10	19	20	33	50	0.1	1.1	0.6	1.5	**6.65E-01**	**5.00E-05**	1.00E+00	2.85E-04
Gvin1_chr7	2	2	1	9	-0.2	1.2	2.8	6.8	**1.00E+00**	**5.00E-05**	1.00E+00	2.92E-04
Gzma_chr13	11	22	10	39	0.9	1.9	2.0	3.9	**1.01E-03**	**5.00E-05**	8.70E-02	2.85E-04
H2-Q2_chr17	0	1	0	2	0.0	1.0	0.6	1.5	**1.29E-01**	**5.00E-05**	9.54E-01	2.85E-04
H2-Q4_chr17	102	122	134	213	0.3	1.2	0.7	1.6	**2.50E-01**	**1.00E-04**	9.92E-01	5.44E-04
H2-Q6_chr17	57	96	97	225	0.8	1.7	1.2	2.3	**3.78E-04**	**5.00E-05**	6.30E-02	2.85E-04
H2-Q7_chr17	21	28	19	55	0.5	1.5	1.8	3.6	**3.30E-01**	**2.14E-02**	9.83E-01	5.61E-02
H2-Q8_chr17	60	77	96	204	0.4	1.3	1.1	2.1	**8.97E-02**	**5.00E-05**	8.35E-01	2.85E-04
H2-Q9_chr17	29	41	36	103	0.5	1.4	1.5	2.9	**1.46E-01**	**5.00E-05**	9.39E-01	2.49E-04
H2-T24_chr17	21	23	32	55	0.1	1.1	0.8	1.7	**8.71E-01**	**1.38E-02**	1.00E+00	4.10E-02
H3f3a_chr1	407	420	376	606	0.0	1.0	0.7	1.6	**8.58E-01**	**1.50E-04**	1.00E+00	7.89E-04
Hace1_chr10	5	5	8	20	-0.1	1.1	1.4	2.7	**7.03E-01**	**5.00E-05**	1.00E+00	2.85E-04
Hars_chr18	18	22	24	47	0.3	1.3	1.0	2.0	**1.34E-01**	**5.00E-05**	9.56E-01	2.85E-04
Hat1_chr2	15	18	17	53	0.3	1.2	1.6	3.1	**2.81E-01**	**5.00E-05**	9.94E-01	2.85E-04
Haus1_chr18	4	6	5	9	0.6	1.5	0.7	1.6	**1.25E-01**	**2.50E-04**	9.50E-01	1.25E-03
Haus4_chr14	4	5	7	13	0.3	1.2	1.0	2.0	**4.18E-01**	**5.00E-05**	1.00E+00	2.85E-04
Haus8_chr8	6	9	6	14	0.6	1.5	1.1	2.2	**4.69E-02**	**2.21E-02**	8.21E-01	5.32E-02
Hbb-b1_chr7	37	434	37	1,011	3.6	11.8	6.2	76.0	**1.78E-15**	**5.00E-05**	2.59E-12	2.85E-04
Hbb-b2_chr7	37	434	104	1,051	3.6	11.8	3.9	14.7	**1.78E-15**	**5.00E-05**	2.59E-12	2.77E-04
Hbq1a_chr11	1	1	0	2	0.0	1.0	0.8	1.8	**9.82E-01**	**5.00E-05**	1.00E+00	2.85E-04
Hcar2_chr5	2	3	4	9	0.3	1.2	1.3	2.5	**4.39E-01**	**5.00E-05**	1.00E+00	2.85E-04
Hdgf_chr3	30	43	50	100	0.5	1.4	1.0	2.0	**1.46E-02**	**5.00E-05**	5.46E-01	2.85E-04
Heatr5a_chr12	6	6	12	21	0.2	1.1	0.7	1.7	**4.00E-01**	**5.00E-05**	1.00E+00	2.85E-04
Hebp1_chr6	26	43	28	99	0.7	1.6	1.8	3.6	**1.80E-03**	**5.00E-05**	1.33E-01	2.85E-04
Hells_chr19	6	6	9	21	0.0	1.0	1.2	2.3	**9.45E-01**	**5.00E-05**	1.00E+00	2.85E-04
Herc6_chr6	9	8	12	25	-0.2	1.1	1.0	2.1	**4.33E-01**	**5.00E-05**	1.00E+00	2.85E-04
Hexim2_chr11	0	1	1	2	0.0	1.0	1.0	2.0	**6.59E-01**	**5.00E-05**	1.00E+00	2.70E-04
Hiatl1_chr13	16	17	25	37	0.1	1.0	0.6	1.5	**7.97E-01**	**3.25E-02**	1.00E+00	6.74E-02
Hint1_chr11	54	59	43	75	0.1	1.1	0.8	1.7	**5.85E-01**	**5.00E-05**	1.00E+00	2.85E-04
Hipk2_chr6	2	2	7	13	-0.3	1.2	0.9	1.9	**5.77E-01**	**1.49E-03**	1.00E+00	5.69E-03
Hirip3_chr7	6	7	7	16	0.2	1.2	1.2	2.2	**4.55E-01**	**5.00E-05**	1.00E+00	2.85E-04
Hist1h1c_chr13	8	11	11	19	0.5	1.4	0.8	1.8	**1.02E-01**	**5.00E-05**	9.38E-01	2.85E-04
Hist1h2bg_chr13	0	1	1	2	0.0	1.0	0.6	1.5	**3.87E-01**	**1.75E-03**	1.00E+00	6.97E-03
Hist1h4i_chr13	3	3	3	4	-0.1	1.1	0.6	1.6	**8.31E-01**	**1.28E-02**	1.00E+00	3.84E-02
Hjurp_chr1	2	3	4	15	0.7	1.6	2.0	4.0	**8.29E-02**	**5.00E-05**	9.16E-01	2.85E-04
Hk1_chr10	11	17	15	34	0.6	1.5	1.3	2.4	**7.91E-03**	**1.52E-02**	4.29E-01	3.98E-02
Hmbs_chr9	7	7	5	160	0.0	1.0	5.6	48.2	**6.61E-01**	**5.00E-05**	9.96E-01	2.85E-04
Hmgcl_chr4	14	17	18	27	0.3	1.2	0.6	1.5	**2.18E-01**	**1.00E-04**	9.89E-01	5.44E-04
Hmgn5_chrX	11	13	9	19	0.2	1.2	1.1	2.1	**3.62E-01**	**5.00E-05**	9.99E-01	2.85E-04
Hmox1_chr8	75	159	116	263	1.1	2.1	1.2	2.3	**9.27E-07**	**5.00E-05**	2.48E-04	2.85E-04
Hook2_chr8	1	2	2	3	0.7	1.6	0.8	1.7	**1.70E-01**	**2.38E-03**	9.60E-01	8.97E-03
Hras_chr7	3	4	4	7	0.2	1.1	0.9	1.9	**7.01E-01**	**3.90E-04**	1.00E+00	1.94E-03
Hs6st1_chr1	11	15	27	56	0.4	1.3	1.1	2.1	**5.89E-02**	**5.00E-05**	8.70E-01	2.85E-04
Hscb_chr5	7	9	8	13	0.3	1.3	0.6	1.5	**3.38E-01**	**9.00E-04**	9.98E-01	3.91E-03
Hsp90aa1_chr12	114	126	170	351	0.1	1.1	1.0	2.1	**5.57E-01**	**5.00E-05**	1.00E+00	2.85E-04
Hspa4l_chr3	5	5	9	17	0.0	1.0	0.9	1.9	**8.86E-01**	**5.00E-05**	1.00E+00	2.85E-04
Hspb6_chr7	1	1	2	4	0.1	1.1	1.4	2.6	**8.15E-01**	**5.00E-05**	1.00E+00	2.85E-04
Hspbap1_chr16	2	2	2	4	0.1	1.1	0.6	1.5	**7.06E-01**	**2.00E-04**	1.00E+00	1.02E-03
Htatip2_chr7	3	4	2	5	0.2	1.2	1.7	3.2	**7.48E-01**	**1.20E-02**	1.00E+00	3.60E-02
Htra2_chr6	17	18	20	32	0.2	1.1	0.7	1.6	**5.40E-01**	**5.00E-05**	1.00E+00	2.85E-04
I830012O16Rik_chr19	2	2	2	7	0.0	1.0	1.8	3.5	**9.16E-01**	**5.00E-05**	1.00E+00	2.85E-04
Ibtk_chr9	11	13	21	37	0.2	1.2	0.8	1.8	**2.71E-01**	**5.00E-05**	9.94E-01	2.85E-04
Ifi27_chr12	14	21	11	34	0.6	1.5	1.8	3.4	**1.18E-01**	**5.00E-05**	9.32E-01	2.85E-04
Ifi27l2a_chr12	52	62	29	130	0.3	1.2	2.2	4.5	**2.87E-01**	**5.00E-05**	9.95E-01	2.85E-04
Ifi35_chr11	15	19	16	31	0.3	1.2	1.0	1.9	**2.13E-01**	**5.00E-05**	9.88E-01	2.85E-04
Ifi47_chr11	30	35	38	84	0.2	1.1	1.2	2.2	**4.34E-01**	**5.00E-05**	1.00E+00	2.85E-04
Ifih1_chr2	3	4	6	17	0.2	1.1	1.4	2.6	**4.94E-01**	**5.00E-05**	1.00E+00	2.85E-04
Ifit1_chr19	2	2	3	13	0.4	1.3	2.4	5.3	**3.51E-01**	**5.00E-05**	9.98E-01	2.85E-04
Ifit2_chr19	5	5	7	16	0.2	1.1	1.2	2.3	**4.78E-01**	**5.00E-05**	1.00E+00	2.85E-04
Ifit3_chr19	3	5	4	24	0.5	1.4	2.6	6.2	**1.25E-01**	**5.00E-05**	9.50E-01	2.85E-04
Ifnlr1_chr4	1	1	1	2	0.0	1.0	0.9	1.9	**8.05E-01**	**5.00E-05**	1.00E+00	2.85E-04
Igsf3_chr3	1	1	2	3	0.0	1.0	0.7	1.6	**1.50E-01**	**5.00E-05**	9.71E-01	2.85E-04
Igtp_chr11	19	20	22	61	0.1	1.1	1.4	2.7	**5.83E-01**	**5.00E-05**	1.00E+00	2.85E-04
Iigp1_chr18	12	11	15	74	-0.1	1.1	2.3	4.9	**7.55E-01**	**5.00E-05**	1.00E+00	2.85E-04
Il12b_chr11	1	1	1	2	0.0	1.0	0.7	1.7	**3.63E-01**	**6.00E-04**	9.99E-01	2.73E-03
Il12rb1_chr8	1	1	1	4	0.1	1.1	1.3	2.4	**1.28E-01**	**5.00E-05**	9.54E-01	2.85E-04

Il13ra1_chrX	7	6	11	17	-0.4	1.3	0.7	1.6	**1.52E-01**	**5.00E-05**	9.72E-01	2.85E-04
Il15_chr8	2	2	2	4	0.3	1.2	1.2	2.3	**6.61E-01**	**1.10E-04**	1.00E+00	6.21E-04
Il1a_chr2	3	3	4	7	-0.1	1.1	0.8	1.8	**8.26E-01**	**5.00E-05**	1.00E+00	2.85E-04
Immp1l_chr2	13	13	10	17	0.0	1.0	0.7	1.7	**9.29E-01**	**5.00E-05**	1.00E+00	2.85E-04
Immp2l_chr12	1	1	1	2	0.2	1.2	0.6	1.5	**7.53E-01**	**3.00E-04**	1.00E+00	1.47E-03
Inhba_chr13	0	0	0	2	0.0	1.0	0.9	1.8	**2.93E-01**	**5.00E-05**	1.00E+00	2.85E-04
Ints8_chr4	11	11	3	25	0.1	1.0	3.0	8.2	**6.40E-01**	**5.00E-05**	1.00E+00	3.24E-04
Irf7_chr7	7	10	8	45	0.4	1.4	2.5	5.8	**2.41E-01**	**5.00E-05**	9.66E-01	2.96E-04
Irf9_chr14	10	12	5	21	0.4	1.3	2.2	4.5	**3.71E-01**	**5.00E-05**	9.75E-01	2.97E-04
Irgc1_chr7	1	2	1	4	1.0	2.0	1.9	3.6	**3.79E-04**	**5.00E-05**	4.30E-02	2.85E-04
Irgm1_chr11	21	25	28	62	0.3	1.2	1.2	2.2	**2.34E-01**	**5.00E-05**	9.91E-01	2.85E-04
Irgm2_chr11	14	17	23	43	0.3	1.2	0.9	1.9	**1.72E-01**	**5.00E-05**	9.82E-01	2.85E-04
Isca2_chr12	9	10	7	13	0.1	1.1	0.9	1.9	**6.58E-01**	**5.00E-05**	1.00E+00	2.85E-04
Itga5_chr15	2	3	5	9	0.1	1.1	0.7	1.7	**7.04E-01**	**5.00E-05**	1.00E+00	2.85E-04
Itgae_chr11	1	2	2	4	0.1	1.1	0.9	1.9	**8.62E-01**	**2.00E-02**	1.00E+00	5.29E-02
Itpa_chr2	12	11	12	24	-0.1	1.1	1.0	1.9	**7.08E-01**	**5.00E-05**	1.00E+00	2.85E-04
Itsn1_chr16	6	7	10	19	0.2	1.1	1.1	2.2	**5.08E-01**	**8.50E-04**	1.00E+00	3.55E-03
Josd2_chr7	4	5	5	16	0.3	1.2	1.6	3.1	**5.93E-01**	**5.00E-05**	1.00E+00	2.85E-04
Katnal1_chr5	2	2	3	6	0.1	1.0	1.1	2.2	**8.74E-01**	**5.00E-05**	1.00E+00	2.85E-04
Kbtbd12_chr6	0	0	1	2	0.0	1.0	0.6	1.6	**8.93E-01**	**5.00E-05**	1.00E+00	2.61E-04
Kcnj5_chr9	1	1	1	2	0.0	1.0	1.0	1.9	**4.80E-01**	**5.00E-05**	1.00E+00	2.85E-04
Kcnj9_chr1	1	1	1	2	0.0	1.0	0.9	1.8	**3.03E-01**	**5.00E-05**	9.96E-01	2.85E-04
Kctd14_chr7	2	2	1	3	0.3	1.3	1.1	2.1	**5.05E-01**	**1.81E-03**	9.83E-01	6.66E-03
Kctd7_chr5	2	2	3	6	0.3	1.2	1.0	2.0	**4.19E-01**	**5.00E-05**	1.00E+00	2.85E-04
Khsrp_chr17	19	30	37	61	0.7	1.6	0.7	1.7	**9.06E-04**	**5.00E-05**	1.16E-01	2.85E-04
Kif1a_chr1	0	0	1	2	0.0	1.0	0.7	1.7	**7.31E-02**	**5.00E-05**	8.94E-01	2.85E-04
Kif20a_chr18	2	2	3	18	0.1	1.1	2.5	5.6	**9.13E-01**	**8.50E-04**	1.00E+00	3.74E-03
Kif20b_chr19	4	4	7	18	-0.2	1.1	1.3	2.5	**4.41E-01**	**5.00E-05**	1.00E+00	2.85E-04
Klf11_chr12	3	3	6	10	0.3	1.2	0.8	1.8	**3.93E-01**	**5.00E-05**	1.00E+00	2.85E-04
Klhl12_chr1	4	5	7	17	0.4	1.3	1.3	2.5	**1.75E-01**	**5.00E-05**	9.84E-01	2.85E-04
Klhl23_chr2	2	2	3	8	0.2	1.1	1.5	2.9	**6.29E-01**	**5.00E-05**	1.00E+00	2.85E-04
Klhl25_chr7	4	4	8	13	0.0	1.0	0.7	1.6	**5.36E-01**	**1.53E-02**	1.00E+00	3.70E-02
Klra17_chr6	5	8	4	9	0.7	1.6	1.1	2.1	**4.37E-02**	**5.00E-05**	7.01E-01	2.85E-04
Klra7_chr6	1	2	1	4	0.6	1.6	1.6	3.1	**4.64E-01**	**1.81E-03**	9.96E-01	7.22E-03
Klrb1f_chr6	2	2	2	4	0.2	1.1	1.1	2.2	**7.92E-01**	**5.00E-05**	1.00E+00	2.85E-04
Klrc2_chr6	1	2	1	2	0.9	1.8	1.1	2.1	**3.14E-01**	**1.27E-02**	9.87E-01	3.80E-02
Klrc3_chr6	2	2	3	6	0.1	1.1	1.1	2.2	**8.82E-01**	**5.00E-05**	1.00E+00	2.85E-04
Klrd1_chr6	11	12	7	11	0.2	1.1	0.6	1.6	**6.29E-01**	**6.00E-04**	1.00E+00	2.73E-03
Klrg1_chr6	1	1	1	2	0.0	1.0	0.7	1.7	**8.28E-01**	**8.00E-04**	1.00E+00	3.53E-03
Lag3_chr6	2	4	5	11	0.7	1.6	1.2	2.3	**6.65E-02**	**5.00E-05**	8.76E-01	2.85E-04
Lancl2_chr6	2	3	3	9	0.6	1.5	1.4	2.6	**7.62E-02**	**5.00E-05**	9.03E-01	2.85E-04
Lap3_chr5	13	16	19	36	0.3	1.2	0.9	1.9	**2.40E-01**	**5.00E-05**	9.92E-01	2.85E-04
Layn_chr9	1	1	1	2	0.0	1.0	0.7	1.7	**7.18E-01**	**6.00E-04**	1.00E+00	2.73E-03
Lbr_chr1	38	47	67	121	0.3	1.3	0.9	1.8	**1.21E-01**	**5.00E-05**	9.50E-01	2.85E-04
Lgals3bp_chr11	17	27	33	73	0.7	1.6	1.2	2.2	**2.78E-03**	**5.00E-05**	1.77E-01	2.85E-04
Lhfpl2_chr13	1	2	2	3	0.6	1.5	0.7	1.6	**1.38E-01**	**5.00E-05**	9.60E-01	2.85E-04
Lilra5_chr7	1	3	1	8	1.8	3.5	2.8	7.0	**1.46E-05**	**5.00E-05**	3.70E-03	2.85E-04
Lilra6_chr7	3	5	4	14	0.6	1.6	2.0	3.9	**3.77E-01**	**6.50E-04**	9.97E-01	2.94E-03
Lipo1_chr19	1	2	2	8	0.8	1.7	2.2	4.7	**4.78E-02**	**5.00E-05**	7.23E-01	2.85E-04
Lmo2_chr2	8	9	6	59	-0.1	1.1	3.5	11.4	**5.26E-01**	**5.00E-05**	9.53E-01	2.97E-04
Lmtk3_chr7	0	0	0	2	0.0	1.0	1.1	2.1	**5.99E-01**	**5.00E-05**	1.00E+00	2.85E-04
Lpar2_chr8	1	3	1	4	1.5	2.8	1.7	3.2	**6.62E-09**	**5.00E-05**	6.37E-06	2.85E-04
Lpcat3_chr6	8	10	13	28	0.3	1.2	1.2	2.2	**4.23E-01**	**5.00E-05**	1.00E+00	2.85E-04
Lpin2_chr17	9	9	1	14	0.1	1.1	3.8	13.9	**6.59E-01**	**5.00E-05**	1.00E+00	2.97E-04
Lrrc39_chr3	1	1	1	2	0.0	1.0	1.2	2.3	**9.51E-01**	**5.55E-03**	1.00E+00	1.76E-02
Lsm2_chr17	3	6	2	5	0.7	1.6	1.0	2.0	**1.86E-01**	**6.82E-03**	9.90E-01	2.14E-02
Lsm3_chr6	21	20	13	28	0.0	1.0	1.1	2.1	**8.87E-01**	**5.00E-05**	1.00E+00	2.85E-04
Lsm4_chr8	15	23	18	29	0.6	1.5	0.7	1.6	**2.55E-02**	**5.00E-05**	6.92E-01	2.85E-04
Lsm5_chr6	20	18	12	25	-0.1	1.1	1.0	2.0	**6.67E-01**	**5.00E-05**	1.00E+00	2.85E-04
Lsm7_chr10	18	21	13	20	0.2	1.1	0.6	1.5	**6.05E-01**	**7.00E-04**	1.00E+00	3.13E-03
Lst1_chr17	20	22	10	18	0.1	1.1	0.9	1.9	**7.85E-01**	**5.00E-05**	1.00E+00	2.85E-04
Lta4h_chr10	20	30	34	52	0.5	1.4	0.6	1.5	**1.37E-02**	**5.00E-05**	5.30E-01	2.85E-04
Ly6a_chr15	70	134	55	158	0.9	1.9	1.5	2.9	**1.00E-05**	**5.00E-05**	2.86E-03	2.85E-04
Ly6c1_chr15	22	30	2	8	0.4	1.3	1.9	3.7	**3.71E-01**	**3.60E-03**	9.16E-01	1.39E-02
Ly6g6f_chr17	1	1	1	3	0.0	1.0	1.4	2.6	**3.32E-01**	**5.00E-05**	9.98E-01	2.85E-04
Ly6k_chr15	3	10	2	10	1.9	3.7	2.3	5.0	**7.87E-06**	**5.00E-05**	2.37E-03	2.85E-04
Lyrm4_chr13	2	3	2	5	0.4	1.3	1.1	2.1	**3.14E-01**	**5.00E-05**	9.97E-01	2.85E-04
Mafg_chr11	7	7	13	26	0.0	1.0	1.0	2.0	**9.63E-01**	**5.00E-05**	1.00E+00	2.85E-04
Magoh_chr4	34	37	27	55	0.1	1.1	1.0	2.1	**5.92E-01**	**5.00E-05**	1.00E+00	2.85E-04
Magohb_chr6	4	4	2	4	0.3	1.2	0.9	1.9	**5.79E-01**	**2.50E-04**	1.00E+00	1.25E-03
Manf_chr9	12	19	14	22	0.6	1.6	0.7	1.6	**4.94E-03**	**5.00E-05**	3.45E-01	2.85E-04
Map2k3_chr11	11	15	21	45	0.5	1.4	1.1	2.1	**3.21E-02**	**5.00E-05**	7.62E-01	2.85E-04
Map4k5_chr12	8	8	13	26	0.0	1.0	1.0	2.0	**9.87E-01**	**5.00E-05**	1.00E+00	2.85E-04
March2_chr17	15	19	2	13	0.3	1.3	2.5	5.7	**3.28E-01**	**5.00E-05**	9.57E-01	3.08E-04
March5_chr19	6	7	8	23	0.1	1.1	1.5	2.8	**6.47E-01**	**5.00E-05**	1.00E+00	3.08E-04
Mb21d1_chr9	1	1	2	4	0.0	1.0	1.0	2.0	**8.99E-01**	**5.00E-05**	1.00E+00	2.85E-04
Mbnl3_chrX	3	4	6	10	0.1	1.0	0.6	1.5	**8.28E-01**	**5.00E-05**	1.00E+00	2.85E-04
Mcm3_chr1	12	19	25	60	0.7	1.6	1.3	2.4	**1.85E-03**	**5.00E-05**	1.88E-01	2.85E-04
Mcm4_chr16	13	18	23	52	0.5	1.4	1.2	2.3	**2.39E-02**	**5.00E-05**	6.72E-01	2.85E-04
Mcm6_chr1	18	23	31	86	0.3	1.2	1.5	2.8	**1.64E-01**	**5.00E-05**	9.80E-01	2.85E-04
Mcm8_chr2	1	1	2	3	-0.2	1.1	1.0	2.0	**6.01E-01**	**5.00E-05**	1.00E+00	2.85E-04

Med21_chr6	19	18	12	27	0.0	1.0	1.2	2.3	**8.97E-01**	**5.00E-05**	1.00E+00	2.85E-04
Med29_chr7	3	3	3	5	0.2	1.2	0.6	1.5	**5.47E-01**	**7.50E-04**	1.00E+00	3.33E-03
Med30_chr15	11	12	9	15	0.2	1.2	0.8	1.8	**4.93E-01**	**5.00E-05**	1.00E+00	2.85E-04
Med6_chr12	10	11	10	17	0.2	1.2	0.8	1.7	**4.79E-01**	**5.00E-05**	1.00E+00	2.85E-04
Med7_chr11	5	5	5	8	0.0	1.0	0.8	1.7	**7.00E-01**	**1.51E-02**	1.00E+00	3.91E-02
Mefv_chr16	4	4	6	10	0.2	1.1	0.8	1.7	**6.40E-01**	**3.75E-03**	1.00E+00	1.26E-02
Mesdc1_chr7	3	5	8	14	0.4	1.4	0.8	1.8	**1.13E-01**	**5.00E-05**	9.42E-01	2.85E-04
Metap1d_chr2	3	7	3	12	1.4	2.6	2.0	3.9	**3.17E-04**	**5.00E-05**	3.81E-02	2.85E-04
Metrn_chr17	3	2	3	5	0.0	1.0	0.7	1.6	**9.78E-01**	**6.50E-04**	1.00E+00	2.93E-03
Metrnl_chr11	1	1	2	3	0.2	1.2	0.7	1.7	**6.40E-01**	**1.00E-04**	1.00E+00	5.44E-04
Mettl7a1_chr15	5	7	6	17	0.5	1.4	1.5	2.8	**8.36E-02**	**5.00E-05**	9.16E-01	2.85E-04
Mettl9_chr7	11	10	14	24	-0.1	1.1	0.8	1.7	**7.34E-01**	**6.90E-03**	1.00E+00	2.28E-02
Mfap3l_chr8	1	1	1	2	0.0	1.0	0.7	1.6	**7.15E-01**	**1.50E-04**	1.00E+00	7.49E-04
Mff_chr1	16	19	19	31	0.2	1.1	0.7	1.7	**4.07E-01**	**5.00E-05**	1.00E+00	2.85E-04
Mfsd12_chr10	3	4	10	15	0.1	1.1	0.6	1.6	**7.71E-01**	**5.00E-05**	1.00E+00	2.85E-04
Mfsd7a_chr5	1	1	2	3	-0.3	1.2	0.8	1.7	**5.62E-01**	**5.00E-05**	1.00E+00	2.85E-04
Mgll_chr6	6	5	7	15	-0.3	1.2	1.1	2.2	**3.06E-01**	**1.31E-02**	9.99E-01	3.53E-02
Mier3_chr13	7	7	11	21	0.2	1.1	0.9	1.8	**4.87E-01**	**5.00E-05**	1.00E+00	2.85E-04
Mmp27_chr9	0	0	0	2	0.0	1.0	1.0	2.0	**6.81E-01**	**5.00E-05**	1.00E+00	2.85E-04
Mmrn1_chr6	1	2	2	4	0.4	1.3	0.8	1.8	**2.98E-01**	**1.28E-03**	9.92E-01	5.04E-03
Mnd1_chr3	1	1	0	3	0.0	1.0	1.7	3.3	**8.63E-01**	**5.00E-05**	1.00E+00	2.85E-04
Mocs1_chr17	4	4	7	17	-0.1	1.1	1.3	2.5	**8.01E-01**	**1.33E-04**	1.00E+00	7.20E-04
Mospd1_chrX	5	5	7	13	0.0	1.0	1.0	2.0	**9.20E-01**	**5.00E-05**	1.00E+00	2.85E-04
Mospd3_chr5	5	8	8	14	0.6	1.6	0.8	1.8	**2.16E-01**	**6.77E-03**	8.21E-01	1.98E-02
Mpc1_chr17	20	21	16	28	0.0	1.0	0.8	1.7	**8.74E-01**	**5.00E-05**	1.00E+00	2.85E-04
Mpc2_chr1	8	10	8	13	0.3	1.2	0.8	1.7	**4.56E-01**	**5.00E-05**	1.00E+00	2.85E-04
Mpl_chr4	1	1	1	2	0.2	1.1	0.7	1.7	**5.26E-01**	**1.45E-02**	9.44E-01	3.92E-02
Mpst_chr15	6	7	1	4	0.3	1.3	2.1	4.1	**3.49E-01**	**1.85E-03**	9.98E-01	7.66E-03
Mri1_chr8	2	4	3	7	1.1	2.1	1.0	2.0	**2.56E-03**	**5.00E-05**	2.34E-01	2.85E-04
Mrm1_chr11	5	7	8	19	0.3	1.2	1.2	2.3	**2.73E-01**	**5.00E-05**	9.94E-01	2.85E-04
Mrpl1_chr5	3	3	3	4	-0.2	1.2	0.7	1.6	**7.12E-01**	**1.61E-02**	1.00E+00	4.49E-02
Mrpl12_chr11	17	18	18	30	0.1	1.1	0.7	1.6	**6.34E-01**	**5.00E-05**	1.00E+00	2.85E-04
Mrpl18_chr17	15	16	16	25	0.2	1.1	0.7	1.6	**5.72E-01**	**5.00E-05**	1.00E+00	2.85E-04
Mrpl20_chr4	21	18	14	27	-0.2	1.2	1.0	2.0	**4.84E-01**	**5.00E-05**	1.00E+00	2.85E-04
Mrpl22_chr11	7	8	6	10	0.1	1.1	0.7	1.6	**7.08E-01**	**2.50E-04**	1.00E+00	1.25E-03
Mrpl27_chr11	10	10	9	15	-0.1	1.1	0.7	1.7	**7.99E-01**	**5.00E-05**	1.00E+00	2.85E-04
Mrpl30_chr1	18	17	12	19	-0.1	1.0	0.7	1.6	**8.60E-01**	**5.00E-05**	1.00E+00	2.85E-04
Mrpl33_chr5	29	30	16	31	0.1	1.0	1.0	2.0	**8.25E-01**	**5.00E-05**	1.00E+00	2.85E-04
Mrpl40_chr16	10	10	8	13	0.1	1.0	0.7	1.6	**8.60E-01**	**5.00E-05**	1.00E+00	2.85E-04
Mrpl41_chr2	4	4	4	7	0.0	1.0	0.8	1.7	**9.67E-01**	**8.50E-04**	1.00E+00	3.72E-03
Mrpl42_chr10	14	15	13	20	0.2	1.1	0.6	1.5	**5.98E-01**	**1.50E-04**	1.00E+00	7.89E-04
Mrpl47_chr3	7	6	6	10	-0.1	1.1	0.6	1.6	**7.50E-01**	**7.50E-04**	1.00E+00	3.33E-03
Mrpl51_chr6	8	10	7	12	0.3	1.2	0.7	1.7	**3.02E-01**	**5.00E-05**	9.96E-01	2.85E-04
Mrpl53_chr6	7	8	7	13	0.1	1.1	0.9	1.9	**8.84E-01**	**2.44E-02**	1.00E+00	6.62E-02
Mrpl54_chr10	9	9	6	11	0.1	1.1	0.7	1.6	**8.36E-01**	**3.00E-04**	1.00E+00	1.47E-03
Mrpl57_chr14	3	3	3	5	0.4	1.3	0.7	1.6	**2.89E-01**	**5.00E-05**	9.95E-01	2.85E-04
Mrps14_chr1	7	8	6	10	0.2	1.1	0.6	1.6	**4.73E-01**	**1.50E-04**	1.00E+00	7.89E-04
Mrps18c_chr5	21	20	12	29	0.0	1.0	1.2	2.3	**9.27E-01**	**5.00E-05**	1.00E+00	2.85E-04
Mrps22_chr9	6	6	6	11	-0.1	1.1	0.9	1.9	**8.20E-01**	**5.00E-05**	1.00E+00	2.85E-04
Mrps28_chr3	6	7	6	10	0.2	1.1	0.8	1.7	**6.35E-01**	**5.00E-05**	1.00E+00	2.85E-04
Mrps36_chr13	5	7	6	10	0.5	1.4	0.7	1.7	**3.87E-01**	**2.50E-04**	9.98E-01	1.28E-03
Ms4a4b_chr19	9	31	10	66	1.8	3.5	2.8	6.7	**5.71E-11**	**5.00E-05**	4.40E-08	2.85E-04
Ms4a4c_chr19	26	36	27	41	0.5	1.4	0.6	1.5	**3.60E-02**	**1.00E-04**	7.71E-01	5.44E-04
Mst1_chr9	0	0	1	2	0.0	1.0	0.9	1.8	**6.34E-02**	**5.00E-05**	1.00E+00	2.85E-04
Mtcp1_chrX	5	6	6	10	0.2	1.1	0.8	1.7	**7.53E-01**	**1.67E-02**	1.00E+00	4.25E-02
Mtfr1_chr3	7	8	11	36	0.3	1.2	1.8	3.4	**2.75E-01**	**5.00E-05**	9.94E-01	2.85E-04
Mthfd1_chr12	9	12	20	32	0.5	1.4	0.7	1.7	**4.50E-02**	**5.00E-05**	8.28E-01	2.85E-04
Mtx2_chr2	10	10	9	19	0.0	1.0	1.0	2.0	**9.53E-01**	**5.00E-05**	1.00E+00	2.85E-04
Muc13_chr16	1	1	1	2	0.0	1.0	0.8	1.7	**8.16E-01**	**2.00E-04**	1.00E+00	1.02E-03
Mx1_chr16	3	3	3	7	0.1	1.1	1.3	2.4	**8.69E-01**	**6.00E-04**	1.00E+00	2.56E-03
Mx2_chr16	3	3	4	7	0.2	1.2	0.9	1.8	**5.20E-01**	**5.00E-05**	1.00E+00	2.82E-04
Mxd3_chr13	1	1	1	13	0.0	1.0	3.5	11.4	**9.70E-01**	**5.50E-04**	1.00E+00	2.52E-03
Mxi1_chr19	2	3	1	6	0.3	1.3	2.6	6.2	**3.20E-01**	**5.00E-05**	9.96E-01	2.97E-04
Mybl1_chr1	1	1	1	2	0.0	1.0	0.7	1.7	**3.85E-01**	**1.50E-04**	1.00E+00	7.89E-04
Myef2_chr2	8	8	8	13	0.0	1.0	0.7	1.6	**7.90E-01**	**3.12E-02**	1.00E+00	7.87E-02
Mylpf_chr7	1	1	1	2	0.0	1.0	1.1	2.2	**9.58E-01**	**2.00E-04**	1.00E+00	1.02E-03
Myo18b_chr5	0	0	1	2	0.0	1.0	1.0	2.0	**2.98E-01**	**5.00E-05**	9.96E-01	2.85E-04
Myo19_chr11	2	2	3	5	0.0	1.0	0.7	1.7	**9.67E-01**	**2.50E-03**	1.00E+00	9.53E-03
Myo1f_chr17	17	23	37	59	0.4	1.4	0.7	1.6	**3.89E-02**	**5.00E-05**	7.91E-01	2.85E-04
Myof_chr19	5	8	11	19	0.6	1.5	0.8	1.7	**1.01E-02**	**5.00E-05**	3.65E-01	2.85E-04
Mzt1_chr14	19	18	21	34	-0.1	1.0	0.7	1.6	**7.98E-01**	**5.00E-05**	1.00E+00	2.85E-04
Naa20_chr2	12	12	8	15	0.0	1.0	0.9	1.9	**9.07E-01**	**4.39E-02**	1.00E+00	8.99E-02
Naa38_chr11	8	8	5	9	0.1	1.0	0.8	1.8	**8.85E-01**	**1.10E-03**	1.00E+00	4.65E-03
Nadk2_chr15	6	7	9	31	0.1	1.1	1.8	3.4	**6.59E-01**	**5.00E-05**	1.00E+00	2.85E-04
Naga_chr15	8	13	14	22	0.6	1.6	0.6	1.6	**1.19E-02**	**5.00E-05**	5.03E-01	2.85E-04
Nampt_chr12	14	14	19	31	0.0	1.0	0.7	1.6	**9.81E-01**	**5.00E-05**	1.00E+00	2.85E-04
Napa_chr7	13	18	22	36	0.4	1.4	0.7	1.6	**5.19E-02**	**5.00E-05**	8.48E-01	2.85E-04
Narf_chr11	10	12	18	41	0.2	1.1	1.2	2.3	**4.33E-01**	**5.00E-05**	1.00E+00	2.85E-04
Nasp_chr4	16	17	10	19	0.1	1.1	0.9	1.8	**7.35E-01**	**2.14E-02**	1.00E+00	5.30E-02
Natd1_chr11	5	5	11	17	0.0	1.0	0.7	1.6	**8.50E-01**	**5.00E-05**	1.00E+00	2.85E-04
Ncaph2_chr15	12	14	20	32	0.2	1.1	0.8	1.7	**5.17E-01**	**3.00E-03**	9.98E-01	1.09E-02

Ncoa4_chr14	32	39	40	125	0.4	1.3	1.6	3.1	**2.69E-01**	**5.00E-05**	9.72E-01	2.99E-04
Ncr1_chr7	6	7	8	14	0.3	1.2	0.9	1.9	**3.60E-01**	**5.00E-05**	9.98E-01	2.85E-04
Ndc1_chr4	2	2	5	8	-0.1	1.0	0.8	1.7	**8.69E-01**	**5.00E-05**	1.00E+00	2.85E-04
Nde1_chr16	12	14	2	9	0.2	1.2	1.9	3.7	**4.43E-01**	**9.40E-03**	9.92E-01	3.18E-02
Ndufa1_chrX	27	28	12	20	0.1	1.0	0.7	1.7	**8.15E-01**	**5.00E-05**	1.00E+00	2.85E-04
Ndufa2_chr18	33	34	22	35	0.1	1.1	0.7	1.6	**7.85E-01**	**7.10E-03**	1.00E+00	2.34E-02
Ndufa4_chr6	75	75	50	115	0.0	1.0	1.2	2.3	**9.70E-01**	**5.00E-05**	1.00E+00	2.85E-04
Ndufa5_chr6	15	19	13	26	0.3	1.3	1.0	2.1	**2.82E-01**	**5.00E-05**	9.94E-01	2.85E-04
Ndufab1_chr7	7	9	5	9	0.4	1.3	0.8	1.8	**2.77E-01**	**1.00E-04**	9.94E-01	5.44E-04
Ndufb2_chr6	9	9	6	13	0.0	1.0	1.1	2.1	**9.64E-01**	**5.00E-05**	1.00E+00	2.85E-04
Ndufb3_chr1	36	45	23	35	0.3	1.3	0.6	1.6	**1.98E-01**	**2.00E-04**	9.87E-01	1.02E-03
Ndufb4_chr16	22	21	15	26	-0.1	1.1	0.8	1.7	**7.76E-01**	**5.00E-05**	1.00E+00	2.85E-04
Ndufb6_chr4	12	14	9	14	0.2	1.2	0.7	1.7	**5.35E-01**	**5.00E-05**	1.00E+00	2.85E-04
Ndufb8_chr19	23	26	20	32	0.2	1.1	0.7	1.6	**5.47E-01**	**5.00E-05**	1.00E+00	2.85E-04
Ndufb9_chr15	26	29	20	41	0.2	1.1	1.0	2.1	**5.44E-01**	**5.00E-05**	1.00E+00	2.85E-04
Ndufc2_chr7	22	22	17	36	0.0	1.0	1.1	2.2	**9.55E-01**	**5.00E-05**	1.00E+00	2.85E-04
Ndufs4_chr13	16	15	9	18	-0.1	1.1	1.0	1.9	**7.23E-01**	**5.00E-05**	1.00E+00	2.85E-04
Ndufs6_chr13	16	19	10	16	0.2	1.2	0.8	1.7	**4.84E-01**	**7.50E-05**	1.00E+00	4.25E-04
Ndufv2_chr17	20	20	15	23	0.0	1.0	0.6	1.5	**9.78E-01**	**3.50E-04**	1.00E+00	1.69E-03
Nedd8_chr14	54	60	39	62	0.1	1.1	0.7	1.6	**5.16E-01**	**5.00E-05**	1.00E+00	2.85E-04
Net1_chr13	9	10	2	5	0.1	1.1	1.6	3.0	**7.39E-01**	**1.25E-03**	1.00E+00	5.42E-03
Neu3_chr7	2	2	4	10	0.1	1.1	1.2	2.4	**7.70E-01**	**5.00E-05**	1.00E+00	2.85E-04
Neurl1a_chr19	0	0	1	2	0.0	1.0	0.7	1.6	**1.01E-01**	**5.00E-05**	9.20E-01	2.49E-04
Nhp2l1_chr15	38	45	34	53	0.2	1.2	0.6	1.5	**2.91E-01**	**1.00E-04**	9.96E-01	5.44E-04
Nkg7_chr7	10	15	11	18	0.6	1.5	0.7	1.6	**5.15E-02**	**1.00E-04**	8.48E-01	5.44E-04
Nlrc5_chr8	14	14	28	60	0.0	1.0	1.1	2.1	**9.52E-01**	**5.00E-05**	1.00E+00	2.85E-04
Nlrp1a_chr11	1	1	1	2	0.0	1.0	0.9	1.9	**5.66E-01**	**5.00E-05**	1.00E+00	2.85E-04
Nlrp1b_chr11	2	2	3	4	0.0	1.0	0.7	1.6	**9.65E-01**	**9.87E-03**	1.00E+00	3.11E-02
Nlrp1c-ps_chr11	1	1	2	3	0.0	1.0	0.6	1.5	**4.99E-01**	**7.00E-04**	1.00E+00	3.10E-03
Nlrp3_chr11	2	3	5	9	0.3	1.2	0.9	1.9	**3.04E-01**	**5.00E-05**	9.96E-01	2.85E-04
Nme1_chr11	23	27	19	35	0.2	1.2	0.9	1.8	**3.20E-01**	**5.00E-05**	9.97E-01	2.85E-04
Nmi_chr2	11	14	10	18	0.4	1.3	0.8	1.8	**3.90E-01**	**4.37E-03**	9.97E-01	1.35E-02
Nmnat1_chr4	2	3	2	4	0.8	1.8	0.7	1.6	**9.49E-02**	**1.50E-03**	9.27E-01	6.08E-03
Nmral1_chr16	3	5	3	14	0.9	1.9	2.0	4.1	**2.67E-02**	**5.00E-05**	6.98E-01	2.85E-04
Nop58_chr1	31	32	31	47	0.0	1.0	0.6	1.5	**8.43E-01**	**5.00E-05**	1.00E+00	2.85E-04
Nos1ap_chr1	1	1	2	4	0.0	1.0	0.9	1.9	**6.38E-01**	**5.00E-05**	1.00E+00	2.85E-04
Npl_chr1	3	4	4	6	0.2	1.1	0.7	1.6	**6.83E-01**	**5.00E-05**	1.00E+00	2.85E-04
Nrgn_chr9	3	7	4	8	1.1	2.2	0.9	1.8	**2.18E-03**	**5.00E-05**	2.07E-01	2.85E-04
Nsmce4a_chr7	24	26	25	38	0.1	1.1	0.6	1.5	**6.24E-01**	**5.00E-05**	1.00E+00	2.85E-04
Nt5c3_chr6	9	11	12	93	0.1	1.1	3.0	8.2	**2.13E-01**	**5.00E-05**	9.25E-01	2.85E-04
Nt5dc2_chr14	2	2	3	8	0.1	1.0	1.4	2.7	**9.53E-01**	**4.07E-02**	1.00E+00	1.01E-01
Nudcd1_chr15	3	3	5	8	0.0	1.0	0.7	1.6	**8.65E-01**	**3.47E-02**	1.00E+00	7.77E-02
Nudcd2_chr11	9	9	9	20	0.0	1.0	1.2	2.3	**9.37E-01**	**5.00E-05**	1.00E+00	2.85E-04
Nudt1_chr5	3	4	3	6	0.2	1.2	0.8	1.7	**6.17E-01**	**1.50E-04**	1.00E+00	7.89E-04
Nudt19_chr7	6	7	7	14	0.1	1.1	0.9	1.9	**6.88E-01**	**5.00E-05**	1.00E+00	2.85E-04
Nudt21_chr8	23	26	30	47	0.2	1.1	0.7	1.6	**5.20E-01**	**5.00E-05**	1.00E+00	2.85E-04
Nudt5_chr2	9	9	12	22	0.0	1.0	0.9	1.8	**8.99E-01**	**5.00E-05**	1.00E+00	2.85E-04
Nudt7_chr8	2	2	2	4	0.3	1.3	0.7	1.7	**6.00E-01**	**8.25E-04**	1.00E+00	3.67E-03
Nudt9_chr5	8	11	11	19	0.5	1.4	0.7	1.7	**8.69E-02**	**5.00E-05**	9.21E-01	2.85E-04
Nup35_chr2	5	4	5	8	-0.3	1.2	0.7	1.6	**3.64E-01**	**5.00E-05**	9.99E-01	2.85E-04
Nup37_chr10	5	4	5	8	-0.1	1.1	0.7	1.6	**8.28E-01**	**3.25E-04**	1.00E+00	1.60E-03
Nup43_chr10	4	5	5	8	0.1	1.1	0.9	1.9	**7.92E-01**	**5.00E-05**	1.00E+00	2.85E-04
Nup85_chr11	12	15	20	33	0.4	1.3	0.7	1.7	**1.36E-01**	**5.00E-05**	9.60E-01	2.85E-04
Nupr1_chr7	4	5	3	7	0.5	1.4	1.2	2.3	**2.91E-01**	**5.00E-05**	9.96E-01	2.85E-04
Nusap1_chr2	4	5	6	59	0.3	1.2	3.3	10.1	**3.05E-01**	**5.00E-05**	9.98E-01	2.85E-04
Nxpe4_chr9	1	3	1	13	1.7	3.2	3.4	10.7	**7.55E-08**	**5.00E-05**	4.40E-05	2.85E-04
Nxt1_chr2	7	8	7	12	0.2	1.1	0.7	1.7	**6.52E-01**	**5.00E-05**	1.00E+00	2.85E-04
Oas1a_chr5	1	4	2	14	1.4	2.7	2.6	6.1	**5.23E-04**	**5.00E-05**	8.17E-02	2.85E-04
Oas2_chr5	1	3	2	29	1.1	2.1	3.9	15.2	**1.90E-03**	**5.00E-05**	1.35E-01	2.85E-04
Oasl1_chr5	1	2	2	11	1.0	2.0	2.4	5.2	**2.11E-02**	**5.00E-05**	6.45E-01	2.85E-04
Odf2_chr2	6	8	1	9	0.6	1.5	3.0	7.9	**2.79E-01**	**5.70E-03**	9.88E-01	2.09E-02
Odf2l_chr3	3	3	3	5	0.0	1.0	0.7	1.7	**9.57E-01**	**1.88E-04**	1.00E+00	9.71E-04
Oip5_chr2	1	1	1	9	0.0	1.0	3.2	9.3	**9.49E-01**	**5.00E-05**	1.00E+00	2.85E-04
Olfr1033_chr2	0	1	0	2	0.0	1.0	1.0	2.0	**2.40E-05**	**5.00E-05**	3.98E-03	2.85E-04
Olfr98_chr17	1	1	2	4	-0.1	1.1	1.1	2.1	**8.04E-01**	**5.00E-05**	1.00E+00	2.85E-04
Olr1_chr6	0	0	0	2	0.0	1.0	0.6	1.5	**4.38E-01**	**5.00E-05**	1.00E+00	2.85E-04
Orc2_chr1	7	6	10	20	-0.2	1.2	1.0	2.0	**6.27E-01**	**5.64E-04**	1.00E+00	2.48E-03
Orc5_chr5	10	10	12	19	0.0	1.0	0.7	1.6	**9.79E-01**	**5.00E-05**	1.00E+00	2.85E-04
Orc6_chr8	5	5	5	22	0.0	1.0	2.2	4.5	**9.53E-01**	**5.00E-05**	1.00E+00	2.85E-04
Osgepl1_chr1	3	3	4	7	-0.2	1.1	0.8	1.8	**5.91E-01**	**5.00E-05**	1.00E+00	2.85E-04
Ost4_chr5	37	39	22	37	0.1	1.1	0.8	1.7	**8.25E-01**	**2.78E-02**	1.00E+00	6.61E-02
Otud5_chrX	33	38	54	89	0.2	1.2	0.7	1.6	**3.29E-01**	**5.00E-05**	9.98E-01	2.85E-04
Pabpc4_chr4	13	15	19	44	0.2	1.1	1.2	2.3	**5.63E-01**	**5.00E-05**	1.00E+00	2.90E-04
Pacsin2_chr15	14	15	3	9	0.0	1.0	1.8	3.6	**8.89E-01**	**4.33E-03**	1.00E+00	1.61E-02
Pafah2_chr4	1	1	2	3	-0.1	1.0	0.7	1.6	**8.89E-01**	**1.00E-04**	1.00E+00	5.44E-04
Palb2_chr7	2	2	4	7	0.1	1.1	0.8	1.7	**8.12E-01**	**5.00E-05**	1.00E+00	2.85E-04
Paqr4_chr17	2	2	3	6	0.3	1.2	0.9	1.9	**6.09E-01**	**7.50E-04**	1.00E+00	3.33E-03
Parp12_chr6	4	4	6	15	0.1	1.1	1.3	2.4	**7.18E-01**	**5.00E-05**	1.00E+00	2.85E-04
Parp9_chr16	13	15	20	31	0.1	1.1	0.7	1.6	**6.78E-01**	**8.75E-03**	1.00E+00	2.79E-02
Pcna_chr2	53	64	64	199	0.3	1.2	1.6	3.1	**2.03E-01**	**5.00E-05**	9.87E-01	2.85E-04
Pcyox1l_chr18	2	2	3	4	0.4	1.3	0.6	1.5	**3.15E-01**	**1.40E-03**	9.97E-01	5.72E-03

Pdcd5_chr7	16	17	11	20	0.1	1.0	0.9	1.8	**8.22E-01**	**5.00E-05**	1.00E+00	2.85E-04
Pdia2_chr17	0	0	0	6	0.0	1.0	2.6	5.9	**5.31E-01**	**5.00E-05**	1.00E+00	2.85E-04
Pdik1l_chr4	5	5	9	13	0.0	1.0	0.6	1.5	**9.61E-01**	**5.00E-05**	1.00E+00	2.85E-04
Pdk1_chr2	5	9	8	18	0.9	1.9	1.2	2.2	**6.32E-05**	**5.00E-05**	9.10E-03	2.85E-04
Pdk3_chrX	6	7	9	14	0.3	1.2	0.7	1.6	**3.16E-01**	**5.00E-05**	9.97E-01	2.85E-04
Pdzd11_chrX	7	8	7	12	0.2	1.1	0.8	1.8	**5.61E-01**	**5.00E-05**	1.00E+00	2.85E-04
Pet100_chr8	4	4	2	5	0.0	1.0	1.0	2.1	**9.99E-01**	**5.00E-05**	1.00E+00	2.85E-04
Pfdn1_chr18	11	12	8	12	0.1	1.1	0.6	1.5	**7.28E-01**	**3.00E-04**	1.00E+00	1.47E-03
Pfdn4_chr2	7	8	5	12	0.1	1.0	1.1	2.1	**8.86E-01**	**5.00E-05**	1.00E+00	2.85E-04
Pfkfb1_chrX	1	1	1	2	0.0	1.0	0.6	1.5	**9.77E-01**	**6.00E-03**	1.00E+00	2.03E-02
Pfkm_chr15	3	3	0	10	0.1	1.1	3.3	10.0	**8.21E-01**	**2.31E-02**	1.00E+00	6.57E-02
Pgap2_chr7	6	7	10	15	0.3	1.2	0.6	1.5	**4.64E-01**	**2.00E-04**	1.00E+00	1.02E-03
Pgp_chr17	5	6	10	20	0.3	1.2	1.0	2.0	**4.60E-01**	**5.00E-05**	1.00E+00	2.85E-04
Phf10_chr17	13	14	19	42	0.0	1.0	1.1	2.1	**8.97E-01**	**5.00E-05**	1.00E+00	2.85E-04
Phf11a_chr14	3	3	3	6	-0.1	1.1	1.0	2.0	**8.58E-01**	**5.00E-05**	1.00E+00	2.85E-04
Phf11d_chr14	2	2	2	4	-0.1	1.1	1.0	1.9	**8.24E-01**	**5.00E-05**	1.00E+00	2.85E-04
Phf5a_chr15	9	12	8	16	0.4	1.3	0.9	1.9	**1.04E-01**	**5.00E-05**	9.38E-01	2.85E-04
Pidd1_chr7	2	3	4	12	0.2	1.2	1.6	3.0	**4.89E-01**	**5.00E-05**	1.00E+00	2.85E-04
Piga_chrX	4	4	5	15	0.1	1.1	1.5	2.8	**7.91E-01**	**5.00E-05**	1.00E+00	2.85E-04
Pigyl_chr6	1	2	1	2	0.4	1.3	0.7	1.6	**2.10E-01**	**5.00E-05**	9.88E-01	2.85E-04
Pik3r1_chr13	9	10	1	13	0.5	1.4	3.7	12.7	**5.38E-01**	**1.48E-02**	1.00E+00	4.49E-02
Pim1_chr17	18	27	32	76	0.6	1.5	1.2	2.3	**8.49E-03**	**5.00E-05**	4.41E-01	2.85E-04
Pin4_chrX	17	20	7	12	0.3	1.2	0.7	1.6	**3.90E-01**	**2.50E-04**	1.00E+00	1.25E-03
Pira1_chr7	0	1	0	3	0.3	1.2	1.6	3.0	**3.17E-01**	**4.36E-02**	9.97E-01	1.07E-01
Pira4_chr7	1	2	1	8	0.7	1.6	2.9	7.7	**5.53E-01**	**7.15E-03**	1.00E+00	2.41E-02
Pira6_chr7	1	2	2	11	0.5	1.4	2.5	5.5	**2.89E-01**	**5.00E-05**	8.64E-01	2.90E-04
Pira7_chr7	1	3	1	8	1.1	2.1	2.9	7.7	**3.52E-01**	**7.38E-03**	9.98E-01	2.41E-02
Pithd1_chr4	9	11	14	22	0.3	1.2	0.6	1.5	**3.15E-01**	**1.50E-04**	9.97E-01	7.89E-04
Pitrm1_chr13	10	11	18	29	0.2	1.2	0.7	1.6	**4.30E-01**	**5.20E-03**	1.00E+00	1.79E-02
Pkmyt1_chr17	4	6	7	13	0.5	1.4	0.8	1.8	**1.52E-01**	**5.00E-05**	9.72E-01	2.85E-04
Pkn2_chr3	12	12	20	32	0.0	1.0	0.7	1.6	**9.13E-01**	**1.00E-04**	1.00E+00	5.44E-04
Pla2g12a_chr3	3	3	2	5	0.0	1.0	1.1	2.2	**9.59E-01**	**2.74E-02**	1.00E+00	6.71E-02
Pla2g16_chr19	5	5	5	12	0.2	1.2	1.3	2.5	**3.87E-01**	**5.00E-05**	1.00E+00	2.85E-04
Pla2g1b_chr5	0	0	0	4	0.0	1.0	2.2	4.5	**4.28E-01**	**2.20E-03**	1.00E+00	8.52E-03
Pla2g4a_chr1	6	5	9	15	-0.3	1.2	0.8	1.7	**3.24E-01**	**5.00E-05**	9.98E-01	2.85E-04
Plau_chr14	2	2	3	5	0.4	1.3	0.6	1.5	**3.82E-01**	**6.00E-04**	1.00E+00	2.73E-03
Plin2_chr4	10	11	16	28	0.1	1.1	0.8	1.7	**6.53E-01**	**5.00E-05**	1.00E+00	2.85E-04
Plod2_chr9	2	3	3	6	0.1	1.1	0.8	1.8	**8.19E-01**	**5.00E-05**	1.00E+00	2.85E-04
Pmm1_chr15	3	4	4	9	0.5	1.5	1.3	2.4	**1.90E-01**	**5.00E-05**	9.86E-01	2.85E-04
Pnmal2_chr7	1	1	1	4	0.2	1.2	1.3	2.5	**8.15E-02**	**5.00E-05**	8.13E-01	2.85E-04
Pno1_chr11	10	11	13	20	0.1	1.1	0.6	1.5	**7.16E-01**	**5.00E-05**	1.00E+00	2.85E-04
Pnpt1_chr11	14	13	16	24	-0.1	1.0	0.6	1.5	**7.82E-01**	**1.50E-04**	1.00E+00	7.89E-04
Pola1_chrX	4	4	7	26	0.1	1.1	1.8	3.5	**7.61E-01**	**5.00E-05**	1.00E+00	2.85E-04
Pola2_chr19	6	7	10	17	0.2	1.1	0.8	1.7	**3.81E-01**	**9.25E-03**	9.91E-01	2.62E-02
Pold1_chr7	10	14	21	34	0.4	1.4	0.7	1.6	**5.19E-02**	**5.00E-05**	8.48E-01	2.85E-04
Pole2_chr12	3	3	4	10	0.0	1.0	1.5	2.8	**9.31E-01**	**5.00E-05**	1.00E+00	2.85E-04
Polh_chr17	4	6	7	19	0.6	1.5	1.4	2.6	**4.99E-02**	**5.00E-05**	8.47E-01	2.85E-04
Polr2k_chr15	19	17	7	18	-0.2	1.1	1.2	2.3	**6.63E-01**	**7.58E-03**	1.00E+00	2.23E-02
Polr3k_chr2	9	9	10	17	0.1	1.1	0.7	1.6	**5.59E-01**	**5.00E-05**	1.00E+00	2.85E-04
Pop1_chr15	2	3	3	5	0.6	1.5	0.8	1.8	**1.22E-01**	**5.00E-05**	9.52E-01	2.85E-04
Pot1b_chr17	11	12	13	25	0.1	1.1	0.9	1.9	**7.38E-01**	**5.00E-05**	1.00E+00	2.85E-04
Ppa1_chr10	7	8	8	14	0.2	1.1	0.8	1.7	**5.34E-01**	**5.00E-05**	1.00E+00	2.85E-04
Ppid_chr3	20	23	20	31	0.2	1.2	0.6	1.5	**3.37E-01**	**5.00E-05**	9.98E-01	2.85E-04
Ppm1l_chr3	2	2	5	7	0.0	1.0	0.6	1.5	**9.97E-01**	**1.00E-04**	1.00E+00	5.44E-04
Ppp1cb_chr5	58	62	92	189	0.1	1.1	1.0	2.1	**6.91E-01**	**5.00E-05**	1.00E+00	2.85E-04
Ppp1r3e_chr14	1	1	2	4	0.2	1.1	1.3	2.5	**2.53E-01**	**5.00E-05**	9.70E-01	2.85E-04
Ppp2r4_chr2	31	38	57	94	0.3	1.2	0.7	1.7	**1.79E-01**	**5.00E-05**	9.85E-01	2.85E-04
Ppp2r5b_chr19	5	6	10	22	0.1	1.1	1.1	2.2	**6.25E-01**	**5.00E-05**	1.00E+00	2.85E-04
Ppwd1_chr13	7	9	9	16	0.4	1.3	0.9	1.9	**1.24E-01**	**5.00E-05**	9.50E-01	2.85E-04
Prdm1_chr10	3	3	5	7	0.1	1.1	0.6	1.5	**6.03E-01**	**5.00E-05**	1.00E+00	2.85E-04
Prdx1_chr4	95	101	78	128	0.1	1.1	0.7	1.6	**6.45E-01**	**5.00E-05**	1.00E+00	2.85E-04
Prdx3_chr19	24	28	30	57	0.2	1.2	0.9	1.9	**3.44E-01**	**5.00E-05**	9.98E-01	2.85E-04
Prelid2_chr18	1	1	1	2	-0.6	1.5	0.9	1.8	**3.08E-01**	**1.75E-03**	9.97E-01	6.97E-03
Prkab1_chr5	11	14	22	36	0.3	1.3	0.7	1.6	**1.64E-01**	**5.00E-05**	9.80E-01	2.85E-04
Prrg2_chr7	1	2	2	3	0.2	1.1	0.7	1.6	**7.39E-01**	**1.60E-03**	1.00E+00	6.43E-03
Psat1_chr19	7	8	10	16	0.2	1.2	0.7	1.6	**4.59E-01**	**5.00E-05**	1.00E+00	2.85E-04
Psip1_chr4	26	25	41	62	0.0	1.0	0.6	1.5	**8.76E-01**	**2.00E-04**	1.00E+00	1.02E-03
Psma1_chr7	52	58	50	88	0.1	1.1	0.8	1.8	**4.97E-01**	**5.00E-05**	1.00E+00	2.85E-04
Psma2_chr13	53	52	44	70	0.0	1.0	0.7	1.6	**9.48E-01**	**5.00E-05**	1.00E+00	2.85E-04
Psma4_chr9	41	43	37	65	0.1	1.0	0.8	1.8	**7.61E-01**	**5.00E-05**	1.00E+00	2.85E-04
Psmb1_chr17	49	52	47	75	0.1	1.1	0.7	1.6	**6.75E-01**	**5.00E-05**	1.00E+00	2.85E-04
Psmb3_chr11	40	42	34	53	0.1	1.0	0.6	1.5	**8.31E-01**	**1.00E-04**	1.00E+00	5.44E-04
Psmb5_chr14	19	24	22	35	0.3	1.3	0.6	1.5	**2.17E-01**	**5.00E-05**	9.89E-01	2.85E-04
Psmb7_chr2	49	50	43	77	0.0	1.0	0.8	1.8	**9.37E-01**	**5.00E-05**	1.00E+00	2.85E-04
Psmc3_chr2	35	41	46	70	0.2	1.2	0.6	1.5	**2.58E-01**	**1.50E-04**	9.93E-01	7.89E-04
Psmc3ip_chr11	2	2	2	5	0.1	1.1	1.6	3.0	**8.96E-01**	**1.19E-02**	1.00E+00	3.62E-02
Psmc6_chr14	35	32	34	72	-0.1	1.1	1.1	2.1	**5.27E-01**	**5.00E-05**	1.00E+00	2.85E-04
Psmd13_chr7	24	26	32	51	0.1	1.1	0.7	1.6	**6.00E-01**	**5.00E-05**	1.00E+00	2.85E-04
Psmd5_chr2	14	16	22	32	0.1	1.1	0.6	1.5	**5.63E-01**	**5.00E-05**	1.00E+00	2.85E-04
Psmd6_chr14	20	22	21	36	0.1	1.1	0.8	1.7	**6.97E-01**	**5.00E-05**	1.00E+00	2.85E-04
Psmd9_chr5	3	4	4	8	0.5	1.4	0.9	1.9	**1.47E-01**	**5.00E-05**	9.68E-01	2.85E-04

Psme3_chr11	32	43	57	123	0.4	1.3	1.1	2.2	**4.47E-02**	**5.00E-05**	8.26E-01	2.85E-04
Psmf1_chr2	5	7	9	17	0.4	1.3	1.0	2.0	**1.62E-01**	**5.00E-05**	9.79E-01	2.85E-04
Psrc1_chr3	1	1	1	4	0.0	1.0	1.9	3.7	**8.98E-01**	**5.00E-05**	1.00E+00	2.70E-04
Pstpip2_chr18	8	6	13	20	-0.3	1.2	0.6	1.5	**3.11E-01**	**1.50E-04**	9.97E-01	7.89E-04
Ptger3_chr3	1	1	1	2	0.1	1.0	1.0	2.0	**1.30E-01**	**1.00E-04**	9.55E-01	5.44E-04
Ptgis_chr2	2	4	4	9	0.6	1.5	1.1	2.2	**1.30E-01**	**5.00E-05**	9.54E-01	2.85E-04
Ptgs1_chr2	10	13	21	33	0.3	1.2	0.7	1.6	**1.96E-01**	**5.00E-05**	9.87E-01	2.85E-04
Ptplad2_chr4	3	2	5	9	-0.3	1.3	1.0	2.0	**3.95E-01**	**5.00E-05**	1.00E+00	2.85E-04
Pvrl1_chr9	1	2	2	4	0.6	1.5	1.1	2.1	**2.51E-03**	**5.00E-05**	2.31E-01	2.85E-04
Pycr1_chr11	0	0	0	2	0.0	1.0	0.7	1.6	**2.42E-01**	**5.00E-05**	1.00E+00	2.85E-04
Pycr2_chr1	9	10	13	20	0.2	1.1	0.6	1.5	**5.44E-01**	**2.00E-04**	1.00E+00	1.02E-03
Pydc3_chr1	5	8	8	17	0.6	1.6	1.0	2.0	**1.29E-02**	**5.00E-05**	5.25E-01	2.85E-04
Pydc4_chr1	2	3	4	11	0.5	1.4	1.5	2.9	**2.19E-01**	**5.00E-05**	9.91E-01	2.85E-04
Pyhin1_chr1	30	59	36	100	1.0	2.0	1.5	2.8	**3.27E-06**	**5.00E-05**	1.12E-03	2.85E-04
Rab27b_chr18	1	1	2	4	0.1	1.1	1.1	2.1	**7.43E-01**	**5.00E-05**	1.00E+00	2.85E-04
Racgap1_chr15	5	7	8	28	0.4	1.3	1.9	3.6	**2.24E-01**	**6.00E-05**	9.90E-01	3.51E-04
Rad21_chr15	38	49	74	118	0.4	1.3	0.7	1.6	**8.26E-02**	**1.50E-04**	9.15E-01	7.89E-04
Rad23a_chr8	13	20	22	69	0.6	1.5	1.6	3.1	**1.11E-02**	**5.00E-05**	4.89E-01	2.85E-04
Rad51b_chr12	0	0	0	2	0.0	1.0	0.8	1.7	**7.05E-01**	**5.00E-05**	1.00E+00	2.49E-04
Rad51c_chr11	1	1	1	2	0.3	1.2	0.7	1.7	**5.39E-01**	**1.00E-04**	1.00E+00	5.44E-04
Rad54b_chr4	1	1	1	4	0.0	1.0	2.0	4.1	**8.71E-01**	**5.00E-05**	1.00E+00	2.85E-04
Rad54l_chr4	2	2	2	12	0.1	1.1	2.4	5.3	**8.79E-01**	**6.00E-05**	1.00E+00	3.51E-04
Ran_chr5	37	49	48	81	0.4	1.3	0.8	1.7	**5.04E-02**	**5.00E-05**	8.48E-01	2.85E-04
Ranbp1_chr16	28	32	38	63	0.2	1.1	0.7	1.7	**4.24E-01**	**5.00E-05**	1.00E+00	2.85E-04
Rangap1_chr15	15	23	25	41	0.6	1.5	0.7	1.7	**5.57E-03**	**3.27E-02**	3.64E-01	6.51E-02
Rap1a_chr3	108	113	105	165	0.1	1.0	0.7	1.6	**7.93E-01**	**5.00E-05**	1.00E+00	2.85E-04
Rasgrp4_chr7	2	3	4	9	0.3	1.2	1.1	2.1	**4.56E-01**	**5.07E-03**	9.99E-01	1.60E-02
Rb1_chr14	23	22	39	60	-0.1	1.0	0.6	1.5	**8.12E-01**	**5.00E-04**	1.00E+00	2.32E-03
Rbbp4_chr4	32	37	42	65	0.2	1.1	0.6	1.6	**3.57E-01**	**5.00E-05**	9.98E-01	2.85E-04
Rbbp8_chr18	5	5	7	18	-0.1	1.0	1.3	2.5	**8.18E-01**	**5.00E-05**	1.00E+00	2.85E-04
Rbks_chr5	2	3	3	5	0.1	1.1	0.8	1.7	**8.10E-01**	**3.00E-04**	1.00E+00	1.47E-03
Rbm38_chr2	23	32	49	112	0.5	1.4	1.2	2.3	**2.20E-02**	**5.00E-05**	6.59E-01	2.85E-04
Rbm43_chr2	8	10	11	15	0.2	1.2	0.7	1.6	**5.71E-01**	**3.90E-02**	1.00E+00	8.41E-02
Rbm44_chr1	0	0	0	5	0.0	1.0	2.5	5.5	**6.46E-01**	**5.00E-05**	1.00E+00	2.85E-04
Rbm47_chr5	2	3	5	8	0.3	1.2	0.8	1.7	**3.01E-01**	**5.00E-05**	9.92E-01	2.85E-04
Rbpms2_chr9	1	2	2	4	0.6	1.5	0.6	1.5	**1.77E-01**	**8.50E-04**	9.84E-01	3.72E-03
Rcc1_chr4	6	7	9	20	0.2	1.1	1.1	2.2	**5.68E-01**	**5.92E-03**	1.00E+00	1.81E-02
Reep4_chr14	4	8	6	17	1.0	2.1	1.5	2.7	**1.05E-03**	**5.00E-05**	1.26E-01	2.85E-04
Reg2_chr6	0	0	0	106	0.0	1.0	6.7	106.5	**6.57E-01**	**5.00E-05**	1.00E+00	2.85E-04
Reg3a_chr6	0	0	0	2	0.0	1.0	0.9	1.9	**1.00E+00**	**5.00E-05**	1.00E+00	2.85E-04
Reg3b_chr6	0	0	0	7	0.0	1.0	2.7	6.7	**1.00E+00**	**5.00E-05**	1.00E+00	2.85E-04
Reln_chr5	0	0	1	2	0.0	1.0	0.8	1.8	**8.10E-01**	**5.00E-05**	1.00E+00	2.85E-04
Relt_chr7	9	10	15	28	0.2	1.2	0.9	1.9	**3.91E-01**	**5.00E-05**	1.00E+00	2.85E-04
Rexo2_chr9	26	35	27	59	0.5	1.4	1.1	2.2	**4.94E-02**	**5.00E-05**	8.46E-01	2.85E-04
Rfc3_chr5	5	7	7	13	0.6	1.5	0.8	1.8	**9.48E-02**	**5.00E-05**	9.27E-01	2.85E-04
Rfc5_chr5	6	7	10	18	0.3	1.2	0.9	1.9	**3.81E-01**	**5.00E-05**	1.00E+00	2.85E-04
Rfesd_chr13	3	3	3	5	0.0	1.0	0.6	1.5	**8.84E-01**	**8.50E-03**	1.00E+00	2.55E-02
Rffl_chr11	6	5	1	6	-0.1	1.1	2.1	4.2	**8.06E-01**	**3.80E-03**	1.00E+00	1.47E-02
Rfwd3_chr8	13	15	25	45	0.3	1.2	0.8	1.8	**2.07E-01**	**5.00E-05**	9.88E-01	2.85E-04
Rgs12_chr5	2	4	3	9	0.6	1.6	1.6	3.0	**3.82E-01**	**5.00E-05**	6.43E-01	2.97E-04
Rgs18_chr1	13	12	14	33	0.0	1.0	1.2	2.3	**9.06E-01**	**5.00E-05**	1.00E+00	2.85E-04
Rhbdd3_chr11	2	3	3	5	0.1	1.1	0.7	1.6	**7.18E-01**	**1.50E-04**	1.00E+00	7.89E-04
Rims3_chr4	3	3	7	14	-0.2	1.1	0.9	1.9	**7.48E-01**	**5.00E-05**	1.00E+00	2.85E-04
Riok3_chr18	22	26	37	58	0.2	1.2	0.6	1.6	**2.92E-01**	**5.00E-05**	9.96E-01	2.85E-04
Rmdn3_chr2	7	8	12	22	0.2	1.1	0.8	1.8	**4.72E-01**	**5.00E-05**	1.00E+00	2.85E-04
Rmi2_chr16	1	1	1	2	0.0	1.0	0.9	1.8	**5.30E-01**	**5.00E-05**	1.00E+00	2.85E-04
Rmrp_chr4	7	91	3	10	3.6	12.3	1.5	2.8	**1.00E-20**	**5.00E-05**	1.00E-20	2.82E-04
Rn45s_chr17	287	0	476	962	-8.2	287.3	1.0	2.0	**1.00E+00**	**6.00E-04**	1.00E+00	2.70E-03
Rnase4_chr14	6	9	7	10	0.6	1.6	0.6	1.5	**3.82E-02**	**7.88E-04**	7.90E-01	3.52E-03
Rnaseh2a_chr8	4	5	4	7	0.4	1.3	0.7	1.6	**2.10E-01**	**1.00E-04**	9.88E-01	5.44E-04
Rnaseh2c_chr19	12	13	12	18	0.1	1.1	0.6	1.5	**6.71E-01**	**4.00E-04**	1.00E+00	1.91E-03
Rnf10_chr5	39	50	88	165	0.4	1.3	0.9	1.9	**6.40E-02**	**5.00E-05**	8.76E-01	2.85E-04
Rnf11_chr4	19	22	29	57	0.2	1.2	1.0	2.0	**3.60E-01**	**5.00E-05**	9.98E-01	2.85E-04
Rnf123_chr9	23	20	47	99	-0.2	1.1	1.1	2.1	**4.16E-01**	**5.00E-05**	1.00E+00	2.85E-04
Rnf139_chr15	13	13	17	27	0.0	1.0	0.7	1.6	**9.84E-01**	**5.00E-05**	1.00E+00	2.85E-04
Rnf168_chr16	5	6	8	12	0.0	1.0	0.6	1.5	**8.39E-01**	**2.00E-04**	1.00E+00	1.02E-03
Rnf26_chr9	4	6	10	23	0.6	1.5	1.2	2.3	**6.44E-02**	**5.00E-05**	8.76E-01	2.85E-04
Rpa2_chr4	8	12	12	21	0.5	1.4	0.8	1.8	**6.69E-02**	**5.00E-05**	8.76E-01	2.85E-04
Rpa3_chr6	15	16	10	32	0.1	1.1	1.7	3.3	**7.43E-01**	**5.00E-05**	1.00E+00	2.85E-04
Rpain_chr11	6	6	6	10	0.0	1.0	0.8	1.7	**9.23E-01**	**1.57E-02**	1.00E+00	4.60E-02
Rpe_chr1	14	15	18	27	0.2	1.1	0.6	1.6	**5.83E-01**	**3.05E-03**	1.00E+00	1.13E-02
Rpgrip1l_chr8	1	1	1	2	0.0	1.0	0.9	1.9	**3.72E-01**	**5.00E-05**	1.00E+00	2.85E-04
Rpl22l1_chr3	108	116	69	152	0.1	1.1	1.1	2.2	**6.36E-01**	**5.00E-05**	1.00E+00	2.85E-04
Rpl31-ps12_chr16	19	16	15	31	-0.3	1.2	1.0	2.0	**4.45E-01**	**5.00E-05**	1.00E+00	2.85E-04
Rpl36al_chr12	152	170	111	178	0.2	1.1	0.7	1.6	**4.51E-01**	**5.00E-05**	1.00E+00	2.85E-04
Rpl39_chrX	822	758	676	1,032	-0.1	1.1	0.6	1.5	**6.17E-01**	**1.50E-04**	1.00E+00	7.89E-04
Rpph1_chr14	2	45	1	10	4.4	20.5	2.9	7.6	**3.77E-15**	**5.00E-05**	4.95E-12	2.82E-04
Rps15a-ps4_chr4	7	6	3	6	-0.2	1.1	0.9	1.9	**6.47E-01**	**5.00E-05**	1.00E+00	2.82E-04
Rps19-ps3_chr4	1	2	1	2	0.9	1.9	0.7	1.6	**9.86E-02**	**1.25E-03**	9.25E-01	5.15E-03
Rps27a_chr11	239	238	255	489	0.1	1.0	1.0	2.0	**9.57E-01**	**2.11E-02**	1.00E+00	4.70E-02
Rps27l_chr9	29	28	17	51	-0.1	1.1	1.6	3.0	**7.81E-01**	**5.00E-05**	1.00E+00	2.85E-04

Rps7_chr12	536	528	427	670	0.0	1.0	0.6	1.6	**9.40E-01**	**1.50E-04**	1.00E+00	7.89E-04
Rtn2_chr7	1	1	1	2	0.2	1.2	0.6	1.6	**3.86E-01**	**1.04E-02**	9.98E-01	2.87E-02
Rtn4rl2_chr2	0	0	0	2	0.0	1.0	0.8	1.8	**4.30E-02**	**5.00E-05**	1.00E+00	2.85E-04
Rtp4_chr16	5	8	5	22	0.6	1.6	2.1	4.3	**3.94E-02**	**5.00E-05**	7.96E-01	2.85E-04
Rwdd3_chr3	1	2	1	2	0.8	1.7	0.6	1.5	**1.80E-01**	**9.73E-03**	9.87E-01	3.03E-02
S100a1_chr3	7	6	5	8	-0.1	1.1	0.8	1.7	**8.67E-01**	**5.00E-05**	1.00E+00	2.85E-04
S100a4_chr3	63	89	40	100	0.5	1.4	1.3	2.5	**3.38E-02**	**5.00E-05**	7.66E-01	2.85E-04
S1pr5_chr9	1	1	1	2	0.0	1.0	0.7	1.6	**6.79E-01**	**1.60E-03**	1.00E+00	6.43E-03
Samd1_chr8	6	7	9	17	0.3	1.2	1.0	2.0	**3.13E-01**	**5.00E-05**	9.97E-01	2.85E-04
Samd11_chr4	2	3	3	21	0.4	1.3	3.0	8.1	**5.38E-01**	**5.00E-05**	1.00E+00	2.85E-04
Samd3_chr10	2	2	2	3	0.3	1.2	0.7	1.6	**4.92E-01**	**1.00E-03**	1.00E+00	4.35E-03
Sap30_chr8	2	3	2	7	0.2	1.1	1.4	2.7	**7.00E-01**	**5.00E-05**	1.00E+00	2.85E-04
Sar1b_chr11	17	17	18	28	0.0	1.0	0.6	1.6	**9.20E-01**	**5.00E-05**	1.00E+00	2.85E-04
Sarnp_chr10	35	40	28	52	0.2	1.1	0.9	1.8	**3.84E-01**	**5.00E-05**	1.00E+00	2.85E-04
Sass6_chr3	3	3	5	12	0.0	1.0	1.3	2.4	**9.49E-01**	**5.00E-05**	1.00E+00	2.85E-04
Scel_chr14	1	1	1	2	0.0	1.0	1.1	2.1	**1.09E-01**	**5.00E-05**	9.38E-01	2.85E-04
Scfd1_chr12	20	18	25	38	-0.1	1.1	0.6	1.5	**5.61E-01**	**5.00E-05**	1.00E+00	2.85E-04
Scly_chr1	7	8	12	20	0.3	1.3	0.7	1.7	**2.23E-01**	**5.00E-05**	9.91E-01	2.85E-04
Scoc_chr8	10	11	10	30	0.1	1.1	1.6	3.0	**6.53E-01**	**5.00E-05**	1.00E+00	2.85E-04
Sdc1_chr12	3	5	7	11	0.7	1.7	0.7	1.6	**9.85E-03**	**5.00E-05**	4.59E-01	2.85E-04
Sdcbp_chr4	52	50	70	150	0.0	1.0	1.1	2.1	**8.01E-01**	**5.17E-04**	1.00E+00	2.32E-03
Sdf2l1_chr16	11	14	16	27	0.4	1.3	0.8	1.7	**1.84E-01**	**5.00E-05**	9.86E-01	2.85E-04
Sdhd_chr9	25	28	26	45	0.2	1.1	0.8	1.7	**4.01E-01**	**5.00E-05**	1.00E+00	2.85E-04
Sec11c_chr18	44	52	36	59	0.2	1.2	0.7	1.6	**2.96E-01**	**5.00E-05**	9.96E-01	2.85E-04
Sec61b_chr4	50	47	32	49	-0.1	1.1	0.6	1.5	**7.32E-01**	**1.50E-04**	1.00E+00	7.89E-04
Sec61g_chr11	36	35	16	59	0.1	1.0	2.0	3.9	**7.44E-01**	**9.17E-05**	1.00E+00	5.18E-04
Selp_chr1	0	1	1	3	0.0	1.0	1.6	3.0	**1.10E-01**	**5.00E-05**	9.38E-01	2.85E-04
Sepn1_chr4	2	3	5	8	0.7	1.6	0.7	1.6	**3.07E-02**	**5.00E-05**	7.45E-01	2.85E-04
Sept3_chr15	1	0	1	2	0.0	1.0	0.9	1.8	**3.05E-01**	**5.00E-05**	9.96E-01	2.85E-04
Sept8_chr11	4	4	5	17	0.0	1.0	1.8	3.5	**8.11E-01**	**5.00E-05**	1.00E+00	3.08E-04
Serpina3b_chr12	0	0	0	2	0.0	1.0	0.7	1.6	**3.18E-01**	**5.00E-05**	1.00E+00	2.85E-04
Serpina3f_chr12	14	14	4	21	0.0	1.0	2.4	5.1	**9.58E-01**	**5.00E-05**	1.00E+00	2.88E-04
Serpini2_chr3	0	0	0	4	0.0	1.0	2.1	4.4	**2.17E-01**	**5.00E-05**	1.00E+00	2.85E-04
Sesn2_chr4	3	5	9	17	0.5	1.4	1.0	2.0	**9.05E-02**	**5.00E-05**	9.27E-01	2.85E-04
Setd8_chr5	14	16	22	47	0.1	1.1	1.1	2.1	**5.18E-01**	**5.00E-05**	1.00E+00	2.85E-04
Sf3b6_chr12	17	18	13	26	0.1	1.1	1.1	2.1	**6.26E-01**	**5.00E-05**	1.00E+00	2.85E-04
Sgk3_chr1	6	6	3	15	0.2	1.2	2.3	4.9	**7.26E-01**	**5.00E-05**	9.08E-01	3.24E-04
Sh2d1b1_chr1	4	6	5	12	0.6	1.5	1.4	2.6	**1.09E-01**	**5.00E-05**	9.38E-01	2.85E-04
Sh2d4a_chr8	1	2	2	6	0.7	1.6	1.5	2.9	**8.04E-02**	**5.00E-05**	9.08E-01	2.85E-04
Sh3glb1_chr3	26	29	38	59	0.2	1.1	0.6	1.6	**4.02E-01**	**5.00E-05**	1.00E+00	2.85E-04
Shfm1_chr6	72	74	44	73	0.0	1.0	0.7	1.7	**8.64E-01**	**5.00E-05**	1.00E+00	2.85E-04
Shmt2_chr10	7	10	12	19	0.4	1.3	0.7	1.6	**2.84E-01**	**2.31E-02**	9.56E-01	5.50E-02
Siglec5_chr7	0	0	0	2	0.0	1.0	0.8	1.7	**7.42E-01**	**5.00E-05**	1.00E+00	2.85E-04
Sirpb1a_chr3	8	10	10	29	0.3	1.2	1.5	2.9	**3.53E-01**	**5.00E-05**	9.98E-01	2.85E-04
Siva1_chr12	4	5	4	8	0.4	1.3	0.9	1.9	**4.46E-01**	**5.00E-05**	1.00E+00	2.85E-04
Six5_chr7	1	2	2	4	0.4	1.3	0.8	1.8	**3.76E-01**	**5.00E-05**	1.00E+00	2.85E-04
Ska2_chr11	6	7	8	23	0.1	1.1	1.5	2.9	**7.69E-01**	**5.00E-05**	1.00E+00	2.85E-04
Skp2_chr15	3	3	4	8	0.1	1.1	1.2	2.3	**7.60E-01**	**5.00E-05**	1.00E+00	2.92E-04
Slamf8_chr1	4	6	6	12	0.6	1.5	0.9	1.8	**4.12E-02**	**5.00E-05**	8.10E-01	2.85E-04
Slamf9_chr1	3	2	3	5	-0.4	1.4	0.7	1.7	**3.28E-01**	**2.50E-04**	9.98E-01	1.25E-03
Slbp_chr5	22	30	28	73	0.4	1.4	1.4	2.6	**4.45E-02**	**5.00E-05**	8.26E-01	2.85E-04
Slc11a1_chr1	13	14	25	41	0.1	1.1	0.7	1.6	**7.01E-01**	**5.00E-05**	1.00E+00	2.85E-04
Slc11a2_chr15	4	5	7	15	0.3	1.2	1.2	2.3	**3.77E-01**	**5.00E-05**	9.95E-01	2.92E-04
Slc14a1_chr18	7	7	2	16	0.0	1.0	2.8	6.9	**6.80E-01**	**5.00E-05**	1.00E+00	2.99E-04
Slc16a1_chr3	10	14	17	55	0.4	1.3	1.7	3.3	**4.91E-02**	**5.00E-05**	8.46E-01	2.85E-04
Slc16a4_chr3	1	1	1	3	0.0	1.0	0.9	1.8	**6.55E-01**	**5.00E-05**	1.00E+00	2.85E-04
Slc22a15_chr3	1	1	1	2	0.0	1.0	0.7	1.7	**7.18E-01**	**5.00E-05**	1.00E+00	2.85E-04
Slc25a17_chr15	7	11	9	17	0.6	1.5	0.9	1.8	**2.14E-02**	**5.00E-05**	6.47E-01	2.85E-04
Slc25a24_chr3	5	5	8	12	0.0	1.0	0.6	1.5	**9.71E-01**	**1.00E-04**	1.00E+00	5.44E-04
Slc25a42_chr8	3	3	6	9	-0.2	1.1	0.6	1.5	**5.70E-01**	**1.50E-04**	1.00E+00	7.89E-04
Slc25a51_chr4	15	19	28	80	0.3	1.3	1.5	2.9	**1.17E-01**	**5.00E-05**	9.46E-01	2.85E-04
Slc26a1_chr5	1	1	2	7	0.0	1.0	1.8	3.4	**7.13E-01**	**5.00E-05**	1.00E+00	2.85E-04
Slc30a9_chr5	13	13	19	32	0.0	1.0	0.8	1.7	**8.75E-01**	**5.00E-05**	1.00E+00	2.85E-04
Slc35g1_chr19	2	2	4	6	-0.3	1.2	0.6	1.5	**3.82E-01**	**5.00E-05**	1.00E+00	2.85E-04
Slc39a4_chr15	1	1	1	2	0.0	1.0	1.0	1.9	**9.85E-02**	**5.00E-05**	9.35E-01	2.85E-04
Slc39a8_chr3	1	2	2	6	0.5	1.4	1.7	3.2	**3.45E-01**	**5.00E-05**	9.96E-01	2.70E-04
Slc43a1_chr2	2	3	1	30	0.6	1.5	4.6	24.3	**2.51E-01**	**5.00E-05**	9.70E-01	2.90E-04
Slc45a4_chr15	2	4	8	14	0.9	1.9	0.7	1.7	**8.10E-02**	**2.23E-02**	9.10E-01	5.48E-02
Slc48a1_chr15	19	26	37	70	0.4	1.3	0.9	1.9	**2.25E-01**	**2.55E-03**	9.91E-01	9.70E-03
Slc6a4_chr11	1	2	2	5	1.0	2.0	1.7	3.3	**3.20E-03**	**5.00E-05**	2.70E-01	2.85E-04
Slc8a2_chr7	0	1	1	2	0.0	1.0	1.0	1.9	**1.25E-01**	**5.00E-05**	9.50E-01	2.85E-04
Slfn1_chr11	15	12	15	32	-0.3	1.2	1.1	2.1	**2.36E-01**	**5.00E-05**	9.66E-01	2.85E-04
Slfn3_chr11	3	2	4	12	-0.3	1.2	1.5	2.9	**4.82E-01**	**5.00E-05**	1.00E+00	2.85E-04
Slfn5_chr11	11	13	17	30	0.2	1.1	0.8	1.8	**3.53E-01**	**5.00E-05**	9.98E-01	2.85E-04
Slfn9_chr11	1	1	2	6	0.1	1.1	1.3	2.5	**7.57E-01**	**5.00E-05**	1.00E+00	2.85E-04
Slmo2_chr2	14	17	16	26	0.2	1.2	0.7	1.6	**3.37E-01**	**5.00E-05**	9.98E-01	2.85E-04
Smap1_chr1	13	17	21	42	0.4	1.3	1.0	2.0	**8.71E-02**	**5.00E-05**	9.22E-01	2.85E-04
Smc4_chr3	49	49	66	117	0.0	1.0	0.8	1.8	**9.47E-01**	**5.00E-05**	1.00E+00	2.85E-04
Smim24_chr10	1	2	2	2	1.1	2.2	0.6	1.5	**8.53E-02**	**3.43E-02**	9.18E-01	8.74E-02
Smim4_chr14	6	6	5	9	0.0	1.0	0.8	1.7	**9.70E-01**	**5.00E-04**	1.00E+00	2.30E-03
Smim7_chr8	10	12	11	20	0.3	1.2	0.8	1.8	**1.94E-01**	**5.00E-05**	9.87E-01	2.85E-04

Smox_chr2	3	4	8	46	0.4	1.4	2.4	5.4	8.47E-01	1.71E-02	1.00E+00	4.72E-02
Snca_chr6	22	39	27	139	0.8	1.8	2.3	4.8	8.19E-02	3.50E-04	3.63E-01	1.62E-03
Snhg1_chr19	30	28	18	35	-0.1	1.1	1.0	1.9	7.84E-01	5.00E-05	1.00E+00	2.82E-04
Snhg3_chr4	15	15	6	16	0.1	1.0	1.5	2.8	8.60E-01	5.00E-05	1.00E+00	2.82E-04
Snhg5_chr9	14	14	11	23	0.0	1.0	1.1	2.1	9.77E-01	5.00E-05	1.00E+00	2.82E-04
Snhg6_chr1	8	8	5	10	0.1	1.1	1.1	2.1	7.85E-01	5.00E-05	1.00E+00	2.82E-04
Snrnp27_chr6	20	20	13	21	0.0	1.0	0.7	1.6	9.55E-01	2.00E-04	1.00E+00	1.02E-03
Snrpb2_chr2	21	21	17	28	0.0	1.0	0.8	1.7	9.33E-01	5.00E-05	1.00E+00	2.85E-04
Snrpd1_chr18	24	26	14	30	0.1	1.1	1.0	2.1	6.92E-01	5.00E-05	1.00E+00	2.85E-04
Snrpd2_chr7	36	44	30	55	0.3	1.2	0.9	1.9	2.32E-01	5.00E-05	9.91E-01	2.85E-04
Snrpe_chr1	63	70	39	77	0.2	1.1	1.0	2.0	4.68E-01	5.00E-05	1.00E+00	2.85E-04
Snrpg_chr6	83	94	49	91	0.2	1.1	0.9	1.9	4.43E-01	5.00E-05	1.00E+00	2.85E-04
Snx10_chr6	7	7	8	17	0.0	1.0	1.1	2.1	9.07E-01	2.47E-02	1.00E+00	4.84E-02
Snx15_chr19	5	8	10	21	0.6	1.5	1.1	2.1	4.67E-02	5.00E-05	8.39E-01	2.85E-04
Snx22_chr9	9	8	11	28	-0.2	1.2	1.3	2.4	6.04E-01	5.00E-05	1.00E+00	2.85E-04
Socs1_chr16	1	2	1	3	0.3	1.2	1.0	1.9	6.29E-01	1.50E-04	1.00E+00	7.89E-04
Sod1_chr16	66	81	56	85	0.3	1.2	0.6	1.5	1.71E-01	1.00E-04	9.81E-01	5.44E-04
Sox12_chr2	1	1	2	3	0.2	1.1	0.7	1.7	2.72E-01	5.00E-05	9.94E-01	2.85E-04
Spata24_chr18	2	2	2	4	0.1	1.1	1.3	2.5	8.90E-01	5.17E-04	1.00E+00	2.34E-03
Spcs1_chr14	29	30	21	45	0.1	1.0	1.1	2.2	8.70E-01	2.50E-04	1.00E+00	1.25E-03
Sphk1_chr11	1	2	1	8	0.1	1.1	2.5	5.5	8.90E-01	5.00E-05	1.00E+00	2.89E-04
Spic_chr10	36	40	41	67	0.1	1.1	0.7	1.7	5.06E-01	5.00E-05	1.00E+00	2.85E-04
Spon2_chr5	1	4	1	2	2.0	4.1	0.6	1.6	4.97E-08	2.90E-03	3.19E-05	1.08E-02
Spp1_chr5	0	0	0	2	0.0	1.0	0.6	1.5	9.64E-01	5.00E-05	1.00E+00	2.61E-04
Sppl2b_chr10	6	6	11	37	0.1	1.0	1.7	3.3	8.05E-01	5.00E-05	1.00E+00	2.85E-04
Srm_chr4	8	12	14	24	0.5	1.4	0.7	1.7	6.08E-02	5.00E-05	8.75E-01	2.85E-04
Srp19_chr18	18	20	14	26	0.1	1.1	0.9	1.9	7.50E-01	5.00E-05	1.00E+00	2.85E-04
Srsf2_chr11	67	86	82	137	0.4	1.3	0.8	1.7	9.05E-02	5.00E-05	9.27E-01	2.85E-04
Srxn1_chr2	2	2	3	6	0.2	1.2	0.9	1.9	6.00E-01	5.00E-05	1.00E+00	2.85E-04
Ssbp3_chr4	6	8	8	13	0.4	1.3	0.7	1.7	1.31E-01	3.18E-02	9.60E-01	7.05E-02
Ssbp4_chr8	7	9	11	22	0.4	1.3	0.9	1.9	1.80E-01	5.00E-05	9.85E-01	2.85E-04
Ssna1_chr2	14	15	13	21	0.1	1.1	0.7	1.6	7.71E-01	5.00E-05	1.00E+00	2.85E-04
Ssr4_chrX	23	22	17	35	0.0	1.0	1.1	2.2	7.62E-01	5.00E-05	1.00E+00	2.90E-04
St3gal2_chr8	6	7	13	23	0.2	1.1	0.8	1.8	4.09E-01	5.00E-05	1.00E+00	2.85E-04
St3gal4_chr9	11	13	17	33	0.2	1.2	0.9	1.9	4.86E-01	5.00E-05	1.00E+00	2.85E-04
St3gal5_chr6	7	10	10	52	0.5	1.4	2.2	4.7	7.64E-02	4.50E-04	9.01E-01	2.06E-03
St3gal6_chr16	7	8	9	22	0.2	1.1	1.3	2.5	5.42E-01	5.00E-05	1.00E+00	2.85E-04
St6galnac1_chr11	0	5	0	10	2.3	5.0	3.4	10.4	2.13E-09	1.67E-02	1.12E-06	4.80E-02
St6galnac2_chr11	3	17	6	31	2.4	5.3	2.5	5.6	1.00E-20	5.00E-05	1.00E-20	2.85E-04
Stat1_chr1	18	23	33	64	0.3	1.2	1.1	2.2	4.69E-01	3.70E-02	9.85E-01	8.35E-02
Stk3_chr15	4	4	6	10	-0.1	1.1	0.7	1.7	7.87E-01	5.00E-05	1.00E+00	2.85E-04
Stk32c_chr7	2	3	2	4	0.7	1.6	0.6	1.5	1.94E-01	3.95E-02	9.64E-01	9.94E-02
Stra13_chr11	13	14	10	16	0.0	1.0	0.7	1.6	9.20E-01	1.50E-04	1.00E+00	7.89E-04
Stradb_chr1	6	8	9	27	0.5	1.4	1.6	2.9	6.53E-02	5.00E-05	8.76E-01	2.85E-04
Stx11_chr10	4	5	8	14	0.3	1.2	0.9	1.9	4.76E-01	2.38E-02	1.00E+00	5.58E-02
Stx3_chr19	2	2	1	2	0.1	1.1	0.6	1.5	7.51E-01	4.65E-02	1.00E+00	1.05E-01
Stxbp4_chr11	1	1	2	3	0.3	1.2	0.7	1.6	3.59E-01	5.00E-05	9.98E-01	2.85E-04
Sub1_chr15	24	28	21	35	0.2	1.2	0.7	1.6	2.80E-01	5.00E-05	9.94E-01	2.85E-04
Sucnr1_chr3	1	2	2	3	0.6	1.5	0.7	1.6	2.23E-01	1.90E-03	9.91E-01	7.48E-03
Sumo1_chr1	64	65	57	88	0.0	1.0	0.6	1.5	9.08E-01	5.00E-05	1.00E+00	2.85E-04
Suox_chr10	5	6	8	13	0.3	1.2	0.7	1.7	2.63E-01	5.00E-05	9.94E-01	2.85E-04
Suv39h1_chrX	7	9	11	18	0.4	1.3	0.7	1.6	1.16E-01	5.00E-05	9.45E-01	2.85E-04
Suv39h2_chr2	1	1	1	3	-0.1	1.1	1.3	2.5	6.46E-01	9.30E-03	1.00E+00	2.96E-02
Suz12_chr11	18	19	29	44	0.0	1.0	0.6	1.5	9.15E-01	4.86E-02	1.00E+00	9.87E-02
Swi5_chr2	39	41	37	56	0.0	1.0	0.6	1.5	8.57E-01	1.00E-04	1.00E+00	5.44E-04
Syce2_chr8	1	2	1	5	0.6	1.5	2.2	4.7	6.15E-01	3.21E-03	1.00E+00	1.20E-02
Synj1_chr16	5	5	8	12	0.2	1.1	0.7	1.6	6.98E-01	3.74E-02	1.00E+00	9.53E-02
Tab3_chrX	4	4	7	16	0.0	1.0	1.1	2.2	8.75E-01	5.00E-05	1.00E+00	2.85E-04
Tac2_chr10	0	0	0	2	0.0	1.0	0.6	1.5	7.44E-01	1.00E-04	1.00E+00	5.50E-04
Tango2_chr16	5	7	8	14	0.3	1.2	0.9	1.8	3.64E-01	5.00E-05	9.99E-01	2.85E-04
Tbc1d31_chr15	3	3	3	6	0.0	1.0	0.9	1.9	9.15E-01	4.15E-03	1.00E+00	1.35E-02
Tbc1d4_chr14	4	7	8	13	0.8	1.7	0.7	1.6	5.76E-04	5.00E-05	5.94E-02	2.85E-04
Tbccd1_chr16	4	5	7	12	0.2	1.1	0.8	1.7	5.53E-01	5.00E-05	1.00E+00	2.85E-04
Tbcel_chr9	10	11	15	28	0.1	1.1	0.8	1.8	5.08E-01	5.00E-05	1.00E+00	2.85E-04
Tbkbp1_chr11	3	3	6	10	0.2	1.2	0.6	1.6	4.35E-01	5.00E-05	1.00E+00	2.85E-04
Tbx21_chr11	2	4	4	7	0.9	1.9	0.8	1.7	6.06E-03	5.00E-05	3.72E-01	2.85E-04
Tcea1_chr1	34	32	43	63	0.0	1.0	0.6	1.5	6.95E-01	1.37E-02	1.00E+00	3.94E-02
Tceb1_chr1	21	23	17	28	0.1	1.1	0.7	1.6	7.36E-01	5.00E-05	1.00E+00	2.85E-04
Tcf19_chr17	3	3	3	13	0.2	1.2	2.3	4.9	6.25E-01	5.00E-05	1.00E+00	2.98E-04
Tctex1d2_chr16	5	6	4	7	0.3	1.2	0.8	1.8	5.25E-01	1.00E-04	1.00E+00	5.44E-04
Tex30_chr1	5	5	4	8	0.0	1.0	1.0	2.0	9.61E-01	5.00E-05	1.00E+00	2.85E-04
Tex9_chr9	2	2	3	8	0.1	1.1	1.6	3.0	6.75E-01	5.00E-05	1.00E+00	2.85E-04
Tfdp2_chr9	3	3	5	30	0.0	1.0	2.6	5.9	8.59E-01	1.93E-04	1.00E+00	9.61E-04
Tff2_chr17	0	0	0	8	0.0	1.0	2.9	7.5	7.56E-01	5.00E-05	1.00E+00	2.85E-04
Tgm2_chr2	22	28	53	94	0.4	1.3	0.8	1.8	5.34E-02	5.00E-05	8.48E-01	2.85E-04
Tgtp1_chr11	3	2	3	5	-0.6	1.5	0.9	1.8	9.16E-02	5.00E-05	9.27E-01	2.85E-04
Tgtp2_chr11	7	7	7	22	-0.1	1.1	1.6	3.0	8.56E-01	5.00E-05	1.00E+00	2.85E-04
Thg1l_chr11	6	6	8	13	0.1	1.1	0.8	1.7	8.31E-01	5.00E-05	1.00E+00	2.85E-04
Thop1_chr10	2	2	4	6	0.1	1.1	0.7	1.6	7.53E-01	5.00E-05	1.00E+00	2.85E-04
Timeless_chr10	3	3	5	9	0.2	1.1	1.0	2.0	6.61E-01	6.45E-03	1.00E+00	2.06E-02
Timm17a_chr1	9	11	9	16	0.3	1.2	0.7	1.7	4.12E-01	5.00E-05	1.00E+00	2.85E-04

Timm23_chr14	25	28	29	44	0.1	1.1	0.6	1.5	**5.32E-01**	**5.00E-05**	1.00E+00	2.85E-04
Timm8a1_chrX	8	8	7	15	0.0	1.0	1.0	2.0	**9.77E-01**	**5.00E-05**	1.00E+00	2.85E-04
Timm8b_chr9	14	13	9	21	-0.1	1.1	1.2	2.3	**8.26E-01**	**5.25E-03**	1.00E+00	1.81E-02
Tinagl1_chr4	11	16	23	40	0.5	1.5	0.8	1.7	**2.62E-02**	**5.00E-05**	6.96E-01	2.85E-04
Tjap1_chr17	0	3	1	6	1.7	3.2	2.5	5.7	**3.08E-02**	**5.00E-05**	8.16E-01	3.24E-04
Tkt_chr14	25	38	46	80	0.6	1.5	0.8	1.7	**2.86E-03**	**5.00E-05**	2.54E-01	2.85E-04
Tlr7_chrX	12	11	18	30	-0.1	1.1	0.8	1.7	**6.89E-01**	**5.00E-05**	1.00E+00	2.85E-04
Tmed6_chr8	0	0	0	2	0.0	1.0	0.8	1.7	**6.57E-01**	**5.00E-05**	1.00E+00	2.85E-04
Tmem106a_chr11	4	5	6	12	0.3	1.3	1.0	1.9	**2.73E-01**	**5.00E-05**	9.94E-01	2.85E-04
Tmem107_chr11	1	1	1	2	0.0	1.0	0.9	1.9	**6.53E-01**	**5.00E-05**	1.00E+00	2.85E-04
Tmem121_chr12	0	1	0	2	0.2	1.2	1.1	2.1	**3.98E-03**	**5.00E-05**	3.11E-01	2.85E-04
Tmem126a_chr7	10	11	8	12	0.1	1.1	0.6	1.5	**7.69E-01**	**1.35E-03**	1.00E+00	5.55E-03
Tmem138_chr19	3	4	4	5	0.4	1.3	0.6	1.5	**4.18E-01**	**3.85E-03**	1.00E+00	1.38E-02
Tmem194_chr10	4	4	6	12	0.2	1.2	1.0	1.9	**3.90E-01**	**5.00E-05**	1.00E+00	2.85E-04
Tmem215_chr4	1	2	2	3	0.9	1.9	0.8	1.7	**6.98E-02**	**7.25E-04**	8.89E-01	3.17E-03
Tmem221_chr8	1	1	1	2	0.4	1.4	1.1	2.1	**3.41E-02**	**5.00E-05**	7.66E-01	2.85E-04
Tmem256_chr11	16	14	11	38	-0.2	1.1	1.7	3.3	**6.73E-01**	**5.00E-05**	1.00E+00	2.85E-04
Tmem258_chr19	41	44	23	41	0.1	1.1	0.8	1.8	**7.15E-01**	**5.00E-05**	1.00E+00	2.85E-04
Tmem29_chrX	2	2	2	3	0.1	1.1	0.7	1.6	**7.81E-01**	**1.33E-02**	1.00E+00	3.90E-02
Tmem38a_chr8	0	1	1	2	0.0	1.0	0.6	1.5	**2.25E-01**	**5.00E-05**	9.91E-01	2.85E-04
Tmem41a_chr16	2	2	2	3	0.4	1.3	0.7	1.6	**5.36E-01**	**5.43E-03**	1.00E+00	1.87E-02
Tmem70_chr1	9	10	9	15	0.1	1.1	0.7	1.6	**7.08E-01**	**5.00E-05**	1.00E+00	2.85E-04
Tmem8_chr17	7	8	13	21	0.3	1.2	0.7	1.6	**2.84E-01**	**5.00E-05**	9.95E-01	2.85E-04
Tmem86b_chr7	2	3	3	7	0.2	1.1	1.4	2.7	**6.70E-01**	**5.00E-05**	1.00E+00	2.85E-04
Tmem9_chr1	5	5	7	12	0.2	1.2	0.9	1.8	**4.98E-01**	**5.00E-05**	1.00E+00	2.85E-04
Tmem97_chr11	3	4	5	8	0.3	1.3	0.7	1.7	**3.89E-01**	**2.00E-04**	1.00E+00	1.02E-03
Tmod1_chr4	0	1	1	15	0.0	1.0	3.9	14.6	**6.72E-01**	**5.00E-05**	1.00E+00	2.85E-04
Tmtc3_chr10	3	3	5	9	-0.2	1.2	0.7	1.7	**4.06E-01**	**5.00E-05**	1.00E+00	2.85E-04
Tmtc4_chr14	1	2	2	4	0.6	1.5	0.8	1.7	**1.04E-01**	**5.00E-05**	9.38E-01	2.85E-04
Tmx1_chr12	27	30	34	57	0.1	1.1	0.7	1.7	**5.45E-01**	**5.00E-05**	1.00E+00	2.85E-04
Tmx4_chr2	6	6	10	17	0.0	1.0	0.8	1.7	**9.27E-01**	**5.00E-05**	1.00E+00	2.85E-04
Tnfsf13_chr11	3	2	3	7	-0.4	1.3	1.3	2.5	**6.50E-01**	**7.33E-04**	1.00E+00	3.37E-03
Tnni3_chr7	1	2	1	2	0.7	1.6	0.7	1.6	**2.48E-01**	**4.50E-04**	9.92E-01	2.12E-03
Tomm40_chr7	9	11	1	4	0.3	1.2	1.8	3.5	**3.36E-01**	**1.88E-02**	9.97E-01	5.88E-02
Tomm5_chr4	15	16	12	21	-0.1	1.1	0.9	1.8	**8.13E-01**	**2.16E-02**	1.00E+00	5.22E-02
Tpcn1_chr5	8	8	19	33	0.0	1.0	0.8	1.8	**8.69E-01**	**5.00E-05**	1.00E+00	2.85E-04
Tpi1_chr6	29	33	33	50	0.2	1.1	0.6	1.5	**4.03E-01**	**2.00E-04**	1.00E+00	1.02E-03
Tppp3_chr8	1	1	1	3	0.0	1.0	1.0	2.0	**9.86E-01**	**5.00E-05**	1.00E+00	2.85E-04
Tpx2_chr2	2	3	2	17	0.3	1.3	2.6	6.1	**3.64E-01**	**7.14E-05**	9.98E-01	4.21E-04
Trappc12_chr12	6	8	1	3	0.4	1.3	1.7	3.2	**3.16E-01**	**1.37E-02**	8.64E-01	4.35E-02
Trim12a_chr7	0	11	0	47	3.5	11.2	5.5	46.6	**1.64E-06**	**1.44E-02**	4.14E-04	4.25E-02
Trim12c_chr7	39	39	11	50	0.0	1.0	2.2	4.5	**9.78E-01**	**5.00E-05**	1.00E+00	2.99E-04
Trim30a_chr7	33	35	46	76	0.1	1.1	0.7	1.6	**5.75E-01**	**5.00E-05**	1.00E+00	2.85E-04
Trim30b_chr7	1	4	1	14	1.8	3.4	3.7	13.4	**5.24E-06**	**5.00E-05**	1.08E-03	2.85E-04
Trim30d_chr7	1	5	1	32	2.2	4.7	5.0	31.6	**2.60E-07**	**5.00E-05**	8.12E-05	2.85E-04
Trim34a_chr7	7	15	11	36	1.1	2.1	1.7	3.2	**1.80E-05**	**5.00E-05**	3.03E-03	2.85E-04
Trim37_chr11	4	5	8	12	0.1	1.1	0.7	1.7	**5.61E-01**	**5.00E-05**	1.00E+00	2.85E-04
Trim59_chr3	22	28	30	78	0.4	1.3	1.4	2.6	**9.32E-02**	**5.00E-05**	8.35E-01	2.85E-04
Trmt1_chr8	2	6	2	9	1.6	3.0	2.1	4.1	**9.90E-03**	**7.50E-04**	4.56E-01	3.46E-03
Trmt10a_chr3	2	2	2	4	0.3	1.2	0.9	1.8	**4.05E-01**	**5.00E-05**	1.00E+00	2.85E-04
Trmt11_chr10	4	4	4	7	0.0	1.0	0.6	1.5	**9.82E-01**	**3.00E-04**	1.00E+00	1.47E-03
Trpc6_chr9	1	1	1	2	0.0	1.0	0.7	1.6	**9.53E-01**	**2.00E-04**	1.00E+00	1.02E-03
Tspan8_chr10	0	1	0	14	0.0	1.0	3.6	11.9	**7.68E-01**	**1.55E-03**	1.00E+00	6.22E-03
Ttc39c_chr18	1	1	1	2	0.0	1.0	0.6	1.6	**7.94E-01**	**2.70E-03**	1.00E+00	1.02E-02
Ttll12_chr15	3	4	8	22	0.6	1.5	1.5	2.8	**3.59E-02**	**5.00E-05**	7.71E-01	2.85E-04
Tuba1b_chr15	61	95	100	282	0.6	1.5	1.5	2.8	**2.71E-03**	**5.00E-05**	1.73E-01	2.85E-04
Tubb3_chr8	0	0	0	2	0.0	1.0	0.7	1.6	**2.97E-01**	**5.00E-05**	1.00E+00	2.85E-04
Tubb5_chr17	71	103	150	228	0.5	1.4	0.6	1.5	**1.71E-02**	**7.00E-04**	5.91E-01	3.13E-03
Tubd1_chr11	4	4	5	9	0.0	1.0	0.7	1.6	**9.19E-01**	**2.50E-04**	1.00E+00	1.28E-03
Tube1_chr10	1	1	1	2	0.0	1.0	0.6	1.6	**9.07E-01**	**1.45E-03**	1.00E+00	5.90E-03
Tuft1_chr3	1	1	2	3	0.2	1.1	0.7	1.6	**7.23E-01**	**2.00E-04**	1.00E+00	1.02E-03
Txndc5_chr13	45	59	73	146	0.4	1.3	1.0	2.0	**5.75E-02**	**5.00E-05**	8.68E-01	2.85E-04
Txnl1_chr18	12	13	14	29	0.1	1.1	1.0	2.0	**7.05E-01**	**5.00E-05**	1.00E+00	2.85E-04
Txnrd2_chr16	5	6	8	28	0.5	1.4	1.8	3.5	**3.59E-01**	**5.00E-05**	9.98E-01	2.85E-04
Tyrobp_chr7	109	95	69	128	-0.2	1.1	0.9	1.8	**3.63E-01**	**5.00E-05**	9.99E-01	2.85E-04
U2af1_chr17	17	20	15	23	0.3	1.2	0.7	1.6	**4.23E-01**	**4.99E-02**	9.98E-01	9.99E-02
Uba7_chr9	34	38	59	91	0.2	1.1	0.6	1.6	**4.17E-01**	**5.00E-05**	1.00E+00	2.85E-04
Ubd_chr17	4	4	2	6	0.0	1.0	1.3	2.5	**9.88E-01**	**5.00E-05**	1.00E+00	2.85E-04
Ube2b_chr11	30	35	31	51	0.2	1.2	0.7	1.6	**3.27E-01**	**5.00E-05**	9.98E-01	2.85E-04
Ube2e3_chr2	14	15	16	27	0.1	1.1	0.7	1.7	**6.91E-01**	**5.00E-05**	1.00E+00	2.85E-04
Ubiad1_chr4	3	7	6	10	1.0	2.0	0.7	1.7	**2.63E-04**	**5.00E-05**	4.78E-02	2.85E-04
Uchl5_chr1	6	7	7	11	0.2	1.2	0.8	1.7	**5.48E-01**	**4.33E-03**	1.00E+00	1.40E-02
Uck2_chr1	7	8	16	25	0.0	1.0	0.6	1.6	**9.09E-01**	**5.00E-05**	1.00E+00	2.85E-04
Ucp2_chr7	75	115	141	236	0.6	1.5	0.7	1.7	**1.22E-02**	**2.00E-04**	5.10E-01	1.02E-03
Uhrf1_chr17	3	4	6	32	0.6	1.5	2.5	5.5	**1.86E-01**	**5.00E-05**	9.56E-01	2.92E-04
Ulbp1_chr10	2	2	3	5	0.0	1.0	0.7	1.6	**9.17E-01**	**1.50E-04**	1.00E+00	7.89E-04
Ulk1_chr5	7	7	16	29	0.1	1.1	0.9	1.8	**5.69E-01**	**5.00E-05**	1.00E+00	2.85E-04
Unc5cl_chr17	2	2	3	4	0.2	1.1	0.6	1.5	**6.13E-01**	**5.00E-04**	1.00E+00	2.32E-03
Ung_chr5	2	2	4	6	0.2	1.2	0.7	1.7	**6.47E-01**	**2.38E-04**	1.00E+00	1.21E-03
Uqcc2_chr17	14	15	10	15	0.1	1.1	0.6	1.5	**6.99E-01**	**1.85E-03**	1.00E+00	7.31E-03
Uqcr10_chr11	29	29	16	31	0.0	1.0	0.9	1.9	**9.49E-01**	**5.00E-05**	1.00E+00	2.85E-04

Uqcr11_chr10	21	21	13	23	0.0	1.0	0.8	1.8	9.06E-01	5.00E-05	1.00E+00	2.85E-04
Uqcrh_chr4	113	115	67	109	0.0	1.0	0.7	1.6	9.22E-01	5.00E-05	1.00E+00	2.85E-04
Uqcrq_chr11	21	20	15	29	-0.1	1.0	0.9	1.9	8.31E-01	5.00E-05	1.00E+00	2.85E-04
Usmg5_chr19	33	31	16	52	-0.1	1.1	1.7	3.2	8.10E-01	5.00E-05	1.00E+00	2.85E-04
Usp1_chr4	19	19	31	55	0.0	1.0	0.8	1.8	9.21E-01	5.00E-05	1.00E+00	2.85E-04
Usp14_chr18	9	10	12	21	0.1	1.1	0.7	1.7	6.24E-01	2.25E-04	1.00E+00	1.15E-03
Usp15_chr10	24	23	39	97	0.0	1.0	1.3	2.5	9.24E-01	5.00E-05	1.00E+00	2.85E-04
Usp18_chr6	3	4	3	20	0.7	1.6	2.6	5.9	6.42E-02	5.00E-05	8.76E-01	2.85E-04
Usp25_chr16	24	29	50	83	0.3	1.2	0.7	1.7	1.96E-01	5.00E-05	9.87E-01	2.85E-04
Usp32_chr11	9	9	17	45	0.0	1.0	1.4	2.7	9.99E-01	5.00E-05	1.00E+00	2.85E-04
Usp49_chr17	2	2	3	9	0.1	1.1	1.5	2.8	6.96E-01	5.00E-05	1.00E+00	2.85E-04
Uxt_chrX	5	5	3	5	0.1	1.0	0.7	1.6	8.83E-01	2.04E-02	1.00E+00	5.69E-02
Vamp8_chr6	42	45	31	56	0.1	1.1	0.9	1.8	7.25E-01	5.00E-05	1.00E+00	2.85E-04
Vangl1_chr3	1	1	2	4	0.3	1.3	1.0	2.0	3.17E-01	5.00E-05	1.00E+00	2.85E-04
Vbp1_chrX	35	38	39	65	0.1	1.1	0.7	1.7	6.61E-01	5.00E-05	1.00E+00	2.85E-04
Vill_chr9	1	1	1	2	0.0	1.0	1.2	2.3	3.93E-01	5.00E-05	9.98E-01	2.85E-04
Vkorc1l1_chr5	7	7	8	13	-0.1	1.1	0.7	1.6	6.99E-01	2.39E-02	1.00E+00	5.79E-02
Vnn3_chr10	1	1	2	3	0.0	1.0	1.0	2.0	9.94E-01	5.00E-05	1.00E+00	2.85E-04
Vps35_chr8	34	32	55	90	-0.1	1.1	0.7	1.6	7.03E-01	1.00E-04	1.00E+00	5.44E-04
Vrk2_chr11	11	12	14	25	0.1	1.1	0.9	1.8	7.67E-01	5.00E-05	1.00E+00	2.85E-04
Vwf_chr6	2	3	6	13	0.7	1.6	1.1	2.1	1.11E-02	5.00E-05	4.89E-01	2.85E-04
Wapal_chr14	25	25	49	79	0.0	1.0	0.7	1.6	8.66E-01	5.00E-05	1.00E+00	2.85E-04
Wbp5_chrX	20	20	15	29	0.0	1.0	0.9	1.9	9.43E-01	5.00E-05	1.00E+00	2.85E-04
Wdr26_chr1	35	35	58	91	0.0	1.0	0.7	1.6	9.87E-01	5.50E-04	1.00E+00	2.52E-03
Wdr60_chr12	1	1	2	4	0.2	1.1	0.8	1.8	6.88E-01	5.00E-05	1.00E+00	2.85E-04
Wdr76_chr2	5	5	8	14	0.1	1.1	0.9	1.9	6.38E-01	5.00E-05	1.00E+00	2.85E-04
Wdr90_chr17	2	3	5	11	0.1	1.1	1.1	2.1	7.73E-01	5.00E-05	1.00E+00	2.85E-04
Wee1_chr7	3	3	5	9	0.0	1.0	1.0	2.0	9.91E-01	5.00E-05	1.00E+00	2.85E-04
Whrn_chr4	1	5	1	7	2.2	4.5	2.3	4.9	8.93E-08	5.00E-05	4.02E-05	2.61E-04
Whsc1_chr5	4	4	7	15	0.1	1.0	1.1	2.1	5.85E-01	2.98E-03	1.00E+00	9.92E-03
Wnk4_chr11	1	1	1	2	0.0	1.0	0.9	1.9	5.41E-01	5.00E-05	1.00E+00	2.85E-04
Xaf1_chr11	2	3	2	6	0.3	1.3	1.3	2.4	3.55E-01	5.00E-05	9.98E-01	2.85E-04
Xcl1_chr1	2	3	1	3	0.2	1.1	1.2	2.3	7.61E-01	2.00E-04	1.00E+00	1.02E-03
Xpnpep1_chr19	9	11	19	35	0.3	1.2	0.9	1.9	2.07E-01	5.00E-05	9.88E-01	2.85E-04
Xrcc6_chr15	10	12	13	20	0.3	1.2	0.6	1.5	3.08E-01	5.00E-05	9.97E-01	2.85E-04
Yars_chr4	8	11	15	24	0.5	1.5	0.7	1.6	2.69E-02	5.00E-05	7.02E-01	2.85E-04
Ydjc_chr16	1	1	2	3	0.3	1.3	0.8	1.8	5.30E-01	5.50E-04	1.00E+00	2.52E-03
Yipf4_chr17	16	20	19	35	0.3	1.2	0.9	1.8	1.71E-01	5.00E-05	9.80E-01	2.85E-04
Yod1_chr1	5	4	8	16	-0.3	1.2	1.0	2.0	5.03E-01	4.50E-04	1.00E+00	2.12E-03
Ypel5_chr17	15	17	15	23	0.2	1.1	0.6	1.5	3.60E-01	5.00E-05	9.98E-01	2.85E-04
Zak_chr2	2	2	3	4	-0.2	1.1	0.8	1.8	7.40E-01	1.34E-02	1.00E+00	3.70E-02
Zbp1_chr2	7	7	7	25	0.2	1.1	1.9	3.9	6.74E-01	5.00E-05	1.00E+00	2.85E-04
Zbtb45_chr7	2	3	6	9	0.5	1.4	0.6	1.6	1.68E-01	5.00E-05	9.80E-01	2.85E-04
Zcchc3_chr2	1	2	2	3	0.4	1.3	0.9	1.9	3.36E-01	5.00E-05	9.98E-01	2.85E-04
Zcrb1_chr15	10	11	8	12	0.1	1.1	0.6	1.5	7.51E-01	2.50E-04	1.00E+00	1.25E-03
Zdhhc14_chr17	3	3	6	9	0.2	1.2	0.6	1.6	5.28E-01	5.00E-05	1.00E+00	2.85E-04
Zdhhc24_chr19	4	5	4	6	0.2	1.2	0.6	1.5	5.66E-01	4.25E-02	1.00E+00	1.03E-01
Zfand6_chr7	39	43	39	65	0.1	1.1	0.7	1.7	4.88E-01	5.00E-05	1.00E+00	2.85E-04
Zfp101_chr17	5	5	6	10	-0.1	1.1	0.7	1.7	7.43E-01	5.00E-05	1.00E+00	2.85E-04
Zfp367_chr13	8	7	11	25	-0.1	1.1	1.2	2.3	5.42E-01	5.00E-05	1.00E+00	2.85E-04
Zfp39_chr11	3	4	6	9	0.1	1.1	0.7	1.6	6.91E-01	5.00E-05	1.00E+00	2.85E-04
Zfp534_chr4	0	4	0	6	1.9	3.8	2.6	6.0	3.95E-14	5.00E-05	9.74E-11	2.85E-04
Zfp808_chr13	4	3	5	16	-0.4	1.4	1.8	3.4	1.44E-01	5.00E-05	9.67E-01	2.85E-04
Zfp933_chr4	4	5	5	9	0.3	1.2	0.7	1.6	2.50E-01	5.00E-05	9.92E-01	2.85E-04
Zfp934_chr13	2	1	2	4	-0.4	1.3	1.3	2.4	4.49E-01	5.00E-05	1.00E+00	2.85E-04
Zfp947_chr17	1	1	1	2	-0.1	1.1	0.7	1.6	8.46E-01	7.50E-04	1.00E+00	3.33E-03
Zfp951_chr5	3	2	3	6	-0.6	1.5	1.0	2.0	1.19E-01	5.00E-05	9.48E-01	2.85E-04
Zgrf1_chr3	1	1	3	6	0.0	1.0	1.2	2.3	9.54E-01	5.00E-05	1.00E+00	2.85E-04
Zmynd19_chr2	6	6	9	14	0.1	1.1	0.7	1.6	7.08E-01	5.00E-05	1.00E+00	2.85E-04
Znhit3_chr11	5	4	4	8	-0.3	1.2	1.0	2.0	6.60E-01	1.79E-02	1.00E+00	5.09E-02
Zranb3_chr1	2	2	3	5	0.3	1.2	0.9	1.9	4.58E-01	5.00E-05	1.00E+00	2.85E-04
Zwint_chr10	9	9	13	22	0.0	1.0	0.8	1.7	9.30E-01	5.00E-05	1.00E+00	2.85E-04
2210010C04Rik_chr6	2	1	2	61	-1.1	2.2	5.3	40.3	3.13E-02	5.00E-05	6.37E-01	2.85E-04
Cd300e_chr11	4	4	6	9	0.2	1.1	0.6	1.5	6.16E-01	1.50E-04	1.00E+00	7.89E-04
Cel_chr2	3	1	4	65	-1.4	2.6	4.1	16.6	1.64E-02	5.00E-05	4.81E-01	2.85E-04
Cela1_chr15	13	7	11	160	-0.9	1.8	3.9	14.5	1.88E-02	5.00E-05	5.03E-01	2.85E-04
Cela3b_chr4	3	1	2	63	-1.4	2.7	4.8	27.3	6.57E-02	5.00E-05	7.70E-01	2.85E-04
Clps_chr17	7	2	4	104	-2.1	4.4	4.6	24.2	5.75E-03	5.00E-05	2.70E-01	2.85E-04
Cpa1_chr6	3	1	3	68	-1.2	2.3	4.7	25.5	3.52E-02	5.00E-05	6.58E-01	2.85E-04
Cpa2_chr6	1	0	1	17	0.0	1.0	4.1	17.3	1.87E-01	5.00E-05	9.45E-01	2.85E-04
Cpb1_chr3	4	1	4	112	-1.9	3.6	4.7	26.9	1.97E-03	5.00E-05	1.38E-01	2.85E-04
Ctrb1_chr8	8	3	6	258	-1.3	2.4	5.4	42.7	1.46E-02	5.00E-05	4.43E-01	2.85E-04
Ctrl_chr8	3	1	2	51	-1.6	3.0	4.4	21.4	2.06E-02	5.00E-05	5.28E-01	2.85E-04
Cyp4f37_chr17	1	2	1	4	0.6	1.6	1.6	3.1	5.04E-03	5.00E-05	3.50E-01	2.85E-04
Gm8221_chr15	0	3	0	3	1.4	2.6	1.8	3.4	1.00E-20	5.00E-05	1.00E-20	2.82E-04
Gp2_chr7	1	1	2	24	-0.6	1.5	3.6	12.5	7.69E-02	5.00E-05	9.03E-01	2.85E-04
Klk1_chr7	2	1	1	24	-0.9	1.8	4.1	17.7	1.91E-01	5.00E-05	9.86E-01	2.85E-04
Klre1_chr6	1	2	1	3	0.6	1.5	1.5	2.8	2.76E-01	5.00E-05	9.94E-01	2.85E-04
Pnlip_chr19	8	3	8	213	-1.4	2.7	4.8	27.9	2.32E-03	5.00E-05	1.54E-01	2.85E-04
Pnliprp1_chr19	3	1	2	65	-1.3	2.5	4.8	27.2	2.82E-02	5.00E-05	6.10E-01	2.85E-04
Pnliprp2_chr19	0	0	0	11	0.0	1.0	3.4	10.9	1.96E-01	5.00E-05	9.48E-01	2.85E-04

Prss2_chr6	8	3	4	107	-1.6	3.1	4.6	24.7	**4.50E-03**	**5.00E-05**	2.50E-01	2.85E-04
Reg1_chr6	2	1	1	88	-0.8	1.8	6.5	87.7	**2.92E-01**	**5.00E-05**	9.83E-01	2.85E-04
Rnase1_chr14	3	1	2	41	-1.4	2.6	4.7	26.1	**6.54E-02**	**5.00E-05**	7.70E-01	2.85E-04
Spink3_chr18	1	0	0	16	0.0	1.0	4.0	15.9	**2.52E-01**	**5.00E-05**	9.92E-01	2.85E-04
Sycn_chr7	4	1	1	29	-1.7	3.1	4.3	20.0	**4.64E-02**	**5.00E-05**	7.18E-01	2.85E-04
Try4_chr6	0	0	0	58	0.0	1.0	5.8	57.5	**1.65E-01**	**5.00E-05**	1.00E+00	2.85E-04
Try5_chr6	1	1	1	62	-0.1	1.1	5.9	61.8	**8.11E-01**	**5.00E-05**	1.00E+00	2.85E-04
Zg16_chr7	2	1	1	36	-0.8	1.8	5.2	35.9	**2.91E-01**	**5.00E-05**	9.82E-01	2.85E-04

Supplemental Table 2: Transcripts down-regulated in spleens from Triple KO mice compared to spleens from WT mice

Shown are a total of 991 transcripts that were down-regulated in Triple KO mice spleens as compared to WT spleens in the RNA-Seq dataset. The symbols and abbreviations used are the same as described in the legend to Supplemental Table 1.

GeneChrom	WT_v1	DoubleKO	WT_v2	TripleKO	floorLog2FC DoubleKO vsWT	Fold Change DoubleKO vs WT	floorLog2FC TripleKO vsWT	Fold Change TripleKO vs WT	p_value DoubleKO vsWT	p_value TripleKO vsWT	q_value DoubleKO vsWT	q_value TripleKO vsWT
Akr1c12_chr13	2	1	2	1	-0.4	1.3	-0.7	1.6	4.64E-01	3.25E-03	1.00E+00	1.19E-02
Alox5_chr6	17	1	37	6	-4.1	16.9	-2.6	5.9	1.00E-20	5.00E-05	1.00E-20	2.85E-04
Bmper_chr9	1	1	2	1	-0.2	1.2	-1.0	2.0	3.93E-01	5.00E-05	1.00E+00	2.85E-04
Ccdc122_chr14	4	3	5	2	-0.7	1.6	-1.2	2.3	8.48E-02	5.00E-05	8.21E-01	2.85E-04
Cyp26b1_chr6	1	0	2	1	0.0	1.0	-0.7	1.7	2.96E-02	5.00E-05	7.33E-01	2.85E-04
Lox_chr18	2	2	3	2	-0.1	1.1	-0.8	1.8	7.47E-01	5.00E-05	1.00E+00	2.85E-04
Lpl_chr8	12	12	18	9	0.0	1.0	-1.1	2.1	8.88E-01	5.00E-05	1.00E+00	2.85E-04
Rgs4_chr1	2	1	2	1	-0.8	1.7	-1.2	2.4	9.38E-04	5.00E-05	1.17E-01	2.85E-04
Serpine2_chr1	5	5	8	5	0.0	1.0	-0.6	1.5	9.13E-01	5.00E-05	1.00E+00	2.85E-04
Zbtb16_chr9	1	1	3	2	-0.5	1.4	-1.0	2.0	4.68E-03	5.00E-05	2.52E-01	2.85E-04
1110059E24Rik_chr19	60	52	55	24	-0.2	1.2	-1.2	2.3	3.01E-01	5.00E-05	9.85E-01	2.85E-04
1700009J07Rik_chr10	1	0	2	1	-0.1	1.1	-0.8	1.7	3.66E-02	2.50E-04	7.60E-01	1.24E-03
1700019G17Rik_chr6	2	2	3	2	0.3	1.3	-0.7	1.6	4.19E-01	8.88E-04	1.00E+00	3.07E-03
1700021K19Rik_chr16	27	32	65	39	0.2	1.2	-0.7	1.7	3.33E-01	5.00E-05	9.98E-01	2.85E-04
1810046K07Rik_chr9	2	1	2	1	-0.3	1.2	-1.1	2.2	5.45E-01	5.00E-05	1.00E+00	2.85E-04
2410089E03Rik_chr15	3	3	6	4	-0.1	1.1	-0.6	1.6	6.60E-01	5.00E-05	1.00E+00	2.85E-04
2410131K14Rik_chr5	4	4	8	5	0.2	1.1	-0.6	1.6	6.05E-01	1.00E-04	1.00E+00	5.44E-04
2610002J02Rik_chr4	6	7	9	5	0.1	1.1	-0.7	1.6	7.30E-01	1.08E-02	1.00E+00	3.23E-02
2610034B18Rik_chr7	2	2	4	3	-0.2	1.1	-0.7	1.6	6.49E-01	3.50E-04	1.00E+00	1.69E-03
2610035D17Rik_chr11	6	3	8	2	-1.3	2.4	-1.7	3.4	6.99E-04	5.00E-05	6.77E-02	2.82E-04
2900052N01Rik_chr9	16	11	17	6	-0.6	1.5	-1.4	2.7	1.56E-02	5.00E-05	4.66E-01	2.82E-04
3830403N18Rik_chrX	3	1	2	0	-1.5	2.8	-1.0	1.9	1.74E-04	5.00E-05	3.38E-02	2.85E-04
4930481A15Rik_chr19	4	1	5	1	-1.8	3.6	-2.3	4.9	2.33E-01	4.45E-03	9.83E-01	1.45E-02
4930523C07Rik_chr1	31	29	18	6	-0.2	1.2	-1.6	3.0	5.23E-01	2.15E-03	1.00E+00	9.41E-03
4932438A13Rik_chr3	15	12	29	19	-0.3	1.3	-0.6	1.5	1.39E-01	2.50E-04	8.88E-01	1.25E-03
4933439K11Rik_chr1	1	1	2	1	-0.2	1.1	-1.2	2.3	7.57E-01	3.50E-03	1.00E+00	1.26E-02
5430435G22Rik_chr1	8	4	10	5	-1.1	2.1	-0.9	1.9	3.00E-04	5.00E-05	5.34E-02	2.85E-04
6330403A02Rik_chr1	1	1	2	1	0.0	1.0	-0.6	1.5	6.29E-01	5.00E-05	1.00E+00	2.85E-04
9030624G23Rik_chr12	1	1	2	1	-0.2	1.2	-0.6	1.6	3.87E-01	3.45E-03	1.00E+00	1.26E-02
9430020K01Rik_chr18	4	3	9	6	-0.1	1.1	-0.6	1.5	5.77E-01	5.00E-05	1.00E+00	2.85E-04
9930014A18Rik_chr15	1	1	2	1	0.0	1.0	-0.8	1.8	8.34E-01	6.55E-03	1.00E+00	2.17E-02
A530099J19Rik_chr13	9	4	13	5	-1.3	2.5	-1.5	2.9	3.03E-06	5.00E-05	6.74E-04	2.85E-04
Abca5_chr11	1	1	2	1	-0.1	1.1	-1.0	2.0	6.87E-01	5.00E-05	1.00E+00	2.85E-04
Abca8a_chr11	5	4	8	4	-0.3	1.2	-1.1	2.1	2.29E-01	5.00E-05	9.91E-01	2.85E-04
Abca8b_chr11	1	1	2	1	-0.1	1.0	-1.0	2.0	3.80E-01	5.00E-05	1.00E+00	2.85E-04
Abi3bp_chr16	4	4	5	2	-0.2	1.1	-1.5	2.8	6.24E-01	5.00E-05	1.00E+00	3.08E-04
Ablim1_chr19	40	46	72	40	0.2	1.2	-0.9	1.8	5.17E-01	3.03E-03	1.00E+00	1.12E-02
Acad10_chr5	2	2	5	3	0.1	1.1	-0.8	1.7	7.09E-01	5.00E-05	1.00E+00	2.85E-04
Ace_chr11	5	4	12	7	-0.4	1.4	-0.7	1.7	1.03E-01	5.00E-05	9.33E-01	2.85E-04
Acta2_chr19	29	33	41	15	0.2	1.1	-1.5	2.8	3.60E-01	5.00E-05	9.98E-01	2.85E-04
Actg2_chr6	3	3	4	1	-0.1	1.1	-1.8	3.4	8.00E-01	5.00E-05	1.00E+00	2.85E-04
Adam19_chr11	20	21	44	22	0.1	1.0	-1.0	2.0	7.55E-01	5.00E-05	1.00E+00	2.85E-04
Adam28_chr14	1	1	2	1	-0.1	1.1	-0.9	1.9	3.54E-01	5.00E-05	1.00E+00	2.61E-04
Adck3_chr1	6	7	16	9	0.4	1.3	-0.8	1.7	5.12E-01	9.78E-03	1.00E+00	2.84E-02
Adcy5_chr16	2	2	6	3	0.1	1.1	-1.2	2.4	6.59E-01	5.00E-05	1.00E+00	2.85E-04
Adcy7_chr8	43	42	79	49	0.0	1.0	-0.7	1.6	8.86E-01	2.34E-02	1.00E+00	6.24E-02
Aff4_chr11	19	18	36	22	-0.1	1.0	-0.7	1.6	8.17E-01	1.00E-04	1.00E+00	5.44E-04
Afp_chr5	1	2	2	1	0.2	1.2	-0.7	1.6	6.15E-01	1.35E-03	1.00E+00	5.55E-03
Ago1_chr4	17	18	38	20	0.0	1.0	-0.9	1.9	9.21E-01	5.00E-05	1.00E+00	2.85E-04
Ak1_chr2	2	3	3	2	0.3	1.2	-0.6	1.5	4.92E-01	7.69E-03	1.00E+00	2.42E-02
Akap12_chr10	8	11	19	10	0.5	1.4	-0.9	1.9	2.53E-02	5.00E-05	6.89E-01	2.85E-04
Akap2_chr4	6	6	12	7	0.3	1.2	-0.8	1.8	5.84E-01	4.72E-02	1.00E+00	9.50E-02
Akna_chr4	46	57	124	82	0.3	1.3	-0.6	1.5	1.59E-01	7.50E-04	9.20E-01	3.33E-03
Akt3_chr1	22	19	36	22	-0.2	1.2	-0.7	1.6	3.16E-01	5.00E-05	9.87E-01	2.85E-04
Aldoc_chr11	1	2	2	1	1.0	2.0	-0.6	1.5	3.50E-02	2.05E-03	7.69E-01	8.00E-03
Alkbh6_chr7	7	8	7	4	0.1	1.1	-0.7	1.6	7.33E-01	5.00E-04	1.00E+00	2.32E-03
Alpl_chr4	4	2	9	4	-0.7	1.7	-1.1	2.2	3.89E-02	5.00E-05	7.91E-01	2.85E-04
Als2cl_chr9	13	8	8	2	-0.9	1.8	-1.8	3.6	3.95E-03	3.43E-02	2.84E-01	9.63E-02
Amotl2_chr9	4	6	12	8	0.4	1.3	-0.6	1.5	1.65E-01	5.00E-05	9.80E-01	2.85E-04
Angel1_chr12	2	3	5	3	0.3	1.2	-0.7	1.6	3.57E-01	5.00E-05	9.98E-01	2.85E-04
Angpt2_chr8	4	3	6	2	-0.5	1.4	-1.6	2.9	1.79E-01	9.20E-03	9.84E-01	2.91E-02
Angptl2_chr2	18	12	38	17	-0.6	1.6	-1.1	2.2	6.05E-03	5.00E-05	2.81E-01	2.85E-04
Ank2_chr3	1	1	3	1	-0.2	1.1	-0.9	1.9	6.38E-01	5.00E-05	1.00E+00	2.85E-04
Ankrd33b_chr15	4	3	9	3	-0.6	1.5	-1.8	3.4	2.00E-02	5.00E-05	5.20E-01	2.85E-04
Ankrd44_chr1	29	34	56	33	0.2	1.2	-0.7	1.7	3.34E-01	5.00E-05	9.90E-01	2.85E-04
Anxa6_chr11	46	64	86	57	0.5	1.4	-0.6	1.5	1.09E-01	7.73E-03	9.14E-01	2.52E-02
Apbb1_chr7	1	2	2	1	0.5	1.4	-1.1	2.1	2.91E-01	5.00E-05	9.91E-01	2.70E-04
Arhgap20_chr9	1	1	2	1	0.3	1.2	-0.7	1.6	5.93E-02	5.00E-05	8.71E-01	2.85E-04
Arhgap24_chr5	6	7	11	7	0.2	1.2	-0.7	1.7	3.39E-01	5.00E-05	9.98E-01	2.85E-04
Arhgap42_chr9	2	1	3	2	-0.7	1.7	-0.7	1.6	4.30E-02	5.00E-05	8.14E-01	2.85E-04
Arhgef11_chr3	7	7	17	10	0.1	1.1	-0.7	1.6	6.26E-01	5.00E-05	1.00E+00	2.85E-04
Arhgef17_chr7	4	4	10	7	-0.1	1.0	-0.6	1.5	8.16E-01	1.00E-04	1.00E+00	5.44E-04
Arhgef18_chr8	36	38	86	44	0.1	1.0	-0.9	1.9	8.01E-01	5.00E-05	1.00E+00	2.85E-04
Arhgef3_chr14	33	42	58	36	0.4	1.3	-0.7	1.6	8.90E-02	5.00E-05	9.27E-01	2.85E-04
Arid1b_chr17	9	11	25	15	0.3	1.3	-0.7	1.6	1.23E-01	5.00E-05	9.50E-01	2.85E-04
Arid3b_chr9	14	16	24	16	0.2	1.2	-0.6	1.5	2.65E-01	5.00E-05	9.94E-01	2.85E-04

Arl4c_chr1	21	23	36	19	0.1	1.1	-0.9	1.8	**7.12E-01**	**5.00E-05**	1.00E+00	2.85E-04
Arl4d_chr11	4	4	5	3	-0.1	1.1	-1.1	2.1	**7.67E-01**	**5.00E-05**	1.00E+00	2.85E-04
Arl5c_chr11	22	23	24	10	0.0	1.0	-1.3	2.4	**8.80E-01**	**5.00E-05**	1.00E+00	2.85E-04
Arnt2_chr7	1	2	3	2	0.3	1.2	-0.9	1.9	**4.34E-01**	**5.00E-05**	1.00E+00	2.85E-04
Aspn_chr13	1	0	2	1	-0.3	1.2	-0.6	1.5	**8.13E-02**	**2.86E-02**	9.10E-01	7.25E-02
Ass1_chr2	7	8	14	9	0.2	1.1	-0.7	1.6	**6.09E-01**	**1.80E-03**	1.00E+00	7.14E-03
Atn1_chr6	11	13	25	17	0.2	1.2	-0.6	1.5	**2.62E-01**	**1.00E-04**	9.94E-01	5.44E-04
Atoh8_chr6	2	2	4	2	0.3	1.2	-0.7	1.6	**4.63E-01**	**1.50E-04**	1.00E+00	7.89E-04
Atp10d_chr5	16	18	24	10	0.2	1.1	-1.3	2.5	**1.00E+00**	**1.17E-02**	1.00E+00	3.47E-02
Atp1a2_chr1	1	1	3	1	-0.2	1.1	-1.5	2.8	**6.10E-01**	**5.00E-05**	1.00E+00	2.85E-04
Axin2_chr11	2	3	5	3	0.4	1.3	-0.7	1.6	**2.59E-01**	**5.00E-05**	9.93E-01	2.85E-04
B3glct_chr5	4	3	7	4	-0.3	1.3	-0.6	1.5	**2.23E-01**	**1.50E-04**	9.91E-01	7.89E-04
B3gnt2_chr11	21	26	33	23	0.3	1.2	-0.6	1.5	**2.91E-01**	**2.27E-02**	9.88E-01	6.00E-02
B3gnt5_chr16	17	18	25	15	0.1	1.1	-0.8	1.7	**6.76E-01**	**9.03E-03**	1.00E+00	2.70E-02
B4galnt1_chr10	24	32	7	1	0.5	1.4	-2.4	5.3	**3.70E-01**	**4.91E-02**	9.67E-01	1.30E-01
Bank1_chr3	99	125	162	81	0.3	1.3	-1.0	2.0	**1.66E-01**	**5.00E-05**	9.80E-01	2.85E-04
BC017612_chr9	5	6	5	3	0.1	1.1	-0.8	1.7	**7.79E-01**	**1.00E-04**	1.00E+00	5.44E-04
Bcar3_chr3	20	26	42	26	0.3	1.3	-0.7	1.6	**1.02E-01**	**5.00E-05**	9.38E-01	2.85E-04
Bcl11b_chr12	3	4	7	3	0.1	1.1	-1.1	2.2	**8.26E-01**	**5.00E-05**	1.00E+00	2.92E-04
Bcl2l14_chr6	1	1	2	1	-0.1	1.0	-0.6	1.5	**4.64E-01**	**3.15E-03**	1.00E+00	1.16E-02
Bcl7a_chr5	13	14	23	15	0.0	1.0	-0.7	1.6	**8.59E-01**	**5.00E-05**	1.00E+00	2.85E-04
Bend5_chr4	6	6	8	5	0.1	1.1	-0.7	1.7	**7.02E-01**	**3.32E-03**	1.00E+00	1.20E-02
Bend6_chr1	1	1	2	1	-0.2	1.1	-0.7	1.7	**6.77E-01**	**1.10E-03**	1.00E+00	4.65E-03
Birc3_chr9	55	62	89	55	0.2	1.1	-0.7	1.6	**4.19E-01**	**5.00E-05**	1.00E+00	2.85E-04
Blk_chr14	84	104	143	89	0.3	1.2	-0.7	1.6	**1.70E-01**	**5.00E-05**	9.80E-01	2.85E-04
Blnk_chr19	52	73	81	51	0.5	1.4	-0.7	1.6	**1.72E-02**	**5.00E-05**	5.91E-01	2.85E-04
Bmf_chr2	11	11	21	12	0.0	1.0	-0.9	1.8	**9.37E-01**	**5.00E-05**	1.00E+00	2.85E-04
Bptf_chr11	17	19	36	23	0.1	1.1	-0.7	1.6	**5.59E-01**	**5.00E-05**	1.00E+00	2.85E-04
Btbd11_chr10	1	1	3	2	0.0	1.0	-0.7	1.7	**8.34E-01**	**5.00E-05**	1.00E+00	2.85E-04
Btg1_chr10	74	99	94	62	0.4	1.3	-0.6	1.5	**8.90E-02**	**4.50E-04**	9.27E-01	2.12E-03
Btnl2_chr17	3	3	4	2	0.2	1.1	-0.8	1.7	**6.18E-01**	**5.00E-05**	1.00E+00	2.85E-04
C130074G19Rik_chr1	3	4	4	2	0.5	1.4	-0.7	1.7	**1.43E-01**	**5.00E-05**	9.67E-01	2.85E-04
C1s2_chr6	3	0	4	0	-1.3	2.5	-2.1	4.2	**7.20E-11**	**5.00E-05**	1.23E-07	2.85E-04
Cables2_chr2	15	18	25	14	0.3	1.2	-0.8	1.8	**1.89E-01**	**5.00E-05**	9.86E-01	2.85E-04
Cacna1a_chr8	1	0	2	0	0.0	1.0	-0.6	1.5	**5.33E-02**	**5.00E-05**	8.48E-01	2.61E-04
Cacna2d1_chr5	1	1	2	1	-0.2	1.2	-0.7	1.6	**1.96E-01**	**5.00E-04**	9.74E-01	2.35E-03
Cacnb1_chr11	2	2	4	2	-0.2	1.1	-0.9	1.9	**6.88E-01**	**4.00E-04**	1.00E+00	1.93E-03
Cacnb3_chr15	4	4	7	5	-0.1	1.1	-0.6	1.5	**7.54E-01**	**9.00E-04**	1.00E+00	3.95E-03
Cadm1_chr9	9	6	7	2	-0.8	1.8	-2.0	4.1	**5.01E-02**	**5.00E-05**	7.55E-01	3.08E-04
Cald1_chr6	27	26	42	27	-0.1	1.1	-0.7	1.6	**6.95E-01**	**5.00E-05**	1.00E+00	2.85E-04
Calhm2_chr19	13	19	25	16	0.5	1.4	-0.6	1.6	**2.18E-02**	**5.00E-05**	6.58E-01	2.85E-04
Camk4_chr18	2	2	4	2	-0.4	1.3	-0.9	1.8	**9.21E-02**	**5.00E-05**	9.27E-01	2.85E-04
Car3_chr3	2	1	2	1	-0.7	1.6	-1.2	2.3	**9.76E-02**	**5.00E-05**	8.43E-01	2.85E-04
Card11_chr5	31	40	69	39	0.4	1.3	-0.8	1.8	**8.13E-02**	**5.00E-05**	9.10E-01	2.85E-04
Carns1_chr19	13	14	22	12	0.1	1.1	-0.8	1.7	**5.46E-01**	**5.00E-05**	1.00E+00	2.85E-04
Casz1_chr4	1	2	3	2	0.3	1.3	-0.6	1.6	**3.88E-01**	**7.98E-03**	1.00E+00	2.45E-02
Cbx7_chr15	18	19	29	17	0.1	1.1	-0.8	1.7	**5.55E-01**	**5.00E-05**	1.00E+00	2.85E-04
Cc2d2a_chr5	1	1	2	2	-0.2	1.2	-0.6	1.6	**5.29E-01**	**1.50E-04**	1.00E+00	7.89E-04
Ccdc109b_chr3	2	1	2	1	-0.5	1.4	-0.8	1.7	**3.73E-01**	**5.00E-05**	1.00E+00	2.85E-04
Ccdc61_chr7	5	4	8	3	-0.2	1.1	-1.5	2.8	**6.03E-01**	**5.00E-05**	1.00E+00	2.85E-04
Ccdc64_chr5	4	4	10	6	-0.2	1.1	-0.8	1.8	**5.77E-01**	**5.00E-05**	1.00E+00	2.85E-04
Ccl19_chr4	65	56	68	24	-0.2	1.2	-1.5	2.8	**3.31E-01**	**5.00E-05**	1.00E+00	2.97E-04
Ccl19_chr4_JH584294_ra	65	56	68	24	-0.2	1.2	-1.5	2.8	**3.31E-01**	**5.00E-05**	9.90E-01	2.49E-04
Ccl21a_chr4	61	28	62	32	-1.1	2.1	-0.9	1.9	**1.18E-05**	**5.00E-05**	3.78E-03	2.92E-04
Ccnj_chr19	8	8	11	7	0.1	1.0	-0.7	1.6	**8.12E-01**	**5.00E-05**	1.00E+00	2.85E-04
Ccr9_chr9	3	2	3	1	-0.4	1.3	-1.1	2.1	**2.72E-01**	**1.97E-02**	9.97E-01	4.47E-02
Cd180_chr13	53	62	87	50	0.2	1.2	-0.8	1.7	**2.55E-01**	**5.00E-05**	9.92E-01	2.85E-04
Cd207_chr6	8	2	10	3	-1.7	3.2	-1.8	3.6	**1.28E-05**	**5.00E-05**	3.53E-03	2.85E-04
Cd209b_chr8	6	3	13	5	-1.0	2.0	-1.4	2.6	**3.10E-01**	**6.82E-03**	8.84E-01	2.06E-02
Cd209d_chr8	5	5	4	1	-0.1	1.0	-1.9	3.8	**8.83E-01**	**5.00E-05**	1.00E+00	2.85E-04
Cd247_chr1	21	17	28	15	-0.3	1.2	-0.9	1.9	**6.41E-01**	**4.54E-02**	1.00E+00	1.11E-01
Cd27_chr6	15	13	21	13	-0.2	1.2	-0.7	1.7	**5.71E-01**	**9.43E-03**	1.00E+00	2.99E-02
Cd28_chr1	11	10	15	9	-0.1	1.0	-0.8	1.7	**7.94E-01**	**5.00E-05**	1.00E+00	2.85E-04
Cd300lg_chr11	4	4	7	3	0.1	1.1	-1.0	2.0	**7.76E-01**	**5.00E-05**	1.00E+00	2.85E-04
Cd37_chr7	205	287	263	151	0.5	1.4	-0.8	1.7	**3.45E-02**	**5.00E-05**	7.66E-01	2.85E-04
Cd3e_chr9	20	22	34	15	0.2	1.1	-1.2	2.3	**5.20E-01**	**5.00E-05**	1.00E+00	2.85E-04
Cd4_chr6	24	29	45	26	0.2	1.2	-0.8	1.7	**2.72E-01**	**5.00E-05**	9.94E-01	2.85E-04
Cd5_chr19	11	12	19	10	0.2	1.2	-0.9	1.9	**3.50E-01**	**5.00E-05**	9.98E-01	2.85E-04
Cd79b_chr11	303	410	333	149	0.4	1.4	-1.2	2.2	**7.84E-02**	**5.00E-05**	9.04E-01	2.85E-04
Cd84_chr1	29	24	8	2	-0.6	1.5	-1.8	3.4	**3.00E-01**	**6.75E-03**	9.65E-01	2.40E-02
Cd8a_chr6	12	11	20	10	-0.1	1.1	-1.0	2.0	**6.71E-01**	**2.00E-04**	1.00E+00	1.03E-03
Cd96_chr16	8	7	11	5	-0.2	1.2	-1.0	2.0	**4.39E-01**	**5.00E-05**	1.00E+00	2.85E-04
Cdc14b_chr13	3	3	4	3	-0.1	1.1	-0.6	1.5	**6.83E-01**	**8.88E-04**	1.00E+00	3.91E-03
Cdh11_chr8	6	6	11	6	0.1	1.0	-0.8	1.8	**8.28E-01**	**5.00E-05**	1.00E+00	2.85E-04
Cdh2_chr18	1	1	2	1	0.0	1.0	-0.7	1.6	**7.07E-01**	**5.00E-05**	1.00E+00	2.85E-04
Cdon_chr9	5	5	9	5	0.0	1.0	-0.9	1.9	**9.91E-01**	**5.00E-05**	1.00E+00	2.85E-04
Ceacam2_chr7	2	2	4	0	-0.4	1.3	-2.0	4.0	**1.00E+00**	**5.85E-03**	1.00E+00	1.84E-02
Cep162_chr9	6	6	9	6	0.0	1.0	-0.7	1.6	**8.92E-01**	**5.00E-05**	1.00E+00	2.85E-04
Cers4_chr8	8	9	12	8	0.2	1.2	-0.6	1.5	**3.31E-01**	**1.00E-04**	9.98E-01	5.44E-04
Ch25h_chr19	1	1	2	1	0.0	1.0	-0.7	1.6	**9.98E-01**	**2.50E-04**	1.00E+00	1.25E-03
Chd2_chr7	26	26	41	26	0.0	1.0	-0.6	1.5	**8.99E-01**	**5.50E-04**	1.00E+00	2.52E-03
Chd3_chr11	45	41	90	49	-0.1	1.1	-0.9	1.8	**5.61E-01**	**5.00E-05**	1.00E+00	2.85E-04
Chd6_chr2	12	11	24	15	-0.1	1.1	-0.7	1.6	**4.89E-01**	**5.00E-05**	1.00E+00	2.85E-04

Chst10_chr1	6	8	10	7	0.5	1.4	-0.7	1.6	**4.03E-02**	**5.00E-05**	6.89E-01	2.85E-04
Chst15_chr7	22	25	54	35	0.1	1.1	-0.6	1.5	**5.10E-01**	**5.00E-05**	1.00E+00	2.85E-04
Cilp_chr9	2	1	4	1	-0.7	1.6	-2.1	4.2	**7.71E-02**	**5.00E-05**	9.03E-01	2.85E-04
Clcf1_chr19	16	19	24	16	0.3	1.2	-0.6	1.5	**2.53E-01**	**4.50E-04**	9.92E-01	2.12E-03
Clcn5_chrX	2	2	4	2	-0.3	1.2	-0.8	1.8	**4.78E-01**	**1.85E-03**	1.00E+00	7.36E-03
Clec14a_chr12	5	4	8	4	-0.1	1.1	-0.8	1.7	**6.89E-01**	**5.00E-05**	1.00E+00	2.85E-04
Clec2i_chr6	28	23	34	19	-0.3	1.2	-0.9	1.8	**3.78E-01**	**4.25E-03**	1.00E+00	1.51E-02
Clec4g_chr8	12	8	14	6	-0.6	1.5	-1.3	2.5	**4.93E-02**	**5.00E-05**	8.46E-01	2.85E-04
Clec9a_chr6	6	3	7	2	-1.1	2.1	-1.7	3.3	**5.31E-02**	**5.00E-05**	4.13E-01	3.08E-04
Clip3_chr7	2	2	5	3	0.2	1.1	-0.6	1.5	**6.27E-01**	**5.00E-04**	1.00E+00	2.32E-03
Clmp_chr9	1	1	3	1	-0.2	1.2	-1.4	2.6	**5.97E-01**	**5.00E-05**	1.00E+00	2.85E-04
Clu_chr14	86	59	152	65	-0.5	1.5	-1.2	2.3	**9.12E-03**	**5.00E-05**	4.45E-01	2.85E-04
Cmtm4_chr8	5	4	10	7	-0.3	1.2	-0.6	1.6	**2.24E-01**	**5.00E-05**	9.64E-01	2.85E-04
Cnn3_chr3	39	49	58	28	0.3	1.3	-1.1	2.1	**1.04E-01**	**5.00E-05**	9.38E-01	2.85E-04
Cnp_chr11	52	68	88	52	0.4	1.3	-0.8	1.7	**7.24E-02**	**5.00E-05**	8.93E-01	2.85E-04
Cnr2_chr4	34	44	70	40	0.4	1.3	-0.8	1.7	**8.04E-02**	**5.00E-05**	9.08E-01	2.85E-04
Cobll1_chr2	4	6	9	5	0.6	1.5	-0.8	1.7	**8.30E-02**	**2.72E-02**	8.70E-01	6.23E-02
Coch_chr12	263	235	481	136	-0.1	1.0	-1.8	3.5	**6.30E-01**	**5.00E-05**	1.00E+00	2.85E-04
Col12a1_chr9	1	1	3	2	0.0	1.0	-0.7	1.6	**9.87E-01**	**1.00E-04**	1.00E+00	5.44E-04
Col16a1_chr4	3	3	6	4	-0.1	1.1	-0.6	1.6	**7.11E-01**	**5.00E-05**	1.00E+00	2.85E-04
Col27a1_chr4	3	2	5	3	-0.3	1.2	-0.8	1.7	**2.62E-01**	**5.00E-05**	9.94E-01	2.85E-04
Col4a5_chrX	1	1	2	1	0.0	1.0	-0.7	1.6	**7.13E-01**	**5.00E-05**	1.00E+00	2.72E-04
Col6a1_chr10	4	5	10	6	0.3	1.2	-0.7	1.6	**3.17E-01**	**5.00E-05**	9.97E-01	2.85E-04
Col6a4_chr9	1	7	2	1	2.9	7.3	-1.2	2.3	**1.00E-20**	**5.00E-05**	1.00E-20	2.85E-04
Col8a2_chr4	4	4	8	4	0.0	1.0	-1.1	2.1	**9.85E-01**	**5.00E-05**	1.00E+00	2.85E-04
Colq_chr14	4	4	7	4	-0.1	1.1	-0.8	1.7	**7.63E-01**	**5.00E-05**	1.00E+00	2.85E-04
Commd6_chr14	22	20	22	1	-0.2	1.1	-4.4	21.8	**5.52E-01**	**1.50E-04**	1.00E+00	8.53E-04
Cplx2_chr13	2	2	4	3	-0.2	1.1	-0.6	1.5	**6.37E-01**	**3.50E-04**	1.00E+00	1.69E-03
Cpxm2_chr7	3	3	5	3	0.2	1.1	-0.9	1.9	**5.90E-01**	**5.00E-05**	1.00E+00	2.85E-04
Cr2_chr1	145	179	226	127	0.3	1.2	-0.8	1.8	**3.54E-01**	**2.00E-04**	9.98E-01	1.02E-03
Crim1_chr17	13	15	29	14	0.2	1.2	-1.1	2.1	**2.88E-01**	**5.00E-05**	9.81E-01	2.85E-04
Cryab_chr9	2	2	3	2	0.3	1.2	-0.8	1.7	**5.24E-01**	**4.50E-04**	1.00E+00	2.12E-03
Csdc2_chr15	1	1	2	1	0.5	1.5	-0.8	1.8	**5.82E-02**	**1.00E-04**	8.69E-01	5.44E-04
Csmd1_chr8	1	1	2	1	0.0	1.0	-1.0	1.9	**6.07E-01**	**5.00E-05**	1.00E+00	2.85E-04
Csrnp2_chr15	2	2	3	2	0.0	1.0	-0.9	1.9	**9.36E-01**	**5.00E-05**	1.00E+00	2.85E-04
Csrp2_chr10	4	4	4	2	-0.2	1.1	-0.7	1.7	**7.27E-01**	**1.35E-03**	1.00E+00	5.55E-03
Ctgf_chr10	19	21	33	16	0.1	1.1	-1.0	2.0	**5.35E-01**	**5.00E-05**	1.00E+00	2.85E-04
Ctso_chr3	25	24	31	18	0.0	1.0	-0.8	1.7	**8.38E-01**	**5.00E-05**	1.00E+00	2.85E-04
Cx3cr1_chr9	6	8	12	8	0.5	1.4	-0.6	1.5	**5.55E-02**	**5.00E-05**	8.56E-01	2.85E-04
Cxcl13_chr5	65	26	59	18	-1.3	2.5	-1.8	3.4	**3.35E-09**	**5.00E-05**	3.59E-06	2.85E-04
Cxx1c_chrX	6	7	8	5	0.3	1.3	-0.6	1.5	**3.47E-01**	**1.05E-03**	9.98E-01	4.47E-03
Cxxc5_chr18	11	14	18	9	0.4	1.3	-1.0	1.9	**8.53E-02**	**5.00E-05**	9.18E-01	2.85E-04
Cybrd1_chr2	1	0	2	1	0.0	1.0	-0.8	1.7	**4.83E-02**	**5.00E-05**	8.46E-01	2.85E-04
Cyp2d22_chr15	3	3	5	3	0.3	1.3	-0.7	1.6	**3.47E-01**	**1.13E-04**	1.00E+00	6.13E-04
Cyp2r1_chr7	1	1	2	1	-0.1	1.1	-0.7	1.6	**7.83E-01**	**3.90E-03**	1.00E+00	1.39E-02
Cyp39a1_chr17	9	6	14	3	-0.5	1.4	-2.1	4.4	**4.21E-02**	**5.00E-05**	8.13E-01	2.85E-04
Cyr61_chr3	5	6	8	3	0.1	1.1	-1.5	2.8	**7.50E-01**	**5.00E-05**	1.00E+00	2.85E-04
D130040H23Rik_chr8	6	4	10	6	-0.5	1.5	-0.7	1.6	**9.10E-02**	**5.00E-05**	8.35E-01	2.85E-04
D430019H16Rik_chr12	2	2	3	2	-0.1	1.1	-0.9	1.9	**6.95E-01**	**5.00E-05**	1.00E+00	2.85E-04
D8Ertd82e_chr8	6	8	17	10	0.5	1.4	-0.7	1.6	**3.03E-02**	**5.00E-05**	7.39E-01	2.85E-04
Daam2_chr17	2	3	6	4	0.3	1.3	-0.7	1.6	**2.03E-01**	**5.00E-05**	9.87E-01	2.85E-04
Dag1_chr9	10	13	27	17	0.4	1.3	-0.7	1.6	**6.26E-02**	**5.00E-05**	7.70E-01	2.85E-04
Dapl1_chr2	14	3	7	0	-2.2	4.5	-2.9	7.5	**3.28E-06**	**5.00E-05**	1.12E-03	2.85E-04
Dbp_chr7	5	2	9	5	-1.3	2.4	-1.0	2.0	**2.59E-02**	**6.05E-03**	6.95E-01	2.04E-02
Dclk1_chr3	5	4	8	3	-0.2	1.2	-1.4	2.7	**4.39E-01**	**6.67E-05**	9.98E-01	3.86E-04
Ddr2_chr1	2	2	5	3	-0.2	1.2	-0.9	1.9	**3.48E-01**	**5.00E-05**	9.98E-01	2.85E-04
Dennd2a_chr6	4	4	10	6	-0.1	1.1	-0.8	1.7	**7.45E-01**	**5.00E-05**	1.00E+00	2.85E-04
Dennd3_chr15	15	18	34	23	0.2	1.2	-0.6	1.5	**3.12E-01**	**5.00E-05**	9.97E-01	2.85E-04
Des_chr1	16	22	35	19	0.5	1.4	-0.9	1.9	**3.91E-02**	**5.00E-05**	7.92E-01	2.85E-04
Dgka_chr10	77	77	122	58	0.0	1.0	-1.1	2.1	**9.48E-01**	**5.00E-05**	1.00E+00	2.85E-04
Dgkd_chr1	55	63	119	63	0.2	1.1	-0.9	1.9	**3.94E-01**	**5.00E-05**	1.00E+00	2.85E-04
Dgke_chr11	4	4	8	5	-0.3	1.2	-0.7	1.6	**2.76E-01**	**5.00E-05**	9.94E-01	2.85E-04
Diras2_chr13	1	1	2	1	0.5	1.4	-0.7	1.6	**2.07E-01**	**1.00E-04**	9.88E-01	5.44E-04
Dkk3_chr7	3	3	5	3	0.0	1.0	-0.6	1.5	**9.56E-01**	**1.00E-04**	1.00E+00	5.44E-04
Dlg2_chr7	1	1	2	1	0.0	1.0	-0.6	1.5	**7.93E-01**	**3.00E-04**	1.00E+00	1.29E-03
Dmd_chrX	2	1	3	2	-0.5	1.5	-0.8	1.8	**3.86E-02**	**5.00E-05**	7.89E-01	2.85E-04
Dnase1l3_chr14	36	35	62	37	-0.1	1.0	-0.7	1.7	**7.85E-01**	**5.00E-05**	1.00E+00	2.85E-04
Dnmbp_chr19	4	5	11	6	0.2	1.2	-0.8	1.8	**3.30E-01**	**5.00E-05**	9.90E-01	2.85E-04
Dntt_chr19	2	1	2	1	-0.6	1.5	-0.9	1.9	**3.49E-01**	**5.00E-05**	9.96E-01	2.85E-04
Dock10_chr1	45	49	90	57	0.1	1.1	-0.7	1.6	**5.90E-01**	**3.00E-04**	1.00E+00	1.47E-03
Dock11_chrX	28	28	56	37	0.0	1.0	-0.6	1.5	**9.82E-01**	**3.50E-04**	1.00E+00	1.69E-03
Dock2_chr11	65	87	138	90	0.4	1.3	-0.6	1.5	**7.56E-02**	**5.50E-04**	9.02E-01	2.52E-03
Dock8_chr19	31	39	79	49	0.3	1.2	-0.7	1.6	**1.82E-01**	**5.00E-05**	9.42E-01	2.85E-04
Dock9_chr14	3	3	6	3	0.0	1.0	-0.6	1.6	**7.21E-01**	**4.96E-02**	1.00E+00	1.04E-01
Dok2_chr14	16	10	22	12	-0.7	1.7	-0.9	1.8	**4.62E-03**	**5.00E-05**	2.52E-01	2.85E-04
Dopey1_chr9	7	7	14	9	0.0	1.0	-0.7	1.6	**9.06E-01**	**1.00E-04**	1.00E+00	5.44E-04
Dph5_chr3	17	17	19	11	0.1	1.0	-0.8	1.7	**7.85E-01**	**5.00E-05**	1.00E+00	2.85E-04
Dpyd_chr3	1	1	2	1	0.0	1.0	-0.6	1.5	**7.59E-01**	**5.00E-04**	1.00E+00	2.32E-03
Draxin_chr4	1	0	2	1	0.0	1.0	-0.9	1.9	**4.25E-04**	**5.00E-05**	6.84E-02	2.85E-04
Dsc2_chr18	2	0	4	1	-1.3	2.4	-2.2	4.5	**4.50E-11**	**5.00E-05**	3.69E-08	2.85E-04
Dsc3_chr18	1	0	2	1	0.0	1.0	-0.8	1.8	**2.75E-06**	**5.00E-05**	1.02E-03	2.85E-04
Dtx1_chr5	41	58	102	62	0.5	1.4	-0.7	1.6	**2.34E-02**	**1.00E-04**	6.69E-01	5.44E-04
Dusp10_chr1	5	5	8	4	-0.1	1.1	-1.1	2.2	**7.18E-01**	**5.00E-05**	1.00E+00	2.85E-04

Dusp16_chr6	9	9	18	10	-0.1	1.1	-0.9	1.8	**6.95E-01**	**5.00E-05**	1.00E+00	2.85E-04
Dusp2_chr2	18	25	28	17	0.4	1.4	-0.7	1.6	**5.25E-02**	**5.00E-05**	8.48E-01	2.85E-04
Dzip1l_chr9	1	1	2	1	-0.2	1.1	-1.2	2.2	**6.38E-01**	**5.00E-05**	1.00E+00	2.85E-04
E330009J07Rik_chr6	2	2	6	3	0.1	1.0	-0.8	1.8	**8.75E-01**	**5.00E-05**	1.00E+00	2.85E-04
Ece1_chr4	13	10	29	18	-0.3	1.3	-0.7	1.7	**1.09E-01**	**5.00E-05**	9.38E-01	2.85E-04
Ednrb_chr14	2	1	3	1	-0.1	1.1	-1.6	3.0	**7.44E-01**	**5.00E-05**	1.00E+00	2.70E-04
Efcc1_chr6	1	1	2	1	0.0	1.0	-0.6	1.5	**2.51E-01**	**1.60E-03**	9.92E-01	6.43E-03
Efnb2_chr8	3	4	7	4	0.2	1.1	-0.8	1.7	**5.14E-01**	**5.00E-05**	1.00E+00	2.85E-04
Ehbp1_chr11	2	2	3	2	0.0	1.0	-0.6	1.5	**9.88E-01**	**4.50E-04**	1.00E+00	1.95E-03
Ehd3_chr17	18	21	37	13	0.2	1.2	-1.5	2.9	**2.91E-01**	**5.00E-05**	9.96E-01	2.85E-04
Eif2ak3_chr6	14	16	28	16	0.2	1.2	-0.8	1.7	**3.05E-01**	**5.00E-05**	9.96E-01	2.85E-04
Elk3_chr10	14	17	25	17	0.2	1.2	-0.6	1.5	**2.68E-01**	**5.00E-05**	9.94E-01	2.85E-04
Ell3_chr2	28	31	37	17	0.1	1.1	-1.1	2.2	**5.82E-01**	**5.00E-05**	1.00E+00	2.85E-04
Eln_chr5	5	6	10	6	0.4	1.4	-0.7	1.6	**7.68E-02**	**5.00E-05**	9.03E-01	2.85E-04
Emid1_chr11	5	5	9	5	0.0	1.0	-0.7	1.7	**9.73E-01**	**5.00E-05**	1.00E+00	2.85E-04
Enah_chr1	1	1	2	2	-0.2	1.2	-0.7	1.6	**3.48E-01**	**5.00E-04**	1.00E+00	2.32E-03
Enc1_chr13	5	5	10	7	-0.1	1.1	-0.6	1.5	**7.16E-01**	**5.00E-05**	1.00E+00	2.85E-04
Enpp2_chr15	22	11	36	13	-1.0	2.0	-1.5	2.8	**7.97E-06**	**5.00E-05**	2.32E-03	2.97E-04
Entpd5_chr12	6	7	11	6	0.3	1.2	-0.9	1.8	**4.34E-01**	**4.00E-04**	9.94E-01	1.89E-03
Epha2_chr4	2	2	5	3	0.2	1.1	-0.6	1.6	**6.56E-01**	**5.00E-05**	1.00E+00	2.85E-04
Epha3_chr16	1	1	2	1	0.0	1.0	-1.2	2.3	**9.48E-01**	**5.00E-05**	1.00E+00	2.85E-04
Ephb6_chr6	2	2	5	2	-0.5	1.4	-1.6	3.1	**2.12E-01**	**5.00E-05**	9.89E-01	2.85E-04
Ephx1_chr1	36	49	59	35	0.4	1.3	-0.8	1.7	**4.70E-02**	**5.00E-05**	8.39E-01	2.85E-04
Epn2_chr11	5	5	10	6	0.0	1.0	-0.6	1.5	**9.31E-01**	**1.75E-04**	1.00E+00	9.25E-04
Erdr1_chrY	21	16	24	11	-0.4	1.3	-1.2	2.2	**1.56E-01**	**5.00E-05**	9.13E-01	2.85E-04
Ero1lb_chr13	24	30	39	24	0.3	1.3	-0.7	1.6	**1.08E-01**	**5.00E-05**	9.38E-01	2.85E-04
Errfi1_chr4	15	11	25	13	-0.5	1.4	-1.0	2.0	**4.14E-02**	**5.00E-05**	6.94E-01	2.85E-04
Esyt1_chr10	55	70	125	75	0.4	1.3	-0.7	1.7	**1.10E-01**	**5.00E-05**	9.38E-01	2.85E-04
Etv1_chr12	1	1	3	1	-0.4	1.3	-0.9	1.8	**3.50E-01**	**5.00E-05**	9.98E-01	2.85E-04
Etv3_chr3	18	22	37	24	0.3	1.2	-0.6	1.5	**2.82E-01**	**6.72E-03**	9.91E-01	1.99E-02
Etv5_chr16	5	4	10	7	-0.1	1.1	-0.6	1.5	**6.10E-01**	**5.00E-05**	1.00E+00	2.85E-04
Eya2_chr2	1	1	3	1	-0.3	1.2	-1.0	2.0	**5.06E-01**	**5.00E-05**	1.00E+00	2.85E-04
Ezr_chr17	68	99	129	84	0.5	1.4	-0.6	1.5	**1.70E-02**	**1.50E-04**	5.91E-01	7.89E-04
F2rl1_chr13	2	1	4	1	-0.8	1.8	-2.0	4.1	**4.32E-02**	**5.00E-05**	6.99E-01	2.85E-04
Fam101b_chr11	13	13	20	12	0.1	1.0	-0.7	1.6	**7.90E-01**	**5.00E-05**	1.00E+00	2.85E-04
Fam102a_chr2	21	24	50	29	0.2	1.2	-0.8	1.7	**3.15E-01**	**5.00E-05**	9.97E-01	2.85E-04
Fam115a_chr6	2	2	4	3	0.1	1.1	-0.6	1.6	**7.42E-01**	**1.50E-04**	1.00E+00	7.89E-04
Fam134b_chr15	13	15	21	13	0.1	1.0	-0.8	1.8	**4.50E-01**	**3.18E-03**	9.97E-01	1.14E-02
Fam13a_chr6	2	1	3	1	-0.5	1.4	-1.3	2.4	**2.33E-01**	**5.00E-05**	9.91E-01	2.85E-04
Fam149a_chr8	2	1	3	2	-0.4	1.3	-0.8	1.8	**2.34E-01**	**5.00E-05**	9.91E-01	2.85E-04
Fam167b_chr4	4	3	4	2	-0.6	1.5	-0.8	1.8	**1.85E-01**	**2.00E-04**	9.86E-01	1.02E-03
Fam169b_chr7	17	17	24	15	0.0	1.0	-0.7	1.6	**8.71E-01**	**5.00E-05**	1.00E+00	2.85E-04
Fam222a_chr5	1	1	2	1	0.1	1.1	-1.0	2.0	**5.12E-01**	**5.00E-05**	1.00E+00	2.85E-04
Fam26e_chr10	2	3	3	2	0.5	1.4	-0.8	1.7	**2.25E-01**	**5.00E-05**	9.91E-01	2.85E-04
Fam35a_chr14	5	4	7	5	-0.2	1.2	-0.6	1.6	**3.75E-01**	**1.00E-04**	1.00E+00	5.44E-04
Fam65b_chr13	34	40	69	37	0.2	1.2	-0.9	1.8	**4.59E-01**	**4.36E-04**	1.00E+00	1.99E-03
Fam84b_chr15	4	4	5	3	0.0	1.0	-0.8	1.8	**9.10E-01**	**5.00E-05**	1.00E+00	2.85E-04
Fat1_chr8	1	1	2	1	0.0	1.0	-0.7	1.6	**9.65E-01**	**5.00E-05**	1.00E+00	2.85E-04
Fat4_chr3	1	1	2	1	0.0	1.0	-0.6	1.5	**3.02E-01**	**5.00E-05**	9.86E-01	2.85E-04
Fbln1_chr15	2	1	4	2	-0.1	1.1	-0.7	1.6	**8.46E-01**	**5.00E-05**	1.00E+00	2.85E-04
Fbln5_chr12	9	14	16	9	0.7	1.6	-0.8	1.8	**1.68E-03**	**5.00E-05**	1.77E-01	2.85E-04
Fbxo21_chr5	5	6	11	7	0.2	1.2	-0.6	1.6	**3.50E-01**	**5.00E-05**	9.98E-01	2.85E-04
Fbxo32_chr15	4	4	7	4	0.2	1.1	-0.8	1.8	**4.81E-01**	**5.00E-05**	1.00E+00	2.85E-04
Fcamr_chr1	5	6	9	6	0.2	1.1	-0.6	1.5	**5.86E-01**	**1.00E-04**	1.00E+00	5.44E-04
Fcrl5_chr3	14	15	23	7	0.1	1.0	-1.6	3.0	**8.27E-01**	**5.00E-05**	1.00E+00	2.85E-04
Fcrla_chr1	36	42	17	5	0.2	1.1	-1.8	3.5	**5.24E-01**	**1.00E-04**	1.00E+00	6.19E-04
Fgf1_chr18	5	5	9	6	0.0	1.0	-0.7	1.6	**9.95E-01**	**5.00E-05**	1.00E+00	2.85E-04
Fgf13_chrX	1	1	3	2	0.1	1.1	-0.8	1.8	**8.57E-01**	**5.00E-05**	1.00E+00	2.85E-04
Fgf2_chr3	1	0	2	1	0.0	1.0	-0.8	1.8	**5.82E-01**	**4.45E-03**	1.00E+00	1.57E-02
Fhl1_chrX	8	8	12	8	0.0	1.0	-0.6	1.5	**8.87E-01**	**5.00E-05**	1.00E+00	2.85E-04
Fkbp9_chr6	9	9	17	11	0.0	1.0	-0.6	1.5	**8.86E-01**	**1.00E-04**	1.00E+00	5.44E-04
Fli1_chr9	33	39	63	41	0.2	1.2	-0.6	1.5	**2.53E-01**	**5.00E-05**	9.92E-01	2.85E-04
Fmnl3_chr15	13	16	27	16	0.3	1.2	-0.8	1.7	**2.08E-01**	**5.00E-05**	9.88E-01	2.85E-04
Fnbp1l_chr3	3	3	5	3	-0.3	1.2	-0.7	1.6	**2.60E-01**	**5.00E-05**	9.93E-01	2.85E-04
Foxk1_chr5	13	15	34	21	0.2	1.1	-0.7	1.6	**4.03E-01**	**5.00E-05**	1.00E+00	2.85E-04
Foxp1_chr6	13	16	24	12	0.3	1.3	-1.0	2.0	**4.08E-01**	**3.58E-03**	9.93E-01	1.18E-02
Fscn1_chr5	8	9	21	11	0.1	1.1	-1.0	2.0	**6.62E-01**	**5.00E-05**	1.00E+00	2.85E-04
Fut10_chr8	1	1	2	1	0.0	1.0	-0.7	1.6	**7.77E-01**	**1.00E-03**	1.00E+00	3.75E-03
Fv1_chr4	5	4	7	4	-0.2	1.2	-0.7	1.6	**5.34E-01**	**3.00E-04**	1.00E+00	1.47E-03
Fxyd1_chr7	5	5	4	2	0.1	1.0	-1.1	2.1	**9.17E-01**	**1.38E-04**	1.00E+00	7.40E-04
Fxyd2_chr9	2	0	2	0	-1.2	2.3	-0.9	1.9	**5.60E-03**	**1.99E-02**	3.64E-01	5.61E-02
Fxyd6_chr9	11	8	17	7	-0.4	1.3	-1.2	2.3	**1.39E-01**	**5.00E-05**	9.62E-01	2.85E-04
G530011O06Rik_chrX	1	1	2	0	-0.3	1.3	-0.8	1.8	**7.12E-01**	**7.75E-03**	1.00E+00	2.49E-02
Gabrq_chrX	3	2	7	2	-0.6	1.5	-1.9	3.8	**1.55E-01**	**5.00E-05**	9.74E-01	2.85E-04
Gadl1_chr4	1	1	2	1	0.0	1.0	-0.7	1.7	**5.41E-01**	**5.00E-05**	1.00E+00	2.85E-04
Gal3st2_chr1	1	0	2	0	-0.2	1.2	-0.9	1.9	**2.25E-06**	**5.00E-05**	8.87E-04	2.85E-04
Galnt4_chr10	7	8	12	8	0.1	1.1	-0.6	1.5	**7.66E-01**	**9.50E-04**	1.00E+00	4.09E-03
Galnt6_chr15	10	11	20	12	0.1	1.1	-0.7	1.6	**6.75E-01**	**1.44E-02**	1.00E+00	3.53E-02
Gas1_chr13	2	3	4	2	0.3	1.2	-0.8	1.7	**4.22E-01**	**5.00E-05**	1.00E+00	2.85E-04
Gas6_chr8	20	23	43	23	0.2	1.1	-0.9	1.8	**3.61E-01**	**5.00E-05**	9.98E-01	2.85E-04
Gata3_chr2	2	2	3	2	0.3	1.3	-0.6	1.6	**3.34E-01**	**2.00E-04**	9.98E-01	1.02E-03
Gcsam_chr16	4	2	5	3	-0.9	1.9	-0.6	1.5	**1.25E-02**	**7.50E-04**	5.13E-01	3.39E-03
Gimap3_chr6	118	131	158	96	0.2	1.1	-0.7	1.6	**4.98E-01**	**5.00E-05**	1.00E+00	2.85E-04

Gimap5_chr6	28	29	39	25	0.1	1.0	-0.7	1.6	**7.74E-01**	**5.00E-05**	1.00E+00	2.85E-04
Gimap6_chr6	132	147	141	85	0.2	1.1	-0.7	1.7	**4.93E-01**	**5.00E-05**	1.00E+00	2.85E-04
Gimap8_chr6	62	62	75	46	0.1	1.1	-0.7	1.6	**6.67E-01**	**1.14E-02**	1.00E+00	3.05E-02
Gipc3_chr10	1	1	2	1	0.0	1.0	-0.9	1.9	**4.17E-01**	**4.50E-04**	1.00E+00	2.12E-03
Gja4_chr4	2	2	3	2	-0.1	1.1	-0.9	1.9	**8.08E-01**	**5.00E-05**	1.00E+00	2.85E-04
Glb1_chr9	6	6	12	7	-0.2	1.1	-0.8	1.8	**6.90E-01**	**1.43E-02**	1.00E+00	4.23E-02
Gltscr1_chr7	11	13	31	20	0.3	1.2	-0.6	1.5	**2.30E-01**	**5.00E-05**	9.91E-01	2.85E-04
Glyctk_chr9	2	2	4	2	-0.1	1.1	-0.8	1.8	**7.33E-01**	**3.29E-03**	1.00E+00	1.11E-02
Gm11346_chr13	7	8	9	5	0.2	1.1	-0.9	1.8	**5.81E-01**	**5.00E-05**	1.00E+00	2.82E-04
Gm13139_chr4	5	1	5	1	-2.4	5.4	-1.8	3.6	**1.32E-05**	**5.00E-05**	3.55E-03	2.85E-04
Gm13152_chr4	2	0	3	1	-1.1	2.1	-1.6	3.1	**2.67E-06**	**5.00E-05**	1.02E-03	2.85E-04
Gm13238_chr4	2	0	2	1	-0.6	1.5	-1.1	2.2	**1.38E-03**	**1.50E-04**	1.50E-01	7.82E-04
Gm13251_chr4	4	1	5	1	-1.8	3.4	-1.8	3.6	**1.30E-03**	**5.00E-05**	1.31E-01	2.49E-04
Gm13889_chr2	1	2	2	1	1.0	1.9	-0.7	1.6	**5.55E-02**	**5.50E-03**	8.56E-01	1.89E-02
Gm19897_chr7	3	4	4	1	0.2	1.2	-1.6	3.1	**6.80E-01**	**1.84E-02**	1.00E+00	5.16E-02
Gm3002_chr14	6	3	9	5	-1.2	2.3	-0.7	1.6	**8.15E-06**	**5.00E-05**	2.25E-03	2.82E-04
Gm4759_chr7	20	14	40	19	-0.5	1.4	-1.1	2.1	**1.74E-02**	**5.00E-05**	4.91E-01	2.82E-04
Gm7120_chr13	5	4	10	3	-0.2	1.1	-1.7	3.3	**7.33E-01**	**5.00E-05**	1.00E+00	2.85E-04
Gpatch11_chr17	7	7	10	5	0.1	1.1	-1.0	2.0	**7.27E-01**	**5.00E-05**	1.00E+00	2.85E-04
Gpc3_chrX	2	3	3	1	0.8	1.7	-1.3	2.5	**4.02E-02**	**5.00E-05**	8.02E-01	2.85E-04
Gpr125_chr5	2	1	3	2	-0.1	1.1	-0.6	1.5	**7.46E-01**	**2.00E-04**	1.00E+00	1.02E-03
Gpr132_chr12	21	27	37	24	0.4	1.3	-0.6	1.6	**9.31E-02**	**5.00E-05**	9.27E-01	2.85E-04
Gpr137b-ps_chr13	10	8	17	3	-0.2	1.2	-2.7	6.3	**3.95E-01**	**5.00E-05**	1.00E+00	2.82E-04
Gpr153_chr4	2	2	5	4	-0.1	1.1	-0.6	1.5	**8.14E-01**	**2.50E-04**	1.00E+00	1.25E-03
Gpr156_chr16	1	1	3	1	-0.2	1.2	-1.5	2.8	**5.29E-01**	**5.00E-05**	1.00E+00	2.85E-04
Gpr176_chr2	1	1	2	1	0.0	1.0	-0.8	1.8	**8.24E-01**	**5.00E-05**	1.00E+00	2.85E-04
Gpr18_chr14	27	40	36	21	0.5	1.5	-0.8	1.7	**1.28E-01**	**9.10E-03**	9.54E-01	2.89E-02
Gpr183_chr14	11	19	17	10	0.7	1.6	-0.8	1.8	**5.08E-02**	**6.60E-03**	8.48E-01	2.20E-02
Gpr4_chr7	1	1	3	1	-0.2	1.2	-1.2	2.3	**5.91E-01**	**5.00E-05**	1.00E+00	2.85E-04
Gpr68_chr12	2	3	5	3	0.2	1.2	-0.6	1.5	**5.65E-01**	**1.82E-02**	1.00E+00	4.89E-02
Gprin3_chr6	1	1	4	2	-0.4	1.3	-0.7	1.6	**3.31E-01**	**2.50E-04**	9.90E-01	1.25E-03
Gpsm1_chr2	3	3	5	3	0.2	1.1	-0.7	1.6	**6.63E-01**	**7.44E-03**	1.00E+00	2.46E-02
Grap2_chr15	43	46	73	45	0.1	1.1	-0.7	1.6	**6.82E-01**	**5.00E-05**	1.00E+00	2.85E-04
Grem2_chr1	1	1	2	1	-0.2	1.2	-1.1	2.1	**5.04E-01**	**5.00E-05**	1.00E+00	2.85E-04
Gstm2_chr3	5	6	5	3	0.4	1.3	-0.8	1.7	**3.46E-01**	**5.00E-05**	9.98E-01	2.85E-04
Gucy1a3_chr3	11	14	21	13	0.3	1.2	-0.7	1.6	**2.17E-01**	**5.00E-05**	9.89E-01	2.85E-04
Gxylt1_chr15	15	13	25	14	-0.2	1.2	-0.8	1.7	**2.55E-01**	**5.00E-05**	9.92E-01	2.85E-04
H2-Eb1_chr17	393	620	522	348	0.7	1.6	-0.6	1.5	**3.44E-02**	**1.90E-03**	7.66E-01	7.48E-03
H2-M2_chr17	5	5	6	2	0.2	1.1	-1.7	3.2	**5.84E-01**	**5.00E-05**	1.00E+00	2.85E-04
Haao_chr17	18	21	23	14	0.2	1.2	-0.7	1.6	**4.01E-01**	**5.00E-05**	1.00E+00	2.85E-04
Hba-a2_chr11	224	437	231	76	0.9	1.9	-1.6	3.0	**4.07E-01**	**5.00E-05**	6.22E-01	2.92E-04
Heatr5b_chr17	6	7	14	9	0.2	1.1	-0.6	1.5	**4.64E-01**	**5.00E-05**	1.00E+00	2.85E-04
Heg1_chr16	13	13	36	24	0.0	1.0	-0.6	1.5	**9.16E-01**	**5.00E-05**	1.00E+00	2.85E-04
Herc3_chr6	15	14	25	14	-0.1	1.1	-0.8	1.7	**6.13E-01**	**5.00E-05**	1.00E+00	2.85E-04
Hes5_chr4	2	2	2	1	0.2	1.1	-1.0	2.0	**7.32E-01**	**1.50E-04**	1.00E+00	7.89E-04
Heyl_chr4	1	1	2	1	0.0	1.0	-0.9	1.9	**8.16E-01**	**5.00E-05**	1.00E+00	2.85E-04
Hhat_chr1	1	1	2	1	0.3	1.2	-1.0	2.0	**5.39E-01**	**5.00E-05**	1.00E+00	2.85E-04
Hip1r_chr5	34	39	73	45	0.2	1.2	-0.7	1.6	**3.22E-01**	**1.00E-04**	9.97E-01	5.44E-04
Hlf_chr11	2	0	3	1	-0.7	1.7	-1.4	2.7	**3.37E-07**	**5.00E-05**	1.76E-04	2.85E-04
Hs3st1_chr5	4	5	8	3	0.4	1.3	-1.5	2.8	**2.47E-01**	**5.00E-05**	9.92E-01	2.85E-04
Hs3st3b1_chr11	3	3	5	3	0.0	1.0	-0.6	1.6	**9.92E-01**	**5.00E-05**	1.00E+00	2.85E-04
Hsd17b7_chr1	3	2	5	2	-0.1	1.1	-1.3	2.5	**6.26E-01**	**5.00E-05**	1.00E+00	2.85E-04
Hspb1_chr5	2	2	2	1	0.3	1.3	-0.8	1.7	**5.28E-01**	**3.40E-03**	1.00E+00	1.24E-02
Hspb7_chr4	1	1	2	1	-0.5	1.5	-1.1	2.2	**8.37E-03**	**5.00E-05**	4.40E-01	2.85E-04
Htra1_chr7	10	13	18	11	0.3	1.2	-0.7	1.7	**2.40E-01**	**5.00E-05**	9.92E-01	2.85E-04
Icosl_chr10	63	73	100	63	0.2	1.2	-0.7	1.6	**3.03E-01**	**2.00E-04**	9.96E-01	1.02E-03
Ifi202b_chr1	7	2	8	0	-1.5	2.9	-3.0	7.9	**3.84E-04**	**3.96E-02**	4.30E-02	9.56E-02
Ifi30_chr8	141	138	175	93	0.0	1.0	-0.9	1.9	**8.59E-01**	**5.00E-05**	1.00E+00	2.85E-04
Ift172_chr5	7	6	13	9	0.0	1.0	-0.6	1.6	**8.41E-01**	**5.00E-05**	1.00E+00	2.85E-04
Ift81_chr5	1	1	2	1	-0.1	1.1	-0.9	1.8	**8.41E-01**	**5.00E-05**	1.00E+00	2.85E-04
Igf2_chr7	2	2	2	1	0.3	1.3	-1.1	2.2	**4.04E-01**	**5.00E-05**	1.00E+00	2.85E-04
Igfbp3_chr11	66	69	106	28	0.1	1.0	-1.9	3.8	**7.66E-01**	**5.00E-05**	1.00E+00	2.85E-04
Igfbp5_chr1	8	7	18	4	-0.1	1.1	-2.2	4.6	**6.18E-01**	**5.00E-05**	1.00E+00	2.85E-04
Il16_chr7	41	51	67	42	0.3	1.3	-0.7	1.6	**1.40E-01**	**5.00E-05**	9.63E-01	2.85E-04
Il27ra_chr8	20	21	35	21	0.1	1.1	-0.7	1.6	**7.41E-01**	**5.00E-05**	1.00E+00	2.85E-04
Il34_chr8	5	6	8	5	0.4	1.3	-0.8	1.7	**2.90E-01**	**5.00E-05**	9.94E-01	2.85E-04
Il4i1_chr7	26	23	42	22	-0.1	1.1	-0.9	1.9	**6.57E-01**	**2.03E-02**	1.00E+00	5.67E-02
Il7r_chr15	28	22	42	24	-0.3	1.3	-0.8	1.7	**1.15E-01**	**5.00E-05**	8.62E-01	2.85E-04
Inadl_chr4	3	4	6	3	0.4	1.3	-1.1	2.1	**2.00E-01**	**5.00E-05**	9.92E-01	2.85E-04
Inpp4b_chr8	9	6	21	10	-0.5	1.4	-1.1	2.1	**3.65E-02**	**5.00E-05**	6.59E-01	2.85E-04
Inppl1_chr7	12	12	28	13	0.0	1.0	-1.1	2.2	**9.17E-01**	**5.00E-05**	1.00E+00	2.85E-04
Irak3_chr10	6	9	12	7	0.4	1.3	-0.8	1.7	**1.02E-01**	**5.00E-05**	9.38E-01	2.85E-04
Irf5_chr6	26	36	45	32	0.4	1.3	-0.6	1.6	**3.49E-01**	**1.20E-02**	8.32E-01	3.69E-02
Irf6_chr1	1	1	2	1	0.1	1.1	-0.7	1.6	**6.12E-01**	**1.50E-04**	1.00E+00	7.89E-04
Irgq_chr7	6	7	13	9	0.2	1.1	-0.6	1.5	**4.06E-01**	**1.50E-04**	1.00E+00	7.89E-04
Irs1_chr1	1	1	2	1	0.0	1.0	-0.6	1.5	**9.71E-01**	**2.00E-04**	1.00E+00	1.02E-03
Islr_chr9	2	2	4	2	0.0	1.0	-1.0	2.0	**8.87E-01**	**5.87E-03**	1.00E+00	1.77E-02
Itga1_chr13	10	10	22	14	-0.1	1.1	-0.6	1.5	**6.49E-01**	**2.00E-04**	1.00E+00	1.02E-03
Itga11_chr9	1	1	2	1	0.0	1.0	-0.8	1.8	**4.58E-01**	**5.00E-05**	1.00E+00	2.85E-04
Itga3_chr11	2	3	5	3	0.4	1.3	-0.8	1.8	**1.99E-01**	**5.00E-05**	9.87E-01	2.85E-04
Itga7_chr10	1	1	2	1	0.0	1.0	-0.7	1.6	**4.15E-01**	**3.50E-04**	1.00E+00	1.69E-03
Itgbl1_chr14	1	1	2	1	-0.2	1.2	-0.8	1.7	**4.70E-01**	**2.00E-04**	1.00E+00	1.02E-03
Itih5_chr2	3	3	6	3	-0.2	1.1	-1.1	2.2	**5.09E-01**	**5.00E-05**	1.00E+00	2.85E-04

Itln1_chr1	1	1	2	0	-0.4	1.3	-0.8	1.8	1.27E-01	5.00E-05	8.77E-01	2.85E-04
Itm2a_chrX	10	7	10	7	-0.4	1.3	-0.7	1.6	1.59E-01	5.00E-05	9.78E-01	2.85E-04
Itpkb_chr1	21	22	50	30	0.1	1.1	-0.7	1.7	6.57E-01	5.00E-05	1.00E+00	2.85E-04
Itpr2_chr6	14	15	34	19	0.1	1.1	-0.8	1.8	6.74E-01	5.00E-05	1.00E+00	2.85E-04
Jag2_chr12	1	1	3	2	0.0	1.0	-0.7	1.6	9.23E-01	2.00E-04	1.00E+00	1.02E-03
Jam3_chr9	6	6	9	5	-0.1	1.1	-0.9	1.9	6.76E-01	5.00E-05	1.00E+00	2.85E-04
Kat6b_chr14	5	4	8	5	-0.1	1.1	-0.7	1.6	6.48E-01	3.27E-02	1.00E+00	8.11E-02
Kbtbd11_chr8	33	32	54	34	-0.1	1.0	-0.7	1.6	7.51E-01	2.00E-04	1.00E+00	1.02E-03
Kcnc3_chr7	2	2	3	1	0.0	1.0	-1.0	2.0	9.04E-01	5.00E-05	1.00E+00	2.85E-04
Kcnk3_chr5	1	1	2	1	0.0	1.0	-1.2	2.2	8.49E-01	5.00E-05	1.00E+00	2.85E-04
Kcnk5_chr14	5	8	11	7	0.5	1.5	-0.6	1.5	2.76E-02	1.00E-04	7.14E-01	5.44E-04
Kctd15_chr7	2	2	3	2	0.4	1.3	-0.7	1.6	3.62E-01	3.50E-04	9.99E-01	1.69E-03
Kdm5b_chr1	7	8	14	9	0.2	1.2	-0.6	1.5	3.19E-01	2.50E-04	9.88E-01	1.25E-03
Kif21b_chr1	42	40	98	43	-0.1	1.1	-1.2	2.3	7.41E-01	5.00E-05	1.00E+00	2.85E-04
Kif3c_chr12	2	2	4	3	0.3	1.2	-0.7	1.6	3.98E-01	2.00E-03	1.00E+00	7.82E-03
Klf12_chr14	3	2	6	2	-0.4	1.4	-1.6	3.0	1.41E-01	5.00E-05	8.94E-01	2.85E-04
Klf2_chr8	22	36	33	21	0.7	1.7	-0.6	1.6	8.59E-04	5.00E-05	1.12E-01	2.85E-04
Klhl13_chrX	2	3	4	3	0.4	1.3	-0.6	1.6	2.36E-01	2.50E-04	9.91E-01	1.25E-03
Klhl24_chr16	30	26	58	37	-0.2	1.2	-0.6	1.6	2.70E-01	1.00E-04	9.94E-01	5.44E-04
Klhl42_chr6	8	8	15	10	0.0	1.0	-0.7	1.6	9.04E-01	5.00E-05	1.00E+00	2.85E-04
Klhl6_chr16	44	45	63	38	0.0	1.0	-0.7	1.6	8.70E-01	5.00E-05	1.00E+00	2.85E-04
Klk1b22_chr7	6	6	6	0	0.0	1.0	-2.6	6.0	9.15E-01	5.00E-05	1.00E+00	2.85E-04
Klri1_chr6	4	2	5	2	-1.2	2.3	-1.1	2.1	1.69E-02	5.00E-05	5.91E-01	2.85E-04
Kremen1_chr11	5	6	12	8	0.1	1.1	-0.6	1.6	7.05E-01	5.00E-05	1.00E+00	2.85E-04
Kynu_chr2	11	12	13	8	0.2	1.1	-0.6	1.5	4.67E-01	3.50E-04	1.00E+00	1.69E-03
L3mbtl3_chr10	10	11	22	12	0.1	1.1	-0.8	1.8	5.13E-01	5.00E-05	1.00E+00	2.85E-04
Lama4_chr10	1	1	2	1	0.0	1.0	-0.9	1.9	7.59E-01	5.00E-05	1.00E+00	2.85E-04
Lama5_chr2	1	1	3	2	0.0	1.0	-0.8	1.8	8.30E-01	5.00E-05	1.00E+00	2.85E-04
Lamb1_chr12	1	1	3	1	0.0	1.0	-0.9	1.9	9.49E-01	5.00E-05	1.00E+00	2.85E-04
Lamb2_chr9	6	9	17	10	0.5	1.4	-0.7	1.6	1.84E-02	5.00E-05	6.02E-01	2.85E-04
Lamb3_chr1	1	1	2	1	0.0	1.0	-0.9	1.9	5.65E-01	5.00E-05	1.00E+00	2.85E-04
Lamc1_chr1	5	6	13	8	0.4	1.3	-0.7	1.6	1.02E-01	5.00E-05	8.50E-01	2.85E-04
Lamc3_chr2	1	1	2	1	0.0	1.0	-0.6	1.6	4.73E-01	2.50E-04	1.00E+00	1.25E-03
Lancl1_chr1	3	3	4	3	-0.1	1.1	-0.7	1.6	7.54E-01	1.58E-02	1.00E+00	3.89E-02
Lat_chr7	28	27	33	20	-0.1	1.1	-0.7	1.6	6.81E-01	5.00E-05	1.00E+00	2.85E-04
Lbh_chr17	74	102	108	66	0.5	1.4	-0.7	1.6	3.66E-02	5.00E-05	7.72E-01	2.85E-04
Lca5_chr9	2	2	3	2	-0.1	1.0	-0.7	1.6	8.72E-01	1.63E-04	1.00E+00	8.62E-04
Ldhb_chr6	5	3	5	2	-0.8	1.7	-1.3	2.4	6.94E-02	5.00E-05	8.81E-01	2.85E-04
Ldlrad3_chr2	4	4	7	4	0.0	1.0	-0.9	1.9	9.26E-01	5.00E-05	1.00E+00	2.85E-04
Ldlrad4_chr18	3	3	8	5	-0.2	1.2	-0.6	1.6	5.43E-01	2.00E-04	1.00E+00	1.02E-03
Lepr_chr4	10	9	19	9	-0.1	1.1	-1.1	2.2	6.44E-01	5.00E-05	1.00E+00	2.85E-04
Leprel1_chr16	8	10	21	13	0.3	1.2	-0.7	1.6	2.77E-01	5.00E-05	9.76E-01	2.85E-04
Lgr4_chr2	1	1	2	1	0.0	1.0	-0.6	1.5	2.54E-01	6.50E-04	9.92E-01	2.93E-03
Limd1_chr9	33	36	71	46	0.1	1.1	-0.6	1.5	5.28E-01	5.00E-05	1.00E+00	2.85E-04
Limd2_chr11	64	75	82	51	0.2	1.2	-0.7	1.6	2.97E-01	5.00E-05	9.96E-01	2.85E-04
Lims2_chr18	2	2	3	1	0.0	1.0	-1.0	1.9	9.73E-01	1.00E-04	1.00E+00	5.44E-04
Lipc_chr9	2	2	3	1	0.0	1.0	-1.4	2.7	9.76E-01	5.00E-05	1.00E+00	2.85E-04
Lipn_chr19	6	2	8	1	-1.5	2.8	-2.9	7.5	3.33E-04	5.00E-05	5.65E-02	2.85E-04
Lix1l_chr3	5	5	9	6	0.0	1.0	-0.6	1.5	8.66E-01	5.00E-05	1.00E+00	2.85E-04
Lmod1_chr1	1	1	2	1	0.1	1.1	-0.7	1.6	5.71E-01	5.00E-05	1.00E+00	2.85E-04
Lpar1_chr4	6	4	7	5	-0.5	1.4	-0.6	1.5	1.34E-01	1.26E-02	9.33E-01	3.72E-02
Lpgat1_chr1	17	17	21	13	0.0	1.0	-0.8	1.7	8.49E-01	2.67E-02	1.00E+00	6.37E-02
Lrat_chr3	2	0	3	2	-1.0	2.0	-1.1	2.2	5.57E-07	5.00E-05	2.79E-04	2.85E-04
Lrch1_chr14	9	10	17	10	0.1	1.0	-0.8	1.7	7.10E-01	8.67E-04	1.00E+00	3.86E-03
Lrrc1_chr9	2	2	4	3	0.0	1.0	-0.7	1.6	9.31E-01	4.75E-04	1.00E+00	2.25E-03
Lrrc61_chr6	6	9	11	7	0.4	1.4	-0.6	1.5	2.11E-01	3.22E-02	9.62E-01	6.63E-02
Lrrc75b_chr10	1	1	2	1	0.0	1.0	-0.8	1.7	5.84E-01	5.00E-05	1.00E+00	2.85E-04
Lrrk2_chr15	25	28	50	33	0.2	1.1	-0.6	1.5	4.46E-01	4.00E-04	1.00E+00	1.91E-03
Lrrn4_chr2	1	1	2	1	0.4	1.4	-0.8	1.7	1.73E-01	5.00E-05	9.82E-01	2.85E-04
Ltbp1_chr17	1	1	2	2	-0.1	1.1	-0.6	1.5	7.86E-01	6.00E-03	1.00E+00	2.04E-02
Ltbp3_chr19	3	3	8	5	0.3	1.3	-0.6	1.5	3.92E-01	2.46E-02	1.00E+00	6.68E-02
Ltbp4_chr7	20	28	70	44	0.5	1.4	-0.7	1.6	2.20E-02	1.50E-04	5.43E-01	7.89E-04
Lurap1l_chr4	2	1	3	1	-0.6	1.6	-1.0	2.0	1.70E-01	5.00E-05	9.80E-01	2.85E-04
Ly75_chr2	5	5	13	9	-0.1	1.1	-0.6	1.5	5.49E-01	5.00E-05	1.00E+00	2.85E-04
Ly86_chr13	108	109	78	51	0.0	1.0	-0.6	1.5	9.67E-01	5.00E-05	1.00E+00	2.85E-04
Mab21l3_chr3	1	1	2	1	0.0	1.0	-0.7	1.6	1.46E-01	5.00E-05	9.68E-01	2.85E-04
Madcam1_chr10	2	0	2	1	-0.9	1.8	-1.1	2.2	8.09E-06	5.00E-05	2.37E-03	2.85E-04
Malt1_chr18	51	52	78	51	0.0	1.0	-0.6	1.6	9.14E-01	1.00E-04	1.00E+00	5.44E-04
Maml2_chr9	9	9	16	8	0.1	1.1	-1.1	2.1	6.29E-01	5.00E-05	1.00E+00	2.85E-04
Maml3_chr3	2	2	4	3	0.1	1.1	-0.6	1.5	6.30E-01	1.00E-04	1.00E+00	5.44E-04
Mamld1_chrX	2	2	3	1	-0.1	1.0	-1.1	2.1	9.05E-01	1.17E-03	1.00E+00	4.64E-03
Manba_chr3	7	8	13	7	0.1	1.1	-0.8	1.7	6.89E-01	5.00E-05	1.00E+00	2.85E-04
Map2_chr1	1	1	2	1	0.0	1.0	-0.6	1.5	1.34E-01	5.00E-05	9.56E-01	2.85E-04
Map2k6_chr11	6	6	9	6	0.0	1.0	-0.7	1.6	9.42E-01	5.00E-05	1.00E+00	2.85E-04
Map3k14_chr11	13	16	31	19	0.3	1.2	-0.8	1.7	1.78E-01	5.00E-05	9.84E-01	2.85E-04
Map3k5_chr10	12	14	25	16	0.2	1.1	-0.6	1.6	3.98E-01	5.00E-05	1.00E+00	2.85E-04
Map4k1_chr7	57	71	110	59	0.3	1.2	-0.9	1.9	1.59E-01	5.00E-05	9.77E-01	2.85E-04
Map4k2_chr19	74	76	138	83	0.0	1.0	-0.7	1.7	8.24E-01	5.00E-05	1.00E+00	2.85E-04
Mapk12_chr15	4	6	5	3	0.8	1.7	-0.6	1.6	1.95E-02	2.50E-04	6.24E-01	1.25E-03
Mapk8ip1_chr2	1	1	2	1	-0.1	1.1	-0.7	1.6	5.79E-01	8.29E-03	1.00E+00	2.66E-02
Marco_chr1	49	35	59	30	-0.5	1.4	-1.0	1.9	2.61E-02	5.00E-05	5.87E-01	2.85E-04
Mark1_chr1	1	1	2	1	0.0	1.0	-1.3	2.4	9.52E-01	5.00E-05	1.00E+00	2.85E-04
Mctp2_chr7	5	4	8	5	-0.2	1.1	-0.6	1.5	4.10E-01	5.00E-05	1.00E+00	2.85E-04

Mcur1_chr13	9	9	16	10	0.1	1.0	-0.6	1.6	**8.12E-01**	**5.00E-05**	1.00E+00	2.85E-04
Mef2d_chr3	31	36	76	51	0.2	1.2	-0.6	1.5	**2.90E-01**	**1.00E-04**	9.82E-01	5.44E-04
Meis2_chr2	1	1	2	1	0.0	1.0	-0.7	1.6	**8.69E-01**	**4.00E-04**	1.00E+00	1.67E-03
Mettl17_chr14	12	11	15	8	-0.2	1.1	-0.9	1.8	**5.53E-01**	**5.00E-05**	1.00E+00	2.85E-04
Mettl23_chr11	17	11	16	7	-0.6	1.6	-1.3	2.4	**2.58E-02**	**5.00E-05**	6.95E-01	2.85E-04
Mfap5_chr6	2	1	2	0	-0.6	1.5	-1.0	2.0	**2.71E-01**	**5.00E-05**	9.94E-01	2.85E-04
Mfge8_chr7	59	55	122	54	-0.1	1.1	-1.2	2.3	**7.09E-01**	**2.50E-04**	1.00E+00	1.25E-03
Mgat4a_chr1	14	14	26	16	0.0	1.0	-0.7	1.6	**9.39E-01**	**5.00E-05**	1.00E+00	2.85E-04
Micall1_chr15	8	8	16	10	0.1	1.1	-0.6	1.6	**6.34E-01**	**5.00E-05**	1.00E+00	2.85E-04
Mid1_chrX	9	10	38	2	-0.5	1.4	-4.3	20.4	**6.28E-01**	**1.36E-02**	1.00E+00	3.75E-02
Miip_chr4	14	9	19	10	-0.6	1.6	-1.0	1.9	**1.34E-02**	**5.00E-05**	5.29E-01	2.85E-04
Mllt6_chr11	38	40	83	49	0.1	1.1	-0.8	1.7	**7.00E-01**	**5.00E-05**	1.00E+00	2.85E-04
Mmp11_chr10	1	1	2	1	0.1	1.0	-1.0	1.9	**8.80E-01**	**5.00E-05**	1.00E+00	2.85E-04
Mmp15_chr8	1	1	2	1	0.2	1.1	-0.8	1.8	**2.06E-01**	**5.00E-05**	9.87E-01	2.85E-04
Mmp17_chr5	2	3	5	2	0.5	1.4	-1.2	2.4	**1.24E-01**	**5.00E-05**	9.50E-01	2.85E-04
Mmp2_chr8	5	5	10	5	0.1	1.0	-1.0	2.1	**8.26E-01**	**5.00E-05**	1.00E+00	2.85E-04
Mmrn2_chr14	5	6	12	7	0.4	1.3	-0.7	1.7	**1.58E-01**	**5.00E-05**	9.77E-01	2.85E-04
Morn1_chr4	1	1	2	1	0.0	1.0	-0.6	1.5	**4.93E-01**	**1.40E-03**	1.00E+00	5.72E-03
Mpdz_chr4	1	2	3	2	0.1	1.1	-0.7	1.7	**7.25E-01**	**5.00E-05**	1.00E+00	2.85E-04
Mras_chr9	4	3	7	4	-0.4	1.3	-0.7	1.6	**1.52E-01**	**5.00E-05**	9.72E-01	2.85E-04
Mrgpre_chr7	3	4	7	4	0.3	1.2	-1.0	2.0	**2.95E-01**	**5.00E-05**	9.96E-01	2.85E-04
Mtss1_chr15	14	17	27	15	0.2	1.2	-0.9	1.9	**4.05E-01**	**1.12E-03**	9.96E-01	4.47E-03
Mturn_chr6	5	5	9	6	-0.2	1.1	-0.6	1.5	**5.81E-01**	**4.00E-04**	1.00E+00	1.91E-03
Mutyh_chr4	3	3	4	3	0.2	1.1	-0.6	1.5	**7.10E-01**	**1.96E-03**	1.00E+00	7.68E-03
Mxra8_chr4	10	12	18	12	0.2	1.2	-0.6	1.6	**3.21E-01**	**5.00E-05**	9.97E-01	2.85E-04
Mybpc2_chr7	1	1	2	1	-0.1	1.1	-1.0	2.0	**6.20E-01**	**5.00E-05**	1.00E+00	2.85E-04
Mycl_chr4	5	5	12	8	-0.2	1.1	-0.7	1.6	**4.95E-01**	**5.00E-05**	1.00E+00	2.85E-04
Myh11_chr16	6	6	4	0	-0.1	1.0	-2.0	3.9	**8.14E-01**	**2.89E-02**	1.00E+00	8.07E-02
Myl9_chr2	17	22	26	15	0.4	1.3	-0.7	1.7	**1.05E-01**	**5.00E-05**	9.38E-01	2.85E-04
Mylip_chr13	32	40	59	38	0.3	1.2	-0.6	1.5	**1.69E-01**	**3.25E-04**	9.80E-01	1.59E-03
Mylk_chr16	11	13	22	13	0.2	1.1	-0.8	1.7	**3.52E-01**	**5.00E-05**	9.98E-01	2.85E-04
Myo1c_chr11	26	31	53	32	0.3	1.2	-0.7	1.7	**3.79E-01**	**6.97E-03**	9.95E-01	2.17E-02
Myo1e_chr9	21	29	46	23	0.5	1.4	-1.0	2.0	**2.85E-02**	**5.00E-05**	7.25E-01	2.85E-04
Myzap_chr9	2	3	4	2	0.1	1.1	-0.6	1.5	**7.38E-01**	**1.45E-03**	1.00E+00	5.90E-03
N4bp2_chr5	9	8	21	13	-0.1	1.1	-0.7	1.6	**7.10E-01**	**5.00E-05**	1.00E+00	2.85E-04
N4bp3_chr11	4	5	7	4	0.5	1.4	-0.7	1.6	**1.47E-01**	**1.15E-03**	9.68E-01	4.84E-03
Naaa_chr5	33	25	51	30	-0.4	1.3	-0.8	1.7	**5.04E-02**	**5.00E-05**	8.45E-01	2.85E-04
Naalad2_chr9	1	1	2	1	0.0	1.0	-0.9	1.8	**4.56E-01**	**5.00E-05**	1.00E+00	2.85E-04
Nbl1_chr4	2	2	4	2	-0.2	1.2	-1.1	2.1	**6.24E-01**	**5.00E-05**	1.00E+00	2.85E-04
Ncoa3_chr2	24	27	54	35	0.2	1.1	-0.6	1.5	**3.98E-01**	**1.00E-04**	1.00E+00	5.44E-04
Ndn_chr7	4	4	6	4	0.1	1.1	-0.7	1.6	**6.80E-01**	**1.50E-04**	1.00E+00	7.89E-04
Ndrg2_chr14	5	4	6	3	-0.1	1.1	-0.9	1.9	**7.33E-01**	**4.07E-02**	1.00E+00	8.50E-02
Nedd4l_chr18	3	3	5	3	0.3	1.2	-0.6	1.6	**2.56E-01**	**5.00E-05**	9.97E-01	2.85E-04
Nek6_chr2	3	2	5	3	-0.3	1.2	-0.9	1.9	**4.69E-01**	**5.00E-05**	9.98E-01	2.85E-04
Neo1_chr9	1	2	3	2	0.3	1.2	-1.0	2.0	**3.97E-01**	**5.00E-05**	1.00E+00	2.85E-04
Nfatc4_chr14	1	2	3	2	0.1	1.1	-0.9	1.8	**8.20E-01**	**1.75E-04**	1.00E+00	8.33E-04
Ngf_chr3	2	2	3	1	-0.2	1.2	-1.3	2.4	**7.41E-01**	**1.50E-04**	1.00E+00	8.06E-04
Nid1_chr13	22	25	51	34	0.2	1.2	-0.6	1.5	**3.01E-01**	**1.50E-04**	9.85E-01	7.89E-04
Nipal3_chr4	8	9	19	13	0.1	1.1	-0.6	1.5	**6.87E-01**	**5.00E-05**	1.00E+00	2.85E-04
Nlrc3_chr16	9	7	21	14	-0.3	1.3	-0.6	1.5	**1.34E-01**	**5.00E-05**	8.81E-01	2.85E-04
Nlrc4_chr17	8	8	16	10	0.0	1.0	-0.6	1.6	**9.30E-01**	**5.00E-05**	1.00E+00	2.85E-04
Nmrk1_chr19	10	7	13	5	-0.5	1.4	-1.4	2.7	**1.07E-01**	**5.00E-05**	8.51E-01	2.85E-04
Nol12_chr15	6	6	7	5	-0.1	1.0	-0.7	1.6	**8.26E-01**	**5.00E-05**	1.00E+00	2.85E-04
Notch2_chr3	26	31	74	45	0.3	1.2	-0.7	1.6	**1.96E-01**	**1.50E-04**	9.87E-01	7.89E-04
Notch3_chr17	4	4	12	6	-0.1	1.1	-1.1	2.1	**7.51E-01**	**5.00E-05**	1.00E+00	2.85E-04
Nphp3_chr9	1	1	2	2	-0.2	1.1	-0.6	1.6	**6.33E-01**	**2.75E-04**	1.00E+00	1.33E-03
Npnt_chr3	12	12	37	23	0.0	1.0	-0.7	1.6	**9.10E-01**	**2.17E-02**	1.00E+00	5.24E-02
Npr2_chr4	3	3	6	4	0.0	1.0	-0.6	1.5	**9.41E-01**	**2.50E-04**	1.00E+00	1.25E-03
Npy1r_chr8	3	3	7	2	-0.3	1.2	-1.8	3.4	**4.18E-01**	**5.00E-05**	1.00E+00	2.85E-04
Nr1d1_chr11	9	4	18	8	-1.1	2.2	-1.1	2.2	**9.83E-05**	**5.00E-05**	1.39E-02	2.85E-04
Nrip2_chr6	1	1	2	1	0.0	1.0	-0.6	1.5	**9.78E-01**	**6.18E-03**	1.00E+00	2.09E-02
Nrm_chr17	12	18	19	12	0.5	1.5	-0.6	1.5	**3.03E-02**	**5.00E-05**	7.39E-01	2.85E-04
Nrn1_chr13	2	1	2	0	-0.6	1.5	-0.8	1.8	**1.32E-01**	**5.00E-05**	9.56E-01	2.85E-04
Nsg2_chr11	12	12	17	8	0.0	1.0	-1.1	2.2	**9.62E-01**	**5.00E-05**	1.00E+00	2.85E-04
Nt5c2_chr19	6	7	4	1	0.1	1.1	-1.7	3.2	**6.48E-01**	**2.00E-03**	1.00E+00	8.84E-03
Nt5e_chr9	6	6	10	6	-0.1	1.1	-0.9	1.9	**7.72E-01**	**5.00E-05**	1.00E+00	2.85E-04
Ntf3_chr6	1	1	2	1	0.0	1.0	-0.8	1.7	**6.65E-01**	**9.50E-04**	1.00E+00	3.57E-03
Ntm_chr9	1	0	2	0	0.0	1.0	-0.7	1.7	**4.99E-02**	**5.00E-05**	8.47E-01	2.85E-04
Olfml1_chr7	6	6	11	5	-0.2	1.1	-1.2	2.3	**5.98E-01**	**5.00E-05**	1.00E+00	2.85E-04
Olfr433_chr1	1	1	2	0	-0.5	1.4	-1.1	2.2	**3.96E-01**	**5.00E-05**	1.00E+00	2.85E-04
Orai2_chr5	19	19	33	20	0.0	1.0	-0.8	1.7	**9.87E-01**	**5.00E-05**	1.00E+00	2.85E-04
Osbpl5_chr7	7	9	16	11	0.4	1.3	-0.6	1.5	**1.23E-01**	**5.00E-05**	9.54E-01	2.85E-04
Otud1_chr2	8	10	12	7	0.4	1.3	-0.7	1.6	**1.12E-01**	**5.00E-05**	9.39E-01	2.85E-04
Pacsin1_chr17	3	3	7	3	0.0	1.0	-1.1	2.1	**8.46E-01**	**3.75E-03**	1.00E+00	1.21E-02
Pam_chr1	9	9	19	11	0.1	1.1	-0.8	1.7	**6.29E-01**	**5.00E-05**	1.00E+00	2.85E-04
Paqr7_chr4	4	4	8	5	-0.1	1.1	-0.8	1.7	**6.49E-01**	**5.00E-05**	1.00E+00	2.85E-04
Pard3b_chr1	2	1	3	2	-0.4	1.3	-1.0	2.0	**1.89E-01**	**5.00E-05**	9.45E-01	2.85E-04
Pard6b_chr2	1	1	2	1	0.0	1.0	-0.7	1.6	**2.03E-01**	**2.00E-04**	9.87E-01	1.02E-03
Pard6g_chr18	1	1	2	1	-0.2	1.1	-0.8	1.7	**5.86E-01**	**5.00E-05**	1.00E+00	2.85E-04
Parm1_chr5	4	4	10	4	-0.3	1.2	-1.2	2.3	**4.04E-01**	**5.00E-05**	1.00E+00	2.85E-04
Parva_chr7	6	6	12	8	0.0	1.0	-0.6	1.5	**8.41E-01**	**5.00E-05**	1.00E+00	2.85E-04
Pcdh15_chr10	1	0	2	0	0.0	1.0	-0.8	1.7	**2.99E-05**	**5.00E-05**	6.05E-03	2.85E-04
Pcp4l1_chr1	4	4	5	2	-0.1	1.0	-1.5	2.9	**8.67E-01**	**5.00E-05**	1.00E+00	2.85E-04

Pcsk6_chr7	1	2	3	1	0.6	1.6	-1.4	2.7	**9.16E-02**	**5.00E-05**	9.27E-01	2.85E-04
Pctp_chr11	5	5	8	5	0.0	1.0	-0.6	1.5	**9.66E-01**	**2.00E-04**	1.00E+00	1.02E-03
Pdcd1lg2_chr19	3	4	5	3	0.5	1.4	-0.8	1.8	**1.22E-01**	**5.00E-05**	9.50E-01	2.85E-04
Pde1a_chr2	1	1	2	1	0.0	1.0	-1.0	2.0	**6.81E-01**	**5.00E-05**	1.00E+00	2.49E-04
Pde3b_chr7	13	12	25	13	-0.1	1.1	-0.9	1.9	**5.45E-01**	**5.00E-05**	1.00E+00	2.85E-04
Pde4b_chr4	15	20	23	13	0.5	1.4	-0.8	1.8	**8.47E-02**	**1.10E-03**	9.04E-01	4.45E-03
Pdia5_chr16	4	4	7	4	-0.2	1.2	-0.7	1.6	**5.56E-01**	**1.50E-04**	1.00E+00	7.89E-04
Pdk4_chr6	8	5	13	5	-0.5	1.5	-1.3	2.5	**4.38E-02**	**5.00E-05**	7.01E-01	2.85E-04
Pdlim3_chr8	2	2	3	1	-0.4	1.3	-1.7	3.3	**3.82E-01**	**5.00E-05**	1.00E+00	2.85E-04
Pdzd2_chr15	1	1	2	1	0.0	1.0	-1.1	2.2	**6.38E-01**	**5.00E-05**	1.00E+00	2.85E-04
Pdzd4_chrX	2	2	4	2	-0.2	1.1	-1.1	2.2	**5.75E-01**	**5.00E-05**	1.00E+00	2.85E-04
Pea15a_chr1	34	33	50	32	0.0	1.0	-0.7	1.6	**8.32E-01**	**5.00E-05**	1.00E+00	2.85E-04
Pecam1_chr11	29	36	56	35	0.3	1.2	-0.7	1.6	**2.90E-01**	**2.75E-03**	9.91E-01	1.02E-02
Peg13_chr15	18	22	32	20	0.3	1.2	-0.7	1.6	**2.28E-01**	**3.50E-04**	9.89E-01	1.68E-03
Pglyrp2_chr17	10	11	20	12	0.2	1.1	-0.7	1.6	**5.04E-01**	**5.00E-05**	1.00E+00	2.85E-04
Phc1_chr6	3	4	8	5	0.4	1.3	-0.7	1.6	**4.04E-01**	**2.19E-02**	9.81E-01	5.28E-02
Pi15_chr1	2	1	2	1	-0.3	1.2	-1.2	2.4	**3.97E-01**	**5.00E-05**	1.00E+00	2.85E-04
Pianp_chr6	9	2	15	1	-2.2	4.6	-3.6	12.5	**2.66E-07**	**5.00E-05**	8.12E-05	2.85E-04
Pik3r4_chr9	14	18	30	19	0.3	1.2	-0.7	1.6	**1.64E-01**	**5.00E-05**	9.80E-01	2.85E-04
Pira2_chr7	16	10	23	14	-0.7	1.6	-0.7	1.6	**1.08E-02**	**8.65E-03**	4.88E-01	2.76E-02
Pkd1_chr17	15	12	40	24	-0.3	1.2	-0.8	1.7	**2.31E-01**	**3.00E-04**	9.66E-01	1.47E-03
Pkia_chr3	4	3	7	4	-0.4	1.3	-0.6	1.5	**1.86E-01**	**1.00E-04**	9.86E-01	5.44E-04
Pla2g5_chr4	14	6	23	7	-1.3	2.5	-1.8	3.4	**1.60E-06**	**5.00E-05**	7.01E-04	2.85E-04
Pla2r1_chr2	1	1	2	1	0.1	1.1	-1.0	2.0	**8.21E-01**	**5.00E-05**	1.00E+00	2.85E-04
Plcd3_chr11	1	0	2	1	-0.6	1.5	-1.3	2.5	**4.08E-04**	**5.00E-05**	6.64E-02	2.85E-04
Plce1_chr19	2	2	4	2	0.3	1.2	-0.9	1.8	**2.59E-01**	**5.00E-05**	9.72E-01	2.85E-04
Plcg1_chr2	18	17	37	22	-0.1	1.1	-0.7	1.7	**5.71E-01**	**5.00E-05**	1.00E+00	2.85E-04
Plekha2_chr8	40	49	67	37	0.3	1.2	-0.9	1.8	**1.63E-01**	**5.00E-05**	9.80E-01	2.85E-04
Plekha7_chr7	1	1	2	1	0.0	1.0	-0.7	1.7	**7.69E-01**	**5.00E-05**	1.00E+00	2.85E-04
Plekhh2_chr17	2	2	4	2	-0.1	1.1	-0.9	1.9	**7.43E-01**	**5.00E-05**	1.00E+00	2.85E-04
Plxdc2_chr2	2	2	5	3	0.1	1.1	-0.8	1.8	**7.34E-01**	**5.00E-05**	1.00E+00	2.85E-04
Pmepa1_chr2	2	2	4	2	0.2	1.1	-0.6	1.6	**5.58E-01**	**2.00E-04**	1.00E+00	1.02E-03
Podn_chr4	2	2	4	2	-0.1	1.1	-0.8	1.8	**8.21E-01**	**5.00E-05**	1.00E+00	2.85E-04
Podnl1_chr8	2	1	3	2	-0.5	1.4	-0.6	1.6	**3.10E-01**	**4.50E-04**	9.97E-01	2.12E-03
Podxl_chr6	3	4	7	5	0.3	1.2	-0.6	1.5	**2.99E-01**	**5.00E-05**	9.96E-01	2.85E-04
Poli_chr18	4	5	10	3	0.2	1.1	-1.7	3.3	**6.93E-01**	**5.00E-05**	1.00E+00	2.97E-04
Polr3h_chr15	6	5	10	5	-0.5	1.4	-1.1	2.2	**3.89E-01**	**2.98E-02**	1.00E+00	7.78E-02
Postn_chr3	3	2	6	2	-0.4	1.4	-1.6	3.0	**4.14E-01**	**5.00E-05**	9.05E-01	2.61E-04
Pou2f1_chr1	5	4	9	5	0.0	1.0	-0.8	1.8	**8.33E-01**	**4.60E-02**	1.00E+00	1.07E-01
Pou6f1_chr15	11	12	22	14	0.1	1.1	-0.7	1.6	**5.83E-01**	**5.00E-05**	1.00E+00	2.85E-04
Ppl_chr16	3	3	5	2	0.0	1.0	-1.5	2.8	**9.28E-01**	**5.00E-05**	1.00E+00	2.85E-04
Ppm1e_chr11	3	3	4	2	0.0	1.0	-0.8	1.7	**9.23E-01**	**5.00E-05**	1.00E+00	2.85E-04
Ppp1r13b_chr12	9	11	20	13	0.3	1.2	-0.7	1.6	**1.77E-01**	**5.00E-05**	9.84E-01	2.85E-04
Ppp1r16b_chr2	19	22	31	20	0.2	1.2	-0.8	1.7	**3.07E-01**	**2.10E-02**	9.93E-01	5.02E-02
Ppp1r3c_chr19	1	1	2	1	0.0	1.0	-0.7	1.6	**9.87E-01**	**1.35E-03**	1.00E+00	5.55E-03
Ppp3ca_chr3	34	45	58	34	0.4	1.3	-0.8	1.7	**6.39E-02**	**5.00E-05**	8.76E-01	2.85E-04
Pqlc2_chr4	9	9	19	10	0.0	1.0	-0.9	1.9	**9.65E-01**	**5.00E-05**	1.00E+00	2.85E-04
Prdm11_chr2	2	1	5	3	-0.2	1.2	-0.7	1.6	**6.47E-01**	**1.50E-04**	1.00E+00	7.89E-04
Prelp_chr1	9	13	21	12	0.6	1.5	-0.8	1.8	**1.31E-02**	**5.00E-05**	5.25E-01	2.85E-04
Prex2_chr1	3	2	9	6	-0.4	1.3	-0.7	1.6	**4.46E-01**	**1.88E-04**	8.37E-01	8.19E-04
Prkca_chr11	6	5	13	8	-0.3	1.2	-0.6	1.5	**2.06E-01**	**5.00E-05**	9.51E-01	2.85E-04
Prkce_chr17	6	7	13	6	0.2	1.2	-1.1	2.2	**3.55E-01**	**5.00E-05**	9.98E-01	2.85E-04
Prkcq_chr2	14	13	24	15	-0.1	1.1	-0.7	1.6	**6.28E-01**	**5.00E-05**	1.00E+00	2.85E-04
Prkcz_chr4	4	2	9	4	-0.8	1.7	-1.2	2.4	**9.85E-03**	**5.00E-05**	4.68E-01	2.85E-04
Prkd1_chr12	1	1	2	1	0.0	1.0	-0.7	1.6	**5.66E-01**	**5.00E-05**	1.00E+00	2.85E-04
Prkd3_chr17	6	6	16	11	0.1	1.1	-0.8	1.8	**8.25E-01**	**3.62E-03**	1.00E+00	1.30E-02
Prmt2_chr10	4	6	7	5	0.4	1.3	-0.6	1.5	**3.58E-01**	**2.96E-02**	9.94E-01	6.21E-02
Prr5_chr15	10	14	19	12	0.5	1.4	-0.7	1.6	**3.45E-02**	**1.50E-04**	7.66E-01	7.89E-04
Prrg3_chrX	1	1	2	1	0.3	1.3	-0.7	1.6	**3.54E-01**	**1.00E-04**	9.98E-01	5.44E-04
Prss12_chr3	2	2	3	1	0.1	1.1	-1.5	2.8	**8.53E-01**	**5.00E-05**	1.00E+00	2.85E-04
Prss23_chr7	4	5	6	4	0.4	1.3	-0.6	1.5	**1.73E-01**	**2.00E-04**	9.82E-01	1.02E-03
Prune2_chr19	1	0	2	0	0.0	1.0	-0.8	1.8	**6.63E-03**	**5.00E-05**	2.90E-01	2.85E-04
Ptgfrn_chr3	3	3	7	5	0.2	1.1	-0.7	1.6	**4.48E-01**	**5.00E-05**	1.00E+00	2.85E-04
Pth1r_chr9	2	1	3	1	-0.2	1.1	-1.5	2.9	**5.59E-01**	**5.00E-04**	1.00E+00	2.44E-03
Ptp4a3_chr15	26	23	38	26	-0.3	1.2	-0.9	1.9	**5.47E-01**	**3.76E-02**	1.00E+00	9.19E-02
Ptpdc1_chr13	2	2	4	2	0.0	1.0	-0.9	1.8	**8.96E-01**	**5.00E-05**	1.00E+00	2.85E-04
Ptpn14_chr1	12	12	29	8	0.1	1.0	-1.9	3.7	**7.99E-01**	**5.00E-05**	1.00E+00	2.85E-04
Ptprcap_chr19	69	100	73	42	0.5	1.4	-0.8	1.7	**1.14E-02**	**5.00E-05**	4.96E-01	2.85E-04
Ptprf_chr4	2	2	6	4	0.1	1.1	-0.7	1.6	**7.84E-01**	**5.00E-05**	1.00E+00	2.85E-04
Ptrf_chr11	11	14	22	13	0.4	1.3	-0.8	1.7	**6.06E-02**	**5.00E-05**	8.75E-01	2.85E-04
Pxdn_chr12	2	2	5	2	-0.3	1.2	-1.5	2.9	**3.96E-01**	**5.00E-05**	1.00E+00	2.85E-04
Pxk_chr14	36	57	65	43	0.7	1.6	-0.6	1.5	**1.81E-03**	**1.75E-04**	1.82E-01	9.15E-04
Pygm_chr19	2	3	5	3	0.4	1.3	-0.7	1.6	**2.64E-01**	**5.00E-05**	9.94E-01	2.85E-04
Rab33b_chr3	10	9	14	9	-0.1	1.1	-0.6	1.5	**7.36E-01**	**5.00E-05**	1.00E+00	2.85E-04
Rab6b_chr9	5	1	10	0	-2.3	5.0	-3.3	9.7	**1.62E-14**	**5.00E-05**	5.03E-11	2.85E-04
Rabep2_chr7	22	24	37	24	0.1	1.1	-0.6	1.6	**6.53E-01**	**5.00E-05**	1.00E+00	2.85E-04
Rai2_chrX	1	1	2	1	0.0	1.0	-1.1	2.1	**7.61E-01**	**5.00E-05**	1.00E+00	2.70E-04
Ralgapa2_chr2	5	3	10	5	-0.5	1.4	-0.9	1.9	**1.96E-02**	**5.00E-05**	5.16E-01	2.85E-04
Ralgds_chr2	4	4	11	7	0.4	1.3	-0.7	1.6	**3.92E-01**	**4.45E-02**	9.85E-01	8.66E-02
Ralgps2_chr1	21	22	50	16	0.0	1.0	-1.7	3.2	**1.00E+00**	**5.98E-03**	1.00E+00	1.86E-02
Rap1gap_chr4	2	2	4	0	-0.2	1.1	-2.1	4.4	**1.00E+00**	**5.00E-05**	1.00E+00	2.74E-04
Rapgef4_chr2	17	11	27	4	-0.7	1.6	-2.7	6.3	**5.23E-03**	**5.00E-05**	2.65E-01	2.85E-04
Rarres2_chr6	23	27	21	13	0.2	1.2	-0.7	1.6	**4.86E-01**	**2.54E-02**	1.00E+00	6.84E-02

Rasa3_chr8	54	64	112	66	0.2	1.2	-0.8	1.7	**2.64E-01**	**5.00E-05**	9.94E-01	2.85E-04
Rasgrp2_chr19	45	51	71	44	0.2	1.1	-0.7	1.6	**3.73E-01**	**5.00E-05**	1.00E+00	2.85E-04
Rasl11a_chr5	2	4	3	2	0.7	1.7	-0.8	1.8	**9.69E-02**	**6.50E-04**	9.33E-01	2.93E-03
Rasl11b_chr5	3	3	4	2	0.0	1.0	-1.3	2.4	**9.42E-01**	**5.00E-05**	1.00E+00	2.85E-04
Rasl12_chr9	1	1	2	1	0.0	1.0	-0.8	1.7	**9.47E-01**	**3.00E-04**	1.00E+00	1.43E-03
Rassf2_chr2	43	52	90	49	0.3	1.2	-0.9	1.9	**2.53E-01**	**5.00E-05**	9.92E-01	2.85E-04
Rassf5_chr1	40	49	73	48	0.3	1.2	-0.6	1.5	**1.61E-01**	**1.50E-04**	9.78E-01	7.89E-04
Rbfox2_chr15	2	2	3	2	-0.1	1.0	-0.6	1.5	**8.85E-01**	**2.07E-02**	1.00E+00	5.61E-02
Rbms3_chr9	3	3	4	2	-0.1	1.1	-0.7	1.7	**6.54E-01**	**7.10E-03**	1.00E+00	2.34E-02
Rcan2_chr17	2	1	4	1	-0.8	1.7	-1.9	3.7	**7.91E-02**	**5.00E-05**	9.03E-01	2.85E-04
Rcn3_chr7	15	18	22	14	0.3	1.3	-0.7	1.6	**1.74E-01**	**1.00E-04**	9.84E-01	5.44E-04
Rdh12_chr12	7	8	8	6	0.2	1.1	-0.6	1.5	**5.94E-01**	**4.50E-04**	1.00E+00	2.12E-03
Reck_chr4	4	4	8	4	0.2	1.1	-0.9	1.9	**5.53E-01**	**5.00E-05**	1.00E+00	2.85E-04
Rem1_chr2	3	2	6	3	-0.1	1.0	-0.9	1.8	**8.92E-01**	**5.00E-05**	1.00E+00	2.85E-04
Rftn1_chr17	20	24	46	28	0.3	1.2	-0.7	1.6	**1.94E-01**	**5.00E-05**	9.87E-01	2.85E-04
Rgma_chr7	1	1	2	1	0.0	1.0	-1.1	2.1	**8.37E-01**	**5.00E-05**	1.00E+00	2.85E-04
Rgs9_chr11	1	1	2	1	-0.3	1.2	-1.0	2.0	**9.37E-02**	**5.00E-05**	8.00E-01	2.85E-04
Rhobtb2_chr14	11	13	24	16	0.2	1.1	-0.6	1.5	**3.76E-01**	**1.00E-04**	1.00E+00	5.44E-04
Rhoh_chr5	13	15	19	9	0.2	1.1	-1.0	2.0	**4.25E-01**	**5.00E-05**	1.00E+00	2.85E-04
Rnd3_chr2	14	11	21	13	-0.3	1.2	-0.7	1.7	**1.77E-01**	**5.00E-05**	9.84E-01	2.85E-04
Robo1_chr16	1	1	2	1	0.0	1.0	-0.7	1.6	**4.70E-01**	**5.00E-05**	1.00E+00	2.85E-04
Rps6ka5_chr12	6	7	11	7	0.3	1.2	-0.7	1.6	**2.84E-01**	**5.00E-05**	9.79E-01	2.85E-04
Rrm2b_chr15	15	13	22	13	-0.2	1.1	-0.7	1.7	**4.04E-01**	**5.00E-05**	1.00E+00	2.85E-04
Rsad1_chr11	2	1	3	2	-0.6	1.5	-0.8	1.8	**9.05E-02**	**5.00E-05**	9.27E-01	2.85E-04
Rundc3b_chr5	2	2	3	2	-0.3	1.2	-0.6	1.5	**3.62E-01**	**7.00E-04**	9.98E-01	3.13E-03
S1pr1_chr3	80	91	133	58	0.2	1.1	-1.2	2.3	**3.94E-01**	**5.00E-05**	1.00E+00	2.85E-04
S1pr3_chr13	14	15	28	12	0.1	1.1	-1.3	2.4	**7.16E-01**	**5.00E-05**	1.00E+00	2.85E-04
S1pr4_chr10	15	19	32	17	0.3	1.3	-0.9	1.9	**1.17E-01**	**5.00E-05**	9.45E-01	2.85E-04
Sash3_chrX	70	90	120	77	0.4	1.3	-0.6	1.6	**9.30E-02**	**1.00E-04**	9.27E-01	5.44E-04
Satb1_chr17	12	14	21	10	0.2	1.2	-1.0	2.0	**4.18E-01**	**3.89E-02**	9.91E-01	7.54E-02
Sbsn_chr7	1	1	2	0	-0.4	1.3	-0.7	1.6	**4.42E-01**	**5.00E-05**	1.00E+00	2.85E-04
Scaper_chr9	5	6	10	6	0.1	1.1	-0.7	1.6	**5.26E-01**	**5.00E-05**	1.00E+00	2.85E-04
Scara3_chr14	2	3	5	3	0.3	1.2	-0.7	1.6	**4.23E-01**	**5.00E-05**	1.00E+00	2.85E-04
Scara5_chr14	1	1	2	1	-0.2	1.2	-1.2	2.3	**5.84E-01**	**5.00E-05**	1.00E+00	2.85E-04
Scd1_chr19	97	120	187	77	0.3	1.2	-1.3	2.4	**2.36E-01**	**5.00E-05**	9.91E-01	2.85E-04
Scin_chr12	1	1	2	1	0.0	1.0	-0.6	1.5	**9.74E-01**	**5.00E-05**	1.00E+00	2.85E-04
Scml4_chr10	10	11	21	9	0.0	1.0	-1.2	2.3	**8.32E-01**	**5.00E-05**	1.00E+00	2.85E-04
Scn2b_chr9	3	3	5	2	-0.1	1.1	-1.3	2.5	**7.67E-01**	**4.90E-03**	1.00E+00	1.71E-02
Scn4b_chr9	1	1	3	0	-0.5	1.4	-1.6	2.9	**4.73E-03**	**5.00E-05**	3.40E-01	2.85E-04
Sdc4_chr2	23	34	39	22	0.6	1.5	-0.8	1.8	**4.15E-03**	**5.00E-05**	3.16E-01	2.85E-04
Sec16b_chr1	1	1	2	1	0.0	1.0	-0.6	1.6	**7.18E-01**	**4.95E-03**	1.00E+00	1.62E-02
Sema4f_chr6	2	2	4	2	0.2	1.1	-0.9	1.9	**6.90E-01**	**5.00E-05**	1.00E+00	2.85E-04
Sema5a_chr15	5	4	11	7	-0.1	1.1	-0.6	1.6	**6.59E-01**	**5.00E-05**	1.00E+00	2.85E-04
Sema7a_chr9	11	13	23	15	0.2	1.2	-0.6	1.5	**2.73E-01**	**1.00E-04**	9.94E-01	5.44E-04
Setbp1_chr18	7	8	15	9	0.2	1.2	-0.7	1.6	**2.99E-01**	**5.00E-05**	9.84E-01	2.85E-04
Setx_chr2	21	20	43	26	-0.1	1.1	-0.7	1.6	**6.72E-01**	**1.00E-04**	1.00E+00	5.44E-04
Sfmbt2_chr2	1	0	2	1	0.0	1.0	-0.8	1.7	**1.75E-01**	**5.00E-05**	9.62E-01	2.49E-04
Sgcd_chr11	1	1	2	1	0.0	1.0	-1.1	2.2	**8.66E-01**	**5.00E-05**	1.00E+00	2.85E-04
Sgpp2_chr1	1	1	2	1	-0.1	1.1	-0.7	1.6	**7.85E-01**	**5.00E-05**	1.00E+00	2.85E-04
Sh3bp4_chr1	1	1	4	2	-0.1	1.0	-0.7	1.6	**8.94E-01**	**5.00E-05**	1.00E+00	2.85E-04
Sh3bp5_chr14	54	66	95	48	0.3	1.2	-1.0	2.0	**1.81E-01**	**5.00E-05**	9.85E-01	2.85E-04
Sh3d19_chr3	2	2	3	2	0.3	1.2	-0.8	1.7	**3.55E-01**	**5.00E-05**	9.98E-01	2.85E-04
Sh3pxd2a_chr19	13	12	31	13	-0.1	1.1	-1.2	2.4	**6.60E-01**	**5.00E-05**	1.00E+00	2.85E-04
Sh3pxd2b_chr11	2	1	4	2	-0.3	1.3	-0.8	1.7	**2.94E-01**	**5.00E-05**	9.83E-01	2.85E-04
Shisa2_chr14	3	3	5	3	0.4	1.3	-0.8	1.8	**1.77E-01**	**5.00E-05**	9.84E-01	2.85E-04
Shroom3_chr5	2	3	3	2	0.3	1.3	-0.8	1.8	**2.87E-01**	**3.92E-02**	9.81E-01	8.91E-02
Sit1_chr4	5	5	7	3	0.0	1.0	-1.0	1.9	**9.60E-01**	**5.00E-05**	1.00E+00	2.85E-04
Ski_chr4	16	17	43	27	0.1	1.1	-0.7	1.6	**6.85E-01**	**5.00E-05**	1.00E+00	2.85E-04
Skil_chr3	10	10	18	12	0.0	1.0	-0.6	1.5	**8.90E-01**	**7.38E-03**	1.00E+00	2.39E-02
Slain1_chr14	6	7	12	7	0.4	1.3	-0.7	1.7	**1.87E-01**	**5.00E-05**	9.86E-01	2.85E-04
Slamf6_chr1	40	32	51	17	-0.3	1.3	-1.6	2.9	**1.18E-01**	**5.00E-05**	8.67E-01	2.85E-04
Slc16a2_chrX	2	1	4	2	-0.1	1.0	-1.2	2.2	**8.55E-01**	**5.00E-05**	1.00E+00	2.85E-04
Slc16a5_chr11	1	1	2	1	-0.3	1.2	-0.6	1.5	**4.79E-01**	**1.35E-03**	1.00E+00	5.55E-03
Slc1a2_chr2	1	1	2	1	-0.1	1.1	-0.9	1.8	**7.59E-01**	**5.00E-05**	1.00E+00	2.85E-04
Slc1a5_chr7	58	48	88	43	-0.3	1.2	-1.1	2.1	**1.99E-01**	**5.00E-05**	9.87E-01	2.85E-04
Slc22a3_chr17	2	1	3	2	-0.1	1.1	-0.9	1.8	**8.49E-01**	**5.00E-05**	1.00E+00	2.85E-04
Slc25a27_chr17	2	1	3	2	-0.7	1.6	-0.8	1.7	**1.04E-01**	**5.00E-05**	9.38E-01	2.85E-04
Slc25a29_chr12	1	2	2	1	0.5	1.4	-0.7	1.6	**3.25E-01**	**6.50E-04**	9.98E-01	2.93E-03
Slc25a53_chrX	13	13	15	10	0.1	1.1	-0.6	1.5	**7.92E-01**	**5.53E-03**	1.00E+00	1.90E-02
Slc2a1_chr4	14	19	30	15	0.4	1.3	-0.9	1.9	**8.43E-02**	**5.00E-05**	9.17E-01	2.85E-04
Slc2a9_chr5	2	2	3	2	0.0	1.0	-0.8	1.7	**9.53E-01**	**7.50E-05**	1.00E+00	3.94E-04
Slc36a2_chr11	1	1	3	1	-0.2	1.1	-1.5	2.8	**7.23E-01**	**5.00E-05**	1.00E+00	2.85E-04
Slc41a2_chr10	3	3	5	3	0.3	1.2	-0.8	1.8	**3.36E-01**	**5.00E-05**	9.98E-01	2.85E-04
Slc4a7_chr14	13	14	21	13	0.1	1.0	-0.7	1.7	**7.56E-01**	**5.00E-05**	1.00E+00	2.85E-04
Slc4a8_chr15	2	2	4	3	-0.1	1.1	-0.6	1.6	**7.43E-01**	**5.00E-05**	1.00E+00	2.85E-04
Slc5a6_chr5	2	2	3	2	0.2	1.1	-0.7	1.6	**6.93E-01**	**4.06E-02**	1.00E+00	9.85E-02
Slc7a11_chr3	2	1	4	2	-0.9	1.9	-1.2	2.2	**3.35E-07**	**5.00E-05**	1.76E-04	2.85E-04
Slc7a2_chr8	10	7	19	10	-0.5	1.4	-0.9	1.8	**2.13E-02**	**5.00E-05**	5.34E-01	2.85E-04
Slfn10-ps_chr11	3	2	6	3	-0.6	1.5	-0.9	1.9	**6.69E-02**	**5.00E-05**	7.70E-01	2.85E-04
Smad3_chr9	11	13	25	17	0.2	1.2	-0.6	1.5	**3.13E-01**	**5.00E-05**	9.97E-01	2.85E-04
Smad4_chr18	18	20	38	24	0.2	1.1	-0.6	1.6	**4.39E-01**	**5.00E-05**	1.00E+00	2.85E-04
Smad7_chr18	6	6	12	7	0.1	1.1	-0.8	1.7	**7.12E-01**	**5.00E-05**	1.00E+00	2.85E-04
Smim14_chr5	37	49	53	33	0.4	1.3	-0.7	1.6	**4.96E-02**	**5.00E-05**	8.46E-01	2.85E-04

Smurf1_chr5	5	5	12	6	0.1	1.1	-0.9	1.9	**7.86E-01**	**1.12E-03**	1.00E+00	4.47E-03
Snai2_chr16	1	1	2	1	0.3	1.2	-0.6	1.5	**5.96E-01**	**7.05E-03**	1.00E+00	2.32E-02
Snn_chr16	87	97	129	74	0.2	1.1	-0.8	1.7	**5.21E-01**	**1.00E-04**	1.00E+00	5.44E-04
Sntb1_chr15	3	2	7	4	-0.3	1.2	-0.9	1.8	**4.96E-01**	**5.00E-05**	1.00E+00	2.85E-04
Snx29_chr16	8	10	23	13	0.2	1.1	-0.8	1.8	**4.68E-01**	**5.00E-05**	1.00E+00	2.85E-04
Snx30_chr4	15	17	30	19	0.2	1.2	-0.7	1.6	**3.27E-01**	**5.00E-05**	9.98E-01	2.85E-04
Snx6_chr12	26	25	35	22	-0.1	1.0	-0.6	1.6	**7.73E-01**	**5.00E-05**	1.00E+00	2.85E-04
Sorcs2_chr5	1	1	2	1	0.0	1.0	-0.9	1.8	**9.57E-01**	**5.00E-05**	1.00E+00	2.85E-04
Spns2_chr11	11	13	24	11	0.2	1.2	-1.1	2.2	**3.33E-01**	**5.00E-05**	9.98E-01	2.85E-04
Sptan1_chr2	24	27	59	37	0.2	1.1	-0.7	1.6	**5.84E-01**	**2.17E-02**	1.00E+00	5.39E-02
Sptbn1_chr11	24	26	59	35	-0.1	1.1	-0.7	1.7	**4.95E-01**	**3.36E-02**	1.00E+00	7.61E-02
Srgap3_chr6	3	3	7	3	-0.1	1.1	-1.0	2.1	**6.80E-01**	**5.00E-05**	1.00E+00	2.85E-04
Srms_chr2	1	1	2	1	0.0	1.0	-0.8	1.7	**6.64E-01**	**5.00E-05**	1.00E+00	2.85E-04
Sspn_chr6	3	3	6	3	-0.1	1.1	-0.8	1.7	**6.08E-01**	**5.00E-05**	1.00E+00	2.85E-04
Ssu2_chr6	1	1	2	1	0.0	1.0	-0.6	1.5	**7.45E-01**	**1.50E-04**	1.00E+00	7.89E-04
St6gal1_chr16	32	44	54	29	0.4	1.3	-0.9	1.9	**1.19E-01**	**1.88E-03**	8.97E-01	6.80E-03
Stac2_chr11	3	5	7	4	0.6	1.5	-0.9	1.8	**4.66E-02**	**5.00E-05**	8.39E-01	2.85E-04
Stambpl1_chr19	8	9	11	6	0.2	1.1	-0.8	1.7	**5.31E-01**	**5.00E-05**	1.00E+00	2.85E-04
Star_chr8	25	16	41	27	-0.7	1.6	-0.6	1.5	**1.07E-03**	**5.00E-05**	9.04E-02	2.85E-04
Stau2_chr1	2	2	3	1	-0.5	1.4	-0.8	1.8	**3.30E-01**	**2.08E-03**	9.95E-01	7.69E-03
Stbd1_chr5	1	1	2	1	0.2	1.2	-0.8	1.8	**6.49E-01**	**2.00E-04**	1.00E+00	1.02E-03
Stk10_chr11	40	49	93	53	0.3	1.2	-0.8	1.8	**1.96E-01**	**5.00E-05**	9.87E-01	2.85E-04
Stk11ip_chr1	13	14	26	16	0.1	1.1	-0.7	1.6	**5.51E-01**	**5.00E-05**	1.00E+00	2.85E-04
Stk38l_chr6	5	5	8	5	-0.1	1.0	-0.7	1.6	**7.99E-01**	**5.00E-05**	1.00E+00	2.85E-04
Stk4_chr2	53	59	101	65	0.2	1.1	-0.6	1.5	**5.10E-01**	**2.50E-04**	1.00E+00	1.25E-03
Ston1_chr17	7	6	17	10	-0.3	1.2	-0.8	1.7	**2.94E-01**	**5.00E-05**	9.83E-01	2.85E-04
Strbp_chr2	8	7	12	7	0.0	1.0	-0.7	1.6	**8.36E-01**	**5.00E-05**	1.00E+00	2.85E-04
Stxbp1_chr2	4	4	10	6	-0.2	1.2	-0.7	1.6	**4.50E-01**	**5.00E-05**	1.00E+00	2.85E-04
Sufu_chr19	6	7	14	8	0.2	1.1	-0.8	1.7	**3.97E-01**	**1.33E-03**	1.00E+00	5.57E-03
Sulf1_chr1	2	1	4	2	-1.1	2.1	-1.5	2.9	**1.35E-02**	**5.00E-05**	4.19E-01	2.72E-04
Swap70_chr7	72	102	133	86	0.5	1.4	-0.6	1.5	**3.54E-02**	**5.50E-04**	7.70E-01	2.52E-03
Syk_chr13	68	83	141	83	0.3	1.2	-0.8	1.7	**3.98E-01**	**5.95E-03**	9.97E-01	1.92E-02
Synj2_chr17	2	2	5	2	0.2	1.1	-1.2	2.3	**6.67E-01**	**5.00E-05**	1.00E+00	2.85E-04
Taf1b_chr12	9	10	6	2	0.2	1.2	-1.9	3.8	**5.35E-01**	**2.50E-04**	1.00E+00	1.42E-03
Tagln_chr9	40	39	44	22	0.0	1.0	-1.0	2.0	**9.08E-01**	**1.80E-03**	1.00E+00	7.14E-03
Tbc1d1_chr5	13	14	28	19	0.1	1.1	-0.6	1.5	**5.57E-01**	**5.00E-05**	1.00E+00	2.85E-04
Tbc1d10c_chr19	73	83	102	67	0.2	1.1	-0.6	1.5	**3.70E-01**	**1.00E-04**	1.00E+00	5.44E-04
Tbc1d30_chr10	2	2	4	1	0.1	1.1	-1.5	2.8	**7.38E-01**	**5.00E-05**	1.00E+00	2.85E-04
Tbx3_chr5	1	1	2	1	0.0	1.0	-0.6	1.5	**7.99E-01**	**5.00E-05**	1.00E+00	2.61E-04
Tcf7_chr11	48	51	100	49	0.1	1.1	-1.0	2.0	**7.32E-01**	**5.00E-05**	1.00E+00	2.85E-04
Tcp11l1_chr2	1	1	4	2	-0.4	1.4	-0.7	1.6	**2.89E-01**	**5.00E-05**	9.81E-01	2.85E-04
Tctn2_chr5	1	1	2	1	0.0	1.0	-0.7	1.7	**6.83E-01**	**5.50E-04**	1.00E+00	2.52E-03
Tead3_chr17	1	0	2	1	0.0	1.0	-0.6	1.5	**5.18E-01**	**4.75E-02**	1.00E+00	1.15E-01
Tec_chr5	13	16	19	11	0.4	1.3	-0.8	1.8	**2.89E-01**	**7.77E-03**	9.85E-01	2.27E-02
Tecpr1_chr5	16	16	36	22	0.1	1.0	-0.7	1.6	**7.67E-01**	**5.00E-05**	1.00E+00	2.85E-04
Tenc1_chr15	11	8	29	19	-0.4	1.3	-0.6	1.5	**6.15E-02**	**1.00E-04**	8.76E-01	5.44E-04
Tet1_chr10	1	1	2	1	0.0	1.0	-0.9	1.8	**2.92E-02**	**5.00E-05**	6.20E-01	2.85E-04
Tgfbr3_chr5	8	9	20	13	0.1	1.1	-0.6	1.5	**6.11E-01**	**5.00E-05**	1.00E+00	2.85E-04
Thbs2_chr17	4	5	10	6	0.2	1.2	-0.9	1.9	**3.98E-01**	**5.00E-05**	1.00E+00	2.85E-04
Them4_chr3	2	1	2	1	-0.1	1.1	-0.7	1.6	**8.19E-01**	**2.85E-03**	1.00E+00	1.07E-02
Themis_chr10	8	6	13	6	-0.5	1.4	-1.0	2.0	**5.38E-02**	**5.00E-05**	7.38E-01	2.85E-04
Thrsp_chr7	1	1	2	1	-0.3	1.3	-0.7	1.6	**4.30E-01**	**1.65E-03**	1.00E+00	6.61E-03
Thy1_chr9	24	32	36	21	0.4	1.3	-0.8	1.7	**6.45E-02**	**5.00E-05**	7.70E-01	2.85E-04
Timp3_chr10	29	29	52	34	0.0	1.0	-0.6	1.5	**9.60E-01**	**5.00E-05**	1.00E+00	2.85E-04
Tlr11_chr14	8	6	11	7	-0.5	1.4	-0.7	1.6	**7.82E-02**	**1.00E-04**	9.04E-01	5.44E-04
Tlr3_chr8	7	6	12	7	-0.3	1.2	-0.7	1.6	**2.46E-01**	**5.00E-05**	9.92E-01	2.85E-04
Tmed8_chr12	16	18	30	19	0.1	1.1	-0.6	1.5	**6.05E-01**	**2.50E-04**	1.00E+00	1.25E-03
Tmem163_chr1	3	4	4	2	0.4	1.3	-1.3	2.4	**2.61E-01**	**5.00E-05**	9.94E-01	2.85E-04
Tmem200b_chr4	2	2	4	2	-0.2	1.2	-1.2	2.4	**6.08E-01**	**5.00E-05**	1.00E+00	2.85E-04
Tmem98_chr11	3	4	6	4	0.4	1.3	-0.6	1.6	**3.06E-01**	**4.00E-04**	9.96E-01	1.91E-03
Tmtc1_chr6	2	2	5	3	-0.2	1.2	-0.8	1.7	**5.71E-01**	**3.09E-02**	1.00E+00	8.01E-02
Tnfrsf1b_chr4	17	4	37	7	-2.2	4.6	-2.4	5.3	**1.00E-20**	**5.00E-05**	1.00E-20	2.85E-04
Tnfrsf22_chr7	3	3	5	3	0.2	1.2	-0.7	1.6	**5.20E-01**	**2.00E-04**	1.00E+00	1.02E-03
Tnfrsf25_chr4	3	3	4	2	0.0	1.0	-0.7	1.7	**9.18E-01**	**1.50E-04**	1.00E+00	7.89E-04
Tnik_chr3	4	5	7	4	0.1	1.1	-1.0	2.0	**7.46E-01**	**8.00E-04**	1.00E+00	3.37E-03
Tnn_chr1	3	1	8	2	-1.6	3.1	-2.1	4.3	**1.82E-09**	**5.00E-05**	9.93E-07	2.85E-04
Tnrc6c_chr11	14	13	29	18	0.0	1.0	-0.7	1.6	**8.37E-01**	**5.00E-05**	1.00E+00	2.85E-04
Tnxb_chr17	14	11	41	20	-0.3	1.2	-1.0	2.0	**1.87E-01**	**5.00E-05**	9.86E-01	2.85E-04
Tox_chr4	3	3	5	3	0.2	1.1	-1.0	2.0	**6.26E-01**	**5.00E-05**	1.00E+00	2.85E-04
Tpm2_chr4	4	5	5	3	0.2	1.2	-0.8	1.7	**5.08E-01**	**5.00E-05**	1.00E+00	2.85E-04
Traf3ip2_chr10	8	10	17	9	0.3	1.2	-0.9	1.9	**2.12E-01**	**5.00E-05**	9.88E-01	2.85E-04
Traf3ip3_chr1	61	62	89	57	0.0	1.0	-0.6	1.5	**9.07E-01**	**2.00E-04**	1.00E+00	1.02E-03
Traf5_chr1	17	23	38	21	0.4	1.3	-0.9	1.8	**1.25E-01**	**5.00E-05**	9.50E-01	2.85E-04
Trib2_chr12	13	13	23	11	-0.1	1.0	-1.1	2.1	**7.66E-01**	**5.00E-05**	1.00E+00	2.85E-04
Trim34b_chr7	5	4	8	1	-0.2	1.1	-2.6	5.9	**6.37E-01**	**5.00E-05**	1.00E+00	2.85E-04
Trim35_chr14	28	34	56	35	0.3	1.2	-0.7	1.6	**1.42E-01**	**5.00E-05**	9.65E-01	2.85E-04
Trim36_chr18	3	3	5	3	0.2	1.1	-0.8	1.7	**5.77E-01**	**5.00E-05**	1.00E+00	2.85E-04
Trim68_chr7	7	7	11	5	0.0	1.0	-1.1	2.1	**9.23E-01**	**5.00E-05**	1.00E+00	2.85E-04
Trp53i11_chr2	32	42	66	42	0.4	1.3	-0.7	1.6	**6.85E-02**	**5.00E-05**	8.77E-01	2.85E-04
Tspan15_chr10	8	9	13	7	0.2	1.2	-0.9	1.9	**3.62E-01**	**5.00E-05**	9.98E-01	2.85E-04
Ttc28_chr5	4	5	13	7	0.1	1.1	-0.8	1.8	**5.26E-01**	**5.00E-05**	1.00E+00	2.85E-04
Tubb2b_chr13	3	3	4	2	-0.3	1.2	-0.8	1.8	**4.06E-01**	**5.00E-05**	1.00E+00	2.85E-04
Tubg2_chr11	2	2	2	1	0.4	1.3	-0.7	1.6	**3.94E-01**	**1.45E-03**	1.00E+00	5.90E-03

Txk_chr5	7	7	10	6	-0.1	1.0	-0.6	1.5	**8.41E-01**	**2.38E-04**	1.00E+00	1.17E-03
Txnip_chr3	123	150	206	122	0.3	1.2	-0.8	1.7	**4.14E-01**	**4.07E-03**	9.98E-01	1.44E-02
Ube2d1_chr10	17	22	21	13	0.4	1.3	-0.6	1.6	**1.30E-01**	**5.00E-05**	9.55E-01	2.85E-04
Ubtd2_chr11	3	3	5	3	0.0	1.0	-0.6	1.5	**9.47E-01**	**2.00E-04**	1.00E+00	1.02E-03
Upb1_chr10	1	1	2	1	-0.1	1.1	-0.6	1.5	**7.92E-01**	**5.00E-05**	1.00E+00	2.85E-04
Usp28_chr9	7	7	13	8	-0.1	1.0	-0.8	1.7	**8.30E-01**	**5.00E-05**	1.00E+00	2.85E-04
Usp53_chr3	4	3	7	4	-0.1	1.1	-0.8	1.7	**6.42E-01**	**5.00E-05**	1.00E+00	2.85E-04
Utp14b_chr1	3	3	5	3	0.2	1.2	-0.8	1.7	**5.91E-01**	**1.41E-03**	1.00E+00	5.76E-03
Utrn_chr10	13	11	28	17	-0.2	1.1	-0.7	1.6	**3.88E-01**	**5.00E-05**	1.00E+00	2.85E-04
Vamp1_chr6	22	24	28	18	0.1	1.0	-0.6	1.6	**7.47E-01**	**5.00E-05**	1.00E+00	2.85E-04
Vangl2_chr1	1	1	3	2	0.6	1.5	-0.6	1.5	**1.41E-01**	**3.55E-03**	9.65E-01	1.29E-02
Vldlr_chr19	2	2	4	1	-0.5	1.4	-2.1	4.4	**1.14E-01**	**5.00E-05**	9.01E-01	2.61E-04
Vmn2r84_chr10	1	1	2	1	0.0	1.0	-0.6	1.6	**3.34E-01**	**5.00E-05**	9.98E-01	2.85E-04
Wdfy4_chr14	50	54	140	78	0.1	1.1	-0.8	1.8	**6.99E-01**	**5.00E-05**	1.00E+00	2.85E-04
Wnt5a_chr14	1	2	2	1	0.3	1.3	-0.6	1.6	**4.65E-01**	**4.23E-03**	1.00E+00	1.44E-02
Wwc2_chr8	3	3	6	4	0.0	1.0	-0.7	1.6	**9.77E-01**	**5.00E-05**	1.00E+00	2.85E-04
Xcr1_chr9	5	3	6	3	-0.8	1.8	-0.9	1.9	**3.07E-03**	**5.00E-05**	2.63E-01	2.85E-04
Xrcc6bp1_chr10	2	2	4	2	0.0	1.0	-1.1	2.2	**9.41E-01**	**5.00E-05**	1.00E+00	2.85E-04
Xylt1_chr7	4	4	12	7	0.2	1.1	-0.7	1.7	**6.02E-01**	**5.00E-05**	1.00E+00	2.85E-04
Xylt2_chr11	5	5	11	7	-0.1	1.1	-0.6	1.5	**6.70E-01**	**3.00E-04**	1.00E+00	1.47E-03
Zbtb10_chr3	3	3	5	2	0.0	1.0	-0.9	1.9	**9.29E-01**	**5.00E-05**	1.00E+00	2.85E-04
Zbtb4_chr11	16	17	31	18	0.1	1.1	-0.8	1.7	**6.19E-01**	**5.00E-05**	1.00E+00	2.85E-04
Zbtb8a_chr4	2	1	3	2	-0.4	1.4	-0.7	1.7	**3.19E-01**	**2.50E-04**	9.97E-01	1.25E-03
Zcchc11_chr4	27	30	50	31	0.1	1.1	-0.7	1.6	**5.60E-01**	**5.00E-05**	1.00E+00	2.85E-04
Zfp109_chr7	1	1	2	1	0.0	1.0	-0.7	1.7	**3.74E-01**	**5.00E-04**	1.00E+00	2.32E-03
Zfp235_chr7	2	2	3	2	-0.1	1.0	-0.7	1.6	**8.52E-01**	**1.00E-04**	1.00E+00	5.44E-04
Zfp239_chr6	2	1	3	2	-0.3	1.3	-0.6	1.6	**5.34E-01**	**7.66E-03**	8.94E-01	2.39E-02
Zfp27_chr7	2	2	3	2	0.1	1.1	-0.6	1.5	**7.78E-01**	**1.43E-03**	1.00E+00	5.90E-03
Zfp275_chrX	7	6	9	6	-0.1	1.1	-0.6	1.5	**6.79E-01**	**2.58E-02**	1.00E+00	6.97E-02
Zfp296_chr7	4	5	6	4	0.3	1.2	-0.7	1.6	**4.50E-01**	**1.50E-04**	1.00E+00	7.89E-04
Zfp318_chr17	19	18	17	6	-0.2	1.1	-1.5	2.9	**6.22E-01**	**9.00E-04**	1.00E+00	4.23E-03
Zfp354c_chr11	2	2	3	2	-0.3	1.2	-0.8	1.7	**4.02E-01**	**5.00E-05**	1.00E+00	2.85E-04
Zfp362_chr4	14	13	27	16	-0.1	1.1	-0.7	1.7	**5.98E-01**	**5.00E-05**	1.00E+00	2.85E-04
Zfp420_chr7	4	4	5	3	-0.1	1.1	-0.7	1.6	**7.15E-01**	**1.50E-04**	1.00E+00	7.89E-04
Zfp46_chr4	4	3	7	4	-0.3	1.2	-0.8	1.8	**3.37E-01**	**5.00E-05**	9.98E-01	2.85E-04
Zfp462_chr4	1	1	2	1	0.0	1.0	-0.6	1.5	**6.56E-01**	**2.00E-04**	1.00E+00	1.02E-03
Zfp60_chr7	6	7	9	6	0.1	1.1	-0.6	1.5	**6.11E-01**	**7.50E-05**	1.00E+00	4.28E-04
Zfp651_chr9	1	1	2	1	0.0	1.0	-0.6	1.5	**6.57E-01**	**2.50E-04**	1.00E+00	1.25E-03
Zfp747_chr7	3	4	5	3	0.3	1.2	-0.6	1.5	**3.56E-01**	**2.00E-04**	9.98E-01	1.02E-03
Zfp764_chr7	4	4	5	3	0.1	1.0	-0.7	1.6	**8.46E-01**	**7.50E-04**	1.00E+00	3.39E-03
Zfp82_chr7	3	3	4	2	0.1	1.1	-1.4	2.7	**8.13E-01**	**5.00E-05**	1.00E+00	2.85E-04
Zfp827_chr8	2	2	4	2	-0.2	1.2	-1.1	2.2	**3.95E-01**	**5.00E-05**	1.00E+00	2.85E-04
Zfp868_chr8	28	16	20	6	-0.9	1.8	-2.2	4.5	**1.68E-04**	**5.00E-05**	2.20E-02	2.85E-04
Zfp949_chr9	27	23	37	5	-0.3	1.2	-3.2	9.4	**3.37E-01**	**5.00E-05**	9.95E-01	2.85E-04
Zfp964_chr8	1	1	2	1	-0.1	1.1	-0.8	1.7	**7.61E-01**	**5.00E-05**	1.00E+00	2.85E-04
Zhx2_chr15	7	10	18	11	0.4	1.4	-0.8	1.7	**4.68E-02**	**5.00E-05**	8.39E-01	2.85E-04
Znf41-ps_chr4	5	1	6	2	-2.2	4.6	-1.5	2.9	**2.67E-08**	**5.00E-05**	1.70E-05	2.82E-04
Zpbp_chr11	1	1	2	1	0.0	1.0	-0.7	1.6	**7.78E-01**	**3.50E-04**	1.00E+00	1.56E-03
Zscan2_chr7	2	2	3	2	0.1	1.1	-0.6	1.6	**8.43E-01**	**6.50E-04**	1.00E+00	2.93E-03
Zscan20_chr4	3	3	6	4	0.2	1.2	-0.7	1.6	**4.50E-01**	**5.00E-05**	1.00E+00	2.85E-04
Zyg11b_chr4	8	8	16	11	-0.1	1.1	-0.6	1.5	**6.35E-01**	**5.00E-05**	1.00E+00	2.85E-04
1700049G17Rik_chr7	3	3	4	2	0.0	1.0	-1.2	2.4	**8.61E-01**	**5.00E-05**	1.00E+00	2.85E-04
4632428C04Rik_chr16	3	3	5	2	0.1	1.1	-0.9	1.9	**6.97E-01**	**5.00E-05**	1.00E+00	2.82E-04
A430078G23Rik_chr8	19	18	39	20	-0.1	1.0	-1.0	1.9	**7.52E-01**	**5.00E-05**	1.00E+00	2.85E-04
Adamts6_chr13	3	3	7	3	0.0	1.0	-1.0	2.0	**9.87E-01**	**5.00E-05**	1.00E+00	2.85E-04
Add3_chr19	22	31	27	7	0.5	1.4	-1.9	3.9	**2.72E-01**	**3.50E-04**	9.38E-01	1.92E-03
Adm_chr7	1	1	2	1	-0.4	1.4	-0.8	1.8	**3.94E-01**	**5.00E-05**	1.00E+00	2.85E-04
Aff3_chr1	12	17	31	13	0.5	1.4	-1.2	2.3	**2.53E-02**	**5.00E-05**	5.78E-01	2.85E-04
Agpat9_chr5	2	3	3	2	0.3	1.3	-0.9	1.9	**3.46E-01**	**5.00E-05**	9.98E-01	2.85E-04
Ankrd37_chr8	3	4	3	2	0.4	1.3	-0.6	1.5	**4.27E-01**	**7.80E-03**	1.00E+00	2.53E-02
Ano1_chr7	2	3	6	2	0.1	1.1	-1.4	2.6	**6.76E-01**	**5.00E-05**	1.00E+00	2.85E-04
Atp1b1_chr1	10	11	16	6	0.1	1.0	-1.5	2.9	**7.94E-01**	**5.00E-05**	1.00E+00	2.85E-04
B3gnt8_chr7	5	6	8	3	0.5	1.4	-1.5	2.7	**2.76E-01**	**1.10E-04**	9.93E-01	6.12E-04
Bach2_chr4	13	16	29	13	0.3	1.2	-1.2	2.3	**1.99E-01**	**5.00E-05**	9.48E-01	2.85E-04
BC094916_chr1	18	12	20	12	-0.5	1.5	-0.8	1.7	**4.14E-02**	**5.00E-05**	6.94E-01	2.85E-04
Cacna1e_chr1	12	11	25	13	-0.1	1.1	-1.0	2.0	**5.75E-01**	**5.00E-05**	1.00E+00	2.85E-04
Cacna1i_chr15	6	8	15	4	0.4	1.3	-1.8	3.5	**6.52E-02**	**5.00E-05**	8.76E-01	2.85E-04
Card6_chr15	17	20	32	16	0.2	1.1	-1.0	2.0	**3.75E-01**	**5.00E-05**	1.00E+00	2.85E-04
Ccr7_chr11	36	46	61	25	0.3	1.3	-1.3	2.4	**9.48E-02**	**5.00E-05**	9.27E-01	2.85E-04
Cd19_chr7	205	259	275	144	0.3	1.3	-0.9	1.9	**2.10E-01**	**5.00E-05**	9.88E-01	2.85E-04
Cd2_chr3	44	54	45	22	0.3	1.2	-1.0	2.0	**1.53E-01**	**5.00E-05**	9.73E-01	2.85E-04
Cd209a_chr8	11	14	12	6	0.3	1.3	-1.0	2.0	**1.85E-01**	**5.00E-05**	9.86E-01	2.85E-04
Cd40lg_chrX	3	3	4	2	0.0	1.0	-1.2	2.2	**9.15E-01**	**5.00E-05**	1.00E+00	2.85E-04
Cd55_chr1	86	100	119	58	0.2	1.2	-1.0	2.0	**3.17E-01**	**5.00E-05**	9.97E-01	2.85E-04
Cd79a_chr7	264	389	256	121	0.6	1.5	-1.1	2.1	**2.71E-02**	**5.00E-05**	7.04E-01	2.85E-04
Chst3_chr10	28	32	54	30	0.2	1.1	-0.9	1.8	**4.13E-01**	**5.00E-05**	1.00E+00	2.85E-04
Clic5_chr17	23	20	43	21	-0.2	1.2	-1.1	2.1	**2.99E-01**	**5.00E-05**	9.84E-01	2.85E-04
Col14a1_chr15	16	17	37	22	0.1	1.1	-0.7	1.7	**6.91E-01**	**5.00E-05**	1.00E+00	2.85E-04
Cpe_chr8	3	4	5	2	0.3	1.2	-1.6	3.0	**4.49E-01**	**5.00E-05**	1.00E+00	2.85E-04
Cpm_chr10	6	7	10	3	0.3	1.2	-1.6	3.1	**2.66E-01**	**5.00E-05**	9.94E-01	2.85E-04
Crisp3_chr17	3	3	3	2	-0.2	1.1	-1.1	2.1	**7.13E-01**	**5.00E-05**	1.00E+00	2.85E-04
Cxcr5_chr9	42	78	80	51	0.9	1.8	-0.6	1.6	**3.50E-05**	**5.00E-05**	8.24E-03	2.85E-04
Cyp21a1_chr17	6	4	11	3	-0.6	1.6	-1.8	3.4	**4.94E-02**	**5.00E-05**	8.46E-01	2.85E-04

Ebf1_chr11	29	32	60	20	0.2	1.1	-1.6	3.0	**4.16E-01**	**5.00E-05**	1.00E+00	2.85E-04
Efr3b_chr12	1	1	2	1	0.0	1.0	-0.9	1.9	**3.65E-01**	**5.00E-05**	9.99E-01	2.85E-04
Egr1_chr18	6	8	13	7	0.4	1.3	-0.8	1.8	**1.05E-01**	**5.00E-05**	9.38E-01	2.85E-04
Faim3_chr1	94	150	154	75	0.7	1.6	-1.0	2.0	**1.60E-03**	**5.00E-05**	1.73E-01	2.85E-04
Fam129c_chr8	36	30	59	17	-0.3	1.2	-1.8	3.5	**1.86E-01**	**5.00E-05**	9.86E-01	2.85E-04
Fchsd2_chr7	32	45	55	28	0.5	1.4	-1.0	2.0	**2.21E-02**	**5.00E-05**	5.43E-01	2.85E-04
Ffar1_chr7	8	9	17	7	0.1	1.1	-1.2	2.2	**7.45E-01**	**5.00E-05**	1.00E+00	2.85E-04
Fndc7_chr3	1	1	2	1	-0.4	1.3	-1.3	2.5	**9.92E-02**	**5.00E-05**	9.21E-01	2.85E-04
Foxo1_chr3	23	30	43	22	0.4	1.3	-0.9	1.9	**9.34E-02**	**5.00E-05**	9.27E-01	2.85E-04
Gdf11_chr10	11	13	22	12	0.3	1.3	-0.8	1.8	**1.78E-01**	**5.00E-05**	9.84E-01	2.85E-04
Gdf6_chr4	5	10	9	5	1.0	2.0	-0.7	1.7	**1.01E-04**	**5.00E-05**	1.41E-02	2.85E-04
Gga2_chr7	24	35	47	26	0.5	1.4	-0.9	1.8	**1.86E-02**	**5.00E-05**	6.08E-01	2.85E-04
H2-Ob_chr17	158	184	205	128	0.2	1.2	-0.7	1.6	**3.86E-01**	**1.50E-04**	1.00E+00	7.89E-04
Havcr1_chr11	2	2	3	0	0.2	1.1	-1.4	2.6	**6.93E-01**	**4.46E-03**	1.00E+00	1.56E-02
Hba-a1_chr11	543	1,058	210	53	1.0	1.9	-2.0	4.1	**3.76E-04**	**6.65E-03**	6.21E-02	2.18E-02
Hepacam2_chr6	5	4	5	3	-0.1	1.0	-0.8	1.8	**8.40E-01**	**5.00E-05**	1.00E+00	2.85E-04
Hivep2_chr10	12	13	28	16	0.1	1.1	-0.9	1.8	**5.20E-01**	**5.00E-05**	1.00E+00	2.85E-04
Hivep3_chr4	2	2	6	3	-0.1	1.1	-0.7	1.7	**7.57E-01**	**5.00E-05**	1.00E+00	2.85E-04
Hs3st3a1_chr11	2	2	3	2	0.2	1.1	-0.8	1.7	**5.90E-01**	**5.00E-05**	1.00E+00	2.85E-04
Ikzf3_chr11	71	76	153	79	0.1	1.1	-1.0	1.9	**6.59E-01**	**5.00E-05**	1.00E+00	2.85E-04
Il5ra_chr6	4	4	6	2	-0.2	1.2	-1.4	2.7	**4.07E-01**	**5.00E-05**	1.00E+00	2.85E-04
Itga8_chr2	5	4	9	3	-0.2	1.2	-1.4	2.7	**3.46E-01**	**5.00E-05**	9.93E-01	2.85E-04
Itk_chr11	16	14	31	14	-0.2	1.2	-1.2	2.2	**2.53E-01**	**5.00E-05**	9.70E-01	2.85E-04
Itpr3_chr17	28	29	69	35	0.0	1.0	-1.0	1.9	**8.93E-01**	**5.00E-05**	1.00E+00	2.85E-04
Jag1_chr2	5	6	10	6	0.3	1.3	-0.7	1.6	**1.71E-01**	**5.00E-05**	9.81E-01	2.85E-04
Jakmip1_chr5	12	14	25	12	0.2	1.1	-1.0	2.0	**4.59E-01**	**5.00E-05**	1.00E+00	2.85E-04
Kcnd3_chr3	1	2	3	1	0.3	1.2	-1.0	1.9	**5.57E-01**	**5.00E-05**	1.00E+00	2.85E-04
Kcnq5_chr1	1	2	3	2	0.2	1.1	-0.8	1.8	**6.02E-01**	**5.00E-05**	1.00E+00	2.85E-04
Klhl14_chr18	5	7	10	5	0.5	1.4	-1.1	2.2	**6.60E-02**	**5.00E-05**	8.76E-01	2.85E-04
Kmo_chr1	29	38	45	29	0.4	1.3	-0.6	1.6	**6.04E-02**	**5.00E-05**	8.74E-01	2.85E-04
Kmt2a_chr9	26	24	57	36	-0.1	1.1	-0.7	1.6	**6.77E-01**	**3.00E-04**	1.00E+00	1.47E-03
L1cam_chrX	3	3	6	3	0.2	1.2	-0.9	1.9	**4.16E-01**	**5.00E-05**	1.00E+00	2.85E-04
Lef1_chr3	11	12	27	9	0.1	1.1	-1.5	2.9	**5.88E-01**	**5.00E-05**	1.00E+00	2.85E-04
Lgals4_chr7	4	4	5	3	0.0	1.0	-1.0	2.0	**9.51E-01**	**5.00E-05**	1.00E+00	2.85E-04
Ltbp2_chr12	3	6	10	4	0.8	1.8	-1.1	2.2	**8.20E-04**	**5.00E-05**	1.11E-01	2.85E-04
Ly6d_chr15	176	226	141	69	0.4	1.3	-1.0	2.1	**9.20E-02**	**5.00E-05**	9.27E-01	2.85E-04
Lynx1_chr15	14	12	26	7	-0.2	1.1	-1.8	3.5	**4.76E-01**	**5.00E-05**	1.00E+00	2.85E-04
Mapk11_chr15	13	21	21	11	0.7	1.6	-0.9	1.9	**1.88E-03**	**5.00E-05**	1.88E-01	2.85E-04
Marveld2_chr13	3	2	5	2	-0.4	1.3	-1.4	2.7	**2.46E-01**	**5.00E-05**	9.98E-01	2.85E-04
Mcoln3_chr3	4	4	6	4	0.1	1.1	-0.8	1.7	**7.54E-01**	**5.00E-05**	1.00E+00	2.85E-04
Mef2c_chr13	29	36	51	26	0.3	1.3	-1.0	1.9	**3.11E-01**	**3.38E-03**	9.93E-01	1.14E-02
Mex3b_chr7	2	2	4	2	0.0	1.0	-0.7	1.6	**9.65E-01**	**5.00E-05**	1.00E+00	2.85E-04
Mfap4_chr11	3	3	4	2	0.1	1.1	-1.2	2.2	**7.95E-01**	**5.00E-05**	1.00E+00	2.85E-04
Mmp12_chr9	2	4	3	1	0.7	1.6	-1.1	2.1	**2.06E-02**	**5.00E-05**	6.41E-01	2.85E-04
Ms4a1_chr19	346	336	447	218	0.0	1.0	-1.0	2.1	**8.82E-01**	**5.00E-05**	1.00E+00	2.85E-04
Nrep_chr18	3	2	4	2	-0.4	1.3	-0.9	1.9	**3.67E-01**	**5.00E-05**	9.90E-01	2.70E-04
Ntn1_chr11	1	1	3	1	-0.3	1.2	-1.3	2.5	**4.63E-01**	**5.00E-05**	1.00E+00	2.85E-04
Ogn_chr13	4	2	5	3	-0.9	1.8	-0.9	1.8	**3.32E-02**	**2.23E-02**	7.65E-01	6.14E-02
Olfml2a_chr2	1	3	5	3	0.8	1.8	-0.6	1.5	**3.39E-02**	**4.00E-04**	7.66E-01	1.91E-03
Olfr164_chr16	3	3	4	2	-0.3	1.2	-1.4	2.6	**5.23E-01**	**5.00E-05**	1.00E+00	2.85E-04
Pax5_chr4	67	89	159	75	0.4	1.3	-1.1	2.1	**4.68E-02**	**5.00E-05**	7.18E-01	2.85E-04
Pgap1_chr1	10	12	18	11	0.2	1.2	-0.7	1.6	**2.93E-01**	**5.00E-05**	9.83E-01	2.85E-04
Pik3c2b_chr1	14	16	33	18	0.1	1.1	-0.9	1.8	**5.03E-01**	**5.00E-05**	1.00E+00	2.85E-04
Plekhg2_chr7	13	13	28	15	0.1	1.0	-1.0	1.9	**5.58E-01**	**4.50E-04**	1.00E+00	2.06E-03
Plxna3_chrX	2	2	3	2	0.0	1.0	-0.6	1.6	**9.05E-01**	**1.50E-04**	1.00E+00	7.89E-04
Prkcb_chr7	54	60	104	61	0.2	1.1	-0.8	1.7	**5.56E-01**	**5.00E-05**	1.00E+00	2.85E-04
Prkcg_chr7	1	2	2	2	0.6	1.5	-0.7	1.6	**1.30E-01**	**5.50E-04**	9.55E-01	2.52E-03
Pxdc1_chr13	18	28	25	13	0.6	1.6	-1.0	2.0	**4.43E-03**	**5.00E-05**	3.28E-01	2.85E-04
Rasgrp1_chr2	26	29	51	23	0.1	1.1	-1.1	2.2	**4.81E-01**	**5.00E-05**	1.00E+00	2.85E-04
Rel_chr11	21	23	44	26	0.1	1.1	-0.7	1.7	**5.47E-01**	**5.00E-05**	1.00E+00	2.85E-04
Rftn2_chr1	3	3	4	2	0.2	1.1	-1.2	2.4	**5.65E-01**	**5.00E-05**	1.00E+00	2.85E-04
Rhof_chr5	16	25	27	15	0.6	1.6	-0.9	1.8	**3.96E-03**	**5.00E-05**	3.11E-01	2.85E-04
Sbk1_chr7	25	29	55	25	0.2	1.2	-1.1	2.2	**3.11E-01**	**5.00E-05**	9.97E-01	2.85E-04
Scn4a_chr11	4	5	9	4	0.2	1.1	-1.0	2.0	**4.11E-01**	**5.00E-05**	1.00E+00	2.85E-04
Sesn3_chr9	19	22	50	27	0.2	1.1	-0.9	1.9	**4.33E-01**	**5.00E-05**	1.00E+00	2.85E-04
Sfn_chr4	4	5	7	4	0.4	1.3	-0.9	1.9	**3.27E-01**	**5.00E-05**	9.98E-01	2.85E-04
Siglecg_chr7	91	107	112	70	0.2	1.2	-0.7	1.6	**2.95E-01**	**5.00E-05**	9.96E-01	2.85E-04
Siglech_chr7	19	16	25	5	-0.3	1.2	-2.2	4.6	**2.59E-01**	**5.00E-05**	9.72E-01	2.85E-04
Slc9a7_chrX	11	12	27	14	0.1	1.1	-0.9	1.9	**6.19E-01**	**5.00E-05**	1.00E+00	2.85E-04
Sox4_chr13	4	4	8	4	0.0	1.0	-0.8	1.8	**9.62E-01**	**5.00E-05**	1.00E+00	2.85E-04
Spib_chr7	107	136	178	75	0.3	1.3	-1.2	2.4	**1.37E-01**	**5.00E-05**	9.60E-01	2.85E-04
Srpk3_chrX	23	28	30	16	0.3	1.2	-0.9	1.9	**2.41E-01**	**5.00E-05**	9.92E-01	2.85E-04
Srpx_chrX	3	3	4	2	0.0	1.0	-1.3	2.5	**9.80E-01**	**5.00E-05**	1.00E+00	2.85E-04
St8sia1_chr6	3	3	5	3	-0.1	1.1	-0.9	1.8	**6.54E-01**	**5.00E-05**	1.00E+00	2.85E-04
Synpo2_chr3	6	9	15	10	0.6	1.5	-0.6	1.5	**4.74E-03**	**5.00E-05**	2.52E-01	2.85E-04
Tdrp_chr8	4	4	7	2	-0.1	1.1	-1.7	3.2	**7.16E-01**	**5.00E-05**	1.00E+00	2.85E-04
Tmie_chr9	2	1	3	1	-0.5	1.4	-1.3	2.5	**2.73E-01**	**5.00E-05**	9.94E-01	2.85E-04
Tnfrsf13c_chr15	49	67	78	31	0.4	1.4	-1.3	2.5	**3.16E-02**	**5.00E-05**	7.56E-01	2.85E-04
Trat1_chr16	5	5	7	4	-0.1	1.0	-0.7	1.7	**8.99E-01**	**3.50E-04**	1.00E+00	1.69E-03
Vipr1_chr9	5	4	9	3	-0.3	1.2	-1.5	2.7	**2.44E-01**	**5.00E-05**	9.68E-01	2.85E-04
Vpreb3_chr10	13	16	12	3	0.2	1.2	-2.1	4.3	**5.23E-01**	**5.00E-05**	1.00E+00	2.85E-04
Xkrx_chrX	7	9	11	5	0.5	1.5	-1.1	2.1	**2.90E-02**	**5.00E-05**	7.30E-01	2.85E-04
Xlr3b_chrX	6	2	6	3	-1.6	3.0	-1.1	2.1	**8.40E-05**	**5.00E-05**	1.77E-02	2.85E-04

Zfp608_chr18	7	9	14	7	0.3	1.3	-0.9	1.9	**1.24E-01**	**5.00E-05**	9.50E-01	2.85E-04
Zfp831_chr2	9	10	20	11	0.2	1.2	-0.9	1.8	**2.53E-01**	**5.00E-05**	9.92E-01	2.85E-04

Supplemental Table 3. Presence of potential TTP binding sites in the transcripts that were up-regulated in the triple KO (TKO) vs WT comparison, compared to the doube KO (DKO) vs WT comparison. Conservation was determined by evaluation of aligned mammalian 3'UTRs in the UCSC genome browser, with the ideal binding site 7 mer being UAUUUAU, and the ideal 9-mer UUAUUUAUU.

	Gene Symbol	Gene Name	Fold change DKO/WT	Fold Change TKO/WT	Significant DKO vs WT	Significant TKO vs WT	Conservation	TTP Binding Sites
1	*Apol11B*	Apolipoprotein L 11b	3.5	367.4	yes	yes	Mouse only	One 8 mer poorly conserved
2	*Ltf*	Lactotransferrin	4.6	81.7	yes	yes	Mouse only	One 9 mer poorly conserved
3	*Gypa*	Gycophorin A	1.9	55.0	no	yes	Mouse only	One 8 mer poorly conserved
4	*Slfn4*	Schlafen 4	1.4	31.5	no	yes	Mouse, Rat	One 7 mer poorly conserved
5	*Tmcc2*	Transmem and coiled coil domain family 2	1.5	23.2	no	yes	Conserved	One 8 mer-9mer overlap poorly, one 9 mer highly conserved
6	*Tfrc*	Transferrin receptor (p90, CD71)	1.1	18.5	no	yes	Conserved	Two 8 mers highly conserved
7	*Abcg4*	ATP-binding cassette, subfamily G, member 4	1.0	17.0	no	yes	Conserved	One 7 mer highly conserved
8	*Oas3*	2'-5' oligoadenylate synthetase 3	1.6	15.5	no	yes	Mouse only	One 7 mer poorly conserved
9	*E2F8*	E2F transcription factor 8	1.4	13.0	no	yes	Conserved	One 8 mer highly conserved
10	*Birc5*	Baculoviral IAP repeat containing 5	1.4	13.0	no	yes	Mouse only	Three 9 mers overlapping poorly conserved
11	*Cenpf*	Centromere protein F, 350/400kDa	1.0	12.0	no	yes	Mouse only	One 7 mer poorly conserved
12	*Sox6*	SRY (sex determining region Y)-box 6	1.0	11.9	no	yes	Conserved	Five 8 mers, one 7 mer highly conserved
13	*Sgol1*	shugoshin-like 1 (S.pombe)	1.0	11.8	no	yes	Mouse only	Two 8 mers poorly conserved
14	*Kif18B*	Kinesin family member 18 b	1.1	11.7	no	yes	Mouse only	One 7 mer poorly conserved
15	*Cdc6*	Cell division cycle 6	1.4	11.7	no	yes	Conserved	One 8 mer highly conserved
16	*Lmo2*	rhombotin-2	-1.1	11.4	no	yes	Conserved	One 7 mer moderately conserved
17	*Gpr146*	probable G-protein coupled receptor 146 isoform	1.0	11.4	no	yes	Conserved	One 7 mer highly conserved

Supplemental Table 3 (continued)

18	*Ccna2*	Cycline A2	1.2	11.3	no	yes	Mouse only	One 8 mer poorly conserved
19	*Tmem56*	transmembrane protein 56	1.0	11.1	no	yes	Conserved	One 7 mer highly, one 9 mer moderately conserved
20	*Depdc1A*	DEP domain-containing protein 1A isoform 1	-1.1	10.5	no	yes	Mouse, Rat	One 8 mer poorly conserved
21	*Clcn3*	H(+)/Cl(-) exchange transporter 3	1.1	9.7	no	yes	Conserved	One 8 mer, one 7 mer , one 8 mer all highly conserved
22	*Anln*	actin-binding protein anillin	-1.0	9.6	no	yes	Conserved	One 7 mer highly, two 7 mers poorly conserved
23	*Kntc1*	kinetochore-associated protein 1	1.0	9.6	no	yes	Conserved	One 8 mer highly conserved
24	*Ifi44*	interferon-induced protein 44	1.3	9.6	no	yes	Mouse, Rat	One 7 mer poorly conserved
25	*Ccne2*	G1/S-specific cyclin-E2 isoform 2	1.0	9.4	no	yes	Conserved	One 8 mer highly conserved
26	*Ccnb1*	G2/mitotic-specific cyclin-B1	1.1	9.4	no	yes	Mouse, Rat	One 9 mer poorly conserved
27	*Slc25A21*	mitochondrial 2-oxodicarboxylate carrier isoform	1.0	9.2	no	yes	Conserved	One 7 mer poorly conserved
28	*Ncapg*	non-SMC condensin I complex, subunit G	1.0	9.2	no	yes	Conserved	Two 8 mers poorly conserved
29	*Prc1*	Protein regulator of cytokinesis 1;	1.2	9.1	no	yes	Conserved	One 8 mer moderately conserved
30	*Clspn*	claspin	1.1	8.8	no	yes	Conserved	One 8 mer highly conserved
31	*Ache*	acetylcholinesterase precursor	1.3	8.6	no	yes	Conserved	One 8 mer moderately conserved
32	*Chac2*	Cation transport regulator-like protein 2	1.1	8.4	no	yes	Mouse only	One 8 mer poorly conserved
33	*Fam109B*	hypothetical protein LOC338368	-1.3	8.4	no	yes	Mouse only	One 8 mer poorly conserved
34	*Kif18A*	kinesin-like protein KIF18A	-1.3	8.3	no	yes	Mouse only	One 7 mer poorly conserved
35	*C530008M17Rik*	hypothetical protein LOC320827	1.0	8.2	no	yes	Conserved	Two 9 mers moderately conserved
36	*Nt5C3*	cytosolic 5'-nucleotidase 3	1.1	8.2	no	yes	Conserved	One 8 mer moderately conserved
37	*Nuf2*	kinetochore protein Nuf2	1.2	8.1	no	yes	Mouse only	One 8 mer poorly conserved
38	*Pif1*	ATP-dependent DNA helicase PIF1	1.0	7.9	no	yes	Conserved	One 8 mer highly, one 8 mer poorly conserved

Supplemental Table 3 (continued)

39	*Odf2*	outer dense fiber protein 2	1.5	7.9	no	yes	Mouse, Rat	One 9 mer poorly conserved
40	*Cenpe*	centromere-associated protein E	-1.0	7.9	no	yes	Mouse only	One 9 mer poorly conserved
41	*Gda*	Guanine Deaminase	1.2	7.8	no	yes	Conserved	One 7 mer moderately conserved
42	*Kif14*	Kinesin family member 14	1.0	7.8	no	yes	Conserved	One 7 mer moderately, one 9 mer poorly conserved
43	*Cenpi*	Centromere protein 1	1.0	7.4	no	yes	Conserved	One 7 mer moderately conserved
44	*C5Ar1*	C5a anaphylatoxin chemotactic receptor	1.0	7.4	no	yes	Mouse only	One 8 mer, one 9 mer poorly conserved
45	*Bub1*	Budding uninhibited by benzimidazoles 1 homologue (S.	-1.1	7.0	no	yes	Conserved	One 7 mer moderately conserved
46	*Lilra5*	Leucocyte immunoglobulin-like receptor, subfamily A (with TM	3.5	7.0	yes	yes	Conserved	One 7 mer moderately, one 7 mer poorly conserved
47	*Kifc1*	kinesin family member C5B	1.4	7.0	no	yes	Conserved	One 7 mer moderately, one 8 mer poorly conserved
48	*Slc14A1*	urea transporter 1	-1.0	6.9	no	yes	Conserved	One 9 mer moderately conserved
49	*Nek2*	Nek2 kinase	1.3	6.7	no	yes	Conserved	One 8 mer moderately conserved
50	*Mmp9*	matrix metalloproteinase-9 precursor	1.4	6.7	no	yes	Mouse only	One 9 mer poorly conserved
51	*Kif2C*	kinesin-like protein KIF2C	1.2	6.6	no	yes	Conserved	One 7 mer moderately conserved
52	*Ppp1R15A*	protein phosphatase 1 regulatory subunit 15A	1.2	6.3	no	yes	Mouse only	Four overlapping 9 mers poorly conserved
53	*Hmgb2*	high mobility group protein B2	1.1	6.3	no	yes	Mouse, Rat	Two 7 mers, one 9 mer poorly conserved
54	*Pip5K1B*	phosphatidylinositol-4-phosphate 5-kinase type-1	1.3	6.2	no	yes	Conserved	One 7 mer highly conserved
55	*Mfsd2B*	Major facilitator superfamily domain-containing protein 2B	1.3	6.1	no	yes	Mouse, Rat	One 7 mer poorly conserved
56	*Usp18*	ubl carboxyl-terminal hydrolase 18	1.6	5.9	no	yes	Conserved	One 7 mer highly conserved
57	*Tfdp2*	transcription factor Dp-2	1.0	5.9	no	yes	Mouse, Rat	One 8 mer poorly conserved
58	*March8*	E3 ubiquitin-protein ligase MARCH8	-1.0	5.9	no	yes	Conserved	One 7 mer moderately conserved
59	*Slc25A37*	mitoferrin-1	1.3	5.8	no	yes	Conserved	One 8 mer highly conserved

Supplemental Table 3 (continued)

60	*C330027C09Rik*	protein CIP2A	-1.1	5.8	no	yes	Conserved	One 7 mer highly, one 8 mer moderately conserved
61	*Tjap1*	tight junction-associated protein 1	3.2	5.7	no	yes	Conserved	One 8 mer moderately conserved
62	*Xpo7*	mRNA for Ran binding protein 16.	1.2	5.6	no	yes	Conserved	One 7 mer highly, one 8 mer moderately conserved
63	*Mpp2*	MAGUK p55 subfamily member 2	1.0	5.6	no	yes	Conserved	Two 8 mers highly, one 7 mer poorly conserved
64	*Slc16A10*	monocarboxylate transporter 10	1.1	5.6	no	yes	Conserved	One 7 mer poorly, one 7 mer moderately, two overlapping 9 mers poorly conserved
65	*4930430F08Rik*	hypothetical protein LOC68281	1.0	5.4	no	yes	Conserved	Three 7 mers moderately conserved
66	*Ncapg2*	condensin-2 complex subunit G2	-1.2	5.4	no	yes	Mouse, Rat	One 9 mer poorly conserved
67	*Slc2A4*	Solute carrier family 2 (Facilitated glucose transporter), member 4	1.0	5.3	no	yes	Conserved	One 8 mer highly conserved
68	*Ube2T*	ubiquitin-conjugating enzyme E2 T	1.1	5.3	no	yes	Conserved	One 8 mer highly conserved
69	*Iqgap3*	IQ motif containing GTPase activating protein 3	1.0	5.3	no	yes	Conserved	One 8 mer highly conserved
70	*Pask*	PAS domain-containing serine/threonine-protein	1.0	5.3	no	yes	Conserved	One 8 mer, one 9 mer both moderately conserved
71	*Ifit1*	interferon-induced protein with	1.3	5.3	no	yes	Mouse, Rat	One 7 mer poorly conserved
72	*Sgol2*	shugoshin-like 2 isoform 1	-1.0	5.3	no	yes	Mouse, Rat	Two 8 mers, one 9 mer both poorly conserved
73	*Cep76*	centrosomal protein of 76 kDa	1.1	5.3	no	yes	Conserved	One 9 mer highly conserved
74	*Troap*	Trophinin-assisting protein	1.0	5.2	no	yes	Conserved	One 9 mer highly conserved
75	*Cep290*	centrosomal protein of 290 kDa	1.1	5.1	no	yes	Conserved	One 8 mer moderately conserved
76	*Ssx2Ip*	afadin- and alpha-actinin-binding protein	1.1	5.0	no	yes	Conserved	One 8 mer highly conserved
77	*E2F2*	transcription factor E2F2	1.4	5.0	no	yes	Conserved	One 8 mer highly conserved
78	*Emilin2*	EMILIN-2 precursor	-1.0	5.0	no	yes	Conserved	One 7 mer moderately conserved
79	*Whrn*	whirlin	4.5	4.9	yes	yes	Conserved	One 8 mer, one 7 mer both highly conserved
80	*Sgk3*	serine/threonine-protein kinase Sgk3	1.2	4.9	no	yes	Conserved	Two 7 mers highly conserved

Supplemental Table 3 (continued)

81	*E2F7*	transcription factor E2F7	1.0	4.8	no	yes	Conserved	One 9 mer moderately conserved
82	*2810417H13Rik*	PCNA-associated factor	1.3	4.8	no	yes	Mouse, Rat	One 7 mer poorly conserved
83	*Bard1*	BRCA1-associated RING domain protein 1	1.1	4.7	no	yes	Conserved	One 8 mer moderately conserved
84	*Mastl*	microtubule-associated serine/threonine-protein	1.0	4.7	no	yes	Conserved	One 8 mer highly, one 8 mer poorly conserved
85	*St3Gal5*	lactosylceramide alpha-2,3-sialyltransferase	1.4	4.7	no	yes	Conserved	One 8 mer highly conserved
86	*Bcl2L1*	bcl-2-like protein 1	1.6	4.7	no	yes	Conserved	One 7 mer highly conserved
87	*Metap2*	methionine aminopeptidase 2	1.1	4.6	no	yes	Conserved	One 7 mer highly conserved
88	*Ccrn4L*	nocturnin	-1.0	4.6	no	yes	Conserved	One 9 mer highly, one 8 mer moderately conserved
89	*Cpeb3*	cytoplasmic polyadenylation element-binding	1.0	4.6	no	yes	Conserved	One 7 mer highly conserved
90	*Cd24A*	signal transducer CD24	1.2	4.6	no	yes	Conserved	One 7 mer moderately conserved
91	*Acp1*	low molecular weight phosphotyrosine protein	1.1	4.5	no	yes	Conserved	One 8 mer moderately conserved
92	*Dusp8*	dual specificity protein phosphatase 8	1.0	4.5	no	yes	Conserved	One 9 mer moderately conserved
93	*Il1Rl1*	interleukin-1 receptor-like 1 isoform a	1.0	4.5	no	yes	Conserved	One 8 mer poorly, one 8 mer moderately conserved
94	*Tmem120B*	transmembrane protein 120B	1.0	4.4	no	yes	Conserved	One 7 mer moderately conserved
95	*Svip*	small VCP/p97-interacting protein	-1.1	4.4	no	yes	Conserved	One 7 mer moderately conserved
96	*Nlrp12*	NACHT, LRR and PYD domains-containing protein	1.0	4.4	no	yes	Mouse only	One 8 mer poorly conserved
97	*Zwilch*	protein zwilch homolog	-1.0	4.2	no	yes	Conserved	One 7 mer moderately conserved
98	*Pi4K2B*	phosphatidylinositol 4-kinase type 2-beta	-1.1	4.2	no	yes	Conserved	One 7 mer moderately conserved
99	*Brip1*	Fanconi anemia group J protein homolog	1.0	4.2	no	yes	Mouse, Rat	One 8 mer poorly conserved
100	*Ranbp10*	ran-binding protein 10	1.1	4.2	no	yes	Conserved	One 7 mer highly conserved
101	*Cenpl*	centromere protein L isoform 2	1.2	4.2	no	yes	Mouse, Rat	One 8 mer poorly conserved

Supplemental Table 3 (continued)

102	*Hagh*	hydroxyacylglutathione hydrolase, mitochondrial	1.2	4.1	no	yes	Conserved	One 7 mer, one 8 mer both highly conserved
103	*Mad2L1*	mitotic spindle assembly checkpoint protein	1.0	4.1	no	yes	Mouse, Rat	One 7 mer poorly conserved
104	*Ccdc34*	coiled-coil domain-containing protein 34	1.2	4.0	no	yes	Mouse, Rat	One 9 mer poorly conserved
105	*5730508B09Rik*	hypothetical protein LOC70617	-1.0	4.0	no	yes	Conserved	One 8 mer highly conserved
106	*Klra2*	killer cell lectin-like receptor 2 isoform 2	1.1	4.0	no	yes	Mouse, Rat	One 8 mer poorly conserved
107	*Dek*	protein DEK	-1.0	4.0	no	yes	Conserved	One 7 mer moderately conserved
108	*Mxd1*	max dimerization protein 1	1.1	4.0	no	yes	Conserved	One 8 mer highly, one 8 mer moderately conserved
109	*Eif2Ak2*	interferon-induced, double-stranded	1.1	3.9	no	yes	Mouse only	One 8 mer poorly conserved
110	*Plk4*	Serine/threonine-protein kinase PLK4	-1.1	3.9	no	yes	Conserved	One 8 mer highly conserved
111	*Gbp10*	guanylate-binding protein 10	1.0	3.9	no	yes	Mouse, Rat	One 9 mer poorly conserved
112	*Gadd45A*	growth arrest and DNA damage-inducible protein	1.3	3.9	no	yes	Conserved	One 8 mer highly conserved
113	*Ppp1R3D*	protein phosphatase 1 regulatory subunit 3D	1.0	3.9	no	yes	Conserved	One 9 mer highly conserved
114	*Gcnt2*	N-acetyllactosaminide	1.0	3.8	no	yes	Conserved	One 8 mer-9 mer overlap moderately conserved
115	*Slc22A23*	solute carrier family 22 member 23	1.1	3.7	no	yes	Conserved	One 8 mer highly conserved
116	*Chtf18*	chromosome transmission fidelity protein 18	1.3	3.7	no	yes	Mouse, Rat	One 7 mer poorly conserved
117	*Cks1B*	cyclin-dependent kinases regulatory subunit 1	1.2	3.6	no	yes	Conserved	One 7 mer moderately conserved
118	*Otub2*	ubiquitin thioesterase OTUB2 isoform 2	1.2	3.5	no	yes	Conserved	One 8 mer moderately, one 7 mer poorly conserved
119	*Igj*	immunoglobulin J chain precursor	1.2	3.5	no	yes	Conserved	One 7 mer moderately conserved
120	*E2F1*	transcription factor E2F1	1.2	3.5	no	yes	Conserved	Two overlapping 8 mers, one 9 mer highly conserved
121	*Mcm2*	DNA replication licensing factor MCM2	1.4	3.5	no	yes	Mouse only	One 8 mer poorly conserved
122	*Ccrl2*	C-C chemokine receptor-like 2	1.7	3.4	no	yes	Conserved	One 7 mer moderately conserved

Supplemental Table 3 (continued)

123	*Xk*	membrane transport protein XK	1.3	3.4	no	yes	Conserved	One 8 mer moderately conserved
124	*Clec4A2*	C-type lectin domain family 4 member A isoform	1.0	3.4	no	yes	Mouse only	One 7 mer poorly conserved
125	*Mtfr1*	mitochondrial fission regulator 1	1.2	3.4	no	yes	Conserved	One 8 mer, one 7 mer both moderately conserved
126	*Fam132B*	hypothetical protein LOC227358 precursor	1.0	3.3	no	yes	Conserved	One 8 mer, one 7 mer both highly conserved
127	*Asb1*	ankyrin repeat and SOCS box protein 1	1.0	3.3	no	yes	Conserved	Two 7 mers moderately, one 9 mer poorly conserved
128	*Cmas*	N-acylneuraminate cytidylyltransferase	1.4	3.3	no	yes	Conserved	One 8 mer highly conserved
129	*Vcan*	versican core protein isoform 3	1.0	3.3	no	yes	Conserved	One 7 mer highly conserved
130	*Arhgap19*	rho GTPase-activating protein 19	1.2	3.3	no	yes	Conserved	One 9 mer highly, one 8 mer moderately conserved
131	*Oaf*	out at first protein homolog precursor	1.0	3.3	no	yes	Conserved	One 7 mer highly conserved
132	*Gch1*	GTP cyclohydrolase 1 precursor	1.0	3.2	no	yes	Conserved	One 8 mer highly conserved
133	*Lbp*	lipopolysaccharide-binding protein precursor	1.0	3.2	no	yes	Conserved	One 7 mer highly conserved
134	*Il1B*	interleukin-1 beta precursor	1.2	3.2	no	yes	Conserved	Three 8 mers (two overlapping) highly conserved
135	*Trak2*	trafficking protein, kinesin binding 2	1.0	3.1	no	yes	Conserved	Two 7 mers moderately conserved
136	*1810033B17Rik*	mast cell-expressed membrane protein 1 homolog	1.1	3.1	no	yes	Mouse, Rat	One 7 mer poorly conserved
137	*Sgms2*	phosphatidylcholine:ceramide	1.0	3.0	no	yes	Conserved	One 8 mer moderately conserved
138	*P2Ry1*	P2Y purinoceptor 1	1.2	3.0	no	yes	Conserved	Two 8 mers both highly conserved
139	*Psmc3Ip*	homologous-pairing protein 2 homolog	1.1	3.0	no	yes	Conserved	One 8 mer highly conserved
140	*Net1*	neuroepithelial cell-transforming gene 1 protein	1.1	3.0	no	yes	Conserved	One 8 mer highly conserved
141	*Mcm5*	DNA replication licensing factor MCM5	1.4	3.0	no	yes	Mouse only	One 8 mer poorly conserved
142	*Gas2L3*	GAS2-like protein 3	1.0	3.0	no	yes	Conserved	One 9 mer highly, one 9 mer poorly conserved
143	*Scoc*	short coiled-coil protein isoform	1.1	3.0	no	yes	Conserved	Two 7 mers both highly conserved

Supplemental Table 3 (continued)

144	*Arl4A*	ADP-ribosylation factor-like protein 4A	-1.0	2.9	no	yes	Conserved	Two 7 mers both moderately conserved
145	*Cd300Lf*	CMRF35-like molecule 1 isoform 1 precursor	1.2	2.9	no	yes	Conserved	One 9 mer highly conserved
146	*Minpp1*	multiple inositol polyphosphate phosphatase 1	1.2	2.9	no	yes	Conserved	One 7 mer highly conserved
147	*Fut1*	galactoside 2-alpha-L-fucosyltransferase 1	1.0	2.9	no	yes	Mouse only	One 8 mer poorly conserved
148	*Csda*	DNA-binding protein A long isoform	1.4	2.8	no	yes	Conserved	One 9 mer highly conserved
149	*March5*	E3 ubiquitin-protein ligase MARCH5	1.1	2.8	no	yes	Conserved	One 8 mer highly, one 9 mer poorly conserved
150	*Fbxo48*	F-box only protein 48	-1.1	2.8	no	yes	Conserved	One 7 mer moderately conserved
151	*Piga*	N-acetylglucosaminyl-phosphatidylinositol	1.1	2.8	no	yes	Conserved	One 8 mer moderately conserved
152	*Usp46*	ubiquitin carboxyl-terminal hydrolase 46	1.0	2.8	no	yes	Conserved	One 7 mer, one 8 mer both highly, one 7 mer poorly conserved
153	*Reep4*	receptor expression-enhancing protein 4	2.1	2.7	no	yes	Conserved	One 8 mer highly conserved
154	*Dck*	deoxycytidine kinase	1.2	2.7	no	yes	Mouse only	One 7 mer poorly conserved
155	*Usp32*	ubiquitin specific protease 32	-1.0	2.7	no	yes	Conserved	One 9 mer highly conserved
156	*Hace1*	E3 ubiquitin-protein ligase HACE1	-1.1	2.7	no	yes	Conserved	One 7 mer moderately conserved
157	*Sh2D1B1*	SH2 domain-containing protein 1B	1.5	2.6	no	yes	Conserved	One 8 mer poorly conserved
158	*Gsr*	glutathione reductase, mitochondrial precursor	-1.1	2.6	no	yes	Conserved	One 7 mer moderately conserved
159	*Ifih1*	interferon-induced helicase C domain-containing	1.1	2.6	no	yes	Mouse, Rat	One 8 mer poorly conserved
160	*Casp4*	caspase-4 precursor	1.1	2.6	no	yes	Mouse, Rat	One 8 mer poorly conserved
161	*Vopp1*	EGFR-coamplified and overexpressed protein	1.2	2.6	no	yes	Mouse, Rat	One 8 mer, one 7 mer both poorly conserved
162	*Ccr2*	C-C chemokine receptor type 2	1.0	2.6	no	yes	Mouse, Rat	One 7 mer poorly conserved
163	*Gca*	grancalcin	1.0	2.6	no	yes	Conserved	One 8 mer highly, one 8 mer moderately conserved

Supplemental Table 3 (continued)

164	*Klhl12*	kelch-like protein 12	1.3	2.5	no	yes	Conserved	One 8 mer highly conserved
165	*Rbbp8*	Retinoblastoma binding protein 8;	-1.0	2.5	no	yes	Conserved	One 8 mer highly conserved
166	*Parvb*	beta-parvin	1.4	2.5	no	yes	Mouse, Rat	One 7 mer poorly conserved
167	*Suv39H2*	Putative uncharacterized protein	-1.1	2.5	no	yes	Mouse only	One 7 mer poorly conserved
168	*Atad2*	ATPase family AAA domain-containing protein 2	1.1	2.5	no	yes	Conserved	One 7 mer highly conserved
169	*Apoo*	apolipoprotein O isoform 2	1.2	2.5	no	yes	Conserved	One 7 mer highly conserved
170	*Tarsl2*	probable threonyl-tRNA synthetase 2,	-1.0	2.5	no	yes	Mouse only	One 7 mer poorly conserved
171	*Tusc1*	tumor suppressor candidate gene 1 protein	1.0	2.5	no	yes	Conserved	One 7 mer moderately conserved
172	*Mfsd9*	major facilitator superfamily domain-containing	1.0	2.4	no	yes	Conserved	Two 7 mers moderately conserved
173	*Tnfsf14*	tumor necrosis factor ligand superfamily member	1.5	2.4	no	yes	Conserved	One 7 mer highly conserved
174	*B4Galt6*	beta-1,4-galactosyltransferase 6	1.3	2.4	no	yes	Conserved	One 9 mer highly conserved
175	*Ncapd3*	condensin-2 complex subunit D3	-1.1	2.4	no	yes	Conserved	One 7 mer, one 8 mer both highly conserved
176	*Brpf3*	Putative uncharacterized protein	1.1	2.4	no	yes	Conserved	One 8 mer highly conserved
177	*Sass6*	Spindle assembly abnormal protein 6 homolog	-1.0	2.4	no	yes	Conserved	One 7 mer moderately conserved
178	*Cdkn2D*	cyclin-dependent kinase 4 inhibitor D	1.2	2.4	no	yes	Conserved	One 8 mer highly conserved
179	*Mx1*	interferon-induced GTP-binding protein Mx1	1.1	2.4	no	yes	Mouse, Rat	One 7 mer poorly conserved
180	*Neu3*	sialidase-3	1.1	2.4	no	yes	Mouse only	One 9 mer poorly conserved
181	*Rhou*	rho-related GTP-binding protein RhoU	1.0	2.4	no	yes	Mouse only	One 7 mer poorly conserved
182	*Creg1*	protein CREG1	1.1	2.4	no	yes	Mouse only	One 7 mer poorly conserved
183	*Agfg2*	arf-GAP domain and FG repeats-containing protein	1.2	2.4	no	yes	Conserved	One 7 mer highly conserved
184	*Xcl1*	lymphotactin precursor	1.1	2.3	no	yes	Conserved	One 8 mer highly conserved

Supplemental Table 3 (continued)

185	*Zfp367*	zinc finger protein 367	-1.1	2.3	no	yes	Conserved	One 8 mer, one 7 mer both highly conserved
186	*Evi5*	ecotropic viral integration site 5 protein	-1.1	2.3	no	yes	Conserved	One 7 mer highly conserved
187	*Timm8B*	mitochondrial import inner membrane translocase	-1.1	2.3	no	yes	Conserved	One 8 mer highly conserved
188	*Lrrc39*	leucine-rich repeat-containing protein 39	1.0	2.3	no	yes	Mouse only	Two overlapping 9 mers poorly conserved
189	*Arhgap11A*	Rho GTPase activating protein 11A	1.1	2.3	no	yes	Conserved	One 8 mer poorly, one 9 mer highly conserved
190	*4930422G04Rik*	Mus musculus adult male testis cDNA, RIKEN full-length enriched	-1.0	2.3	no	yes	Mouse, Rat	Three 7 mers poorly conserved
191	*Apold1*	apolipoprotein L domain-containing protein 1	1.0	2.3	no	yes	Mouse, Rat	Two 8 mers poorly conserved
192	*Rgs18*	regulator of G-protein signaling 18	-1.0	2.3	no	yes	Mouse only	One 7 mer poorly conserved
193	*Pdgfc*	platelet-derived growth factor C	1.0	2.3	no	yes	Conserved	One 8 mer highly conserved
194	*Endod1*	endonuclease domain-containing 1 protein	1.0	2.3	no	yes	Conserved	One 8 mer highly conserved
195	*Cox7A2*	cytochrome c oxidase subunit 7A2, mitochondrial	-1.0	2.3	no	yes	Conserved	One 8 mer highly conserved
196	*Slc11A2*	natural resistance-associated macrophage protein	1.2	2.3	no	yes	Conserved	One 7 mer highly conserved
197	*Pls1*	plastin-1	1.3	2.2	no	yes	Conserved	One 8 mer moderately conserved
198	*Thbs1*	thrombospondin-1	1.7	2.2	no	yes	Conserved	One 8 mer, one 9 mer, one 7 mer all highly conserved
199	*Slc16A3*	monocarboxylate transporter 4	1.3	2.2	no	yes	Conserved	One 8 mer moderately conserved
200	*Cln8*	protein CLN8	-1.0	2.2	no	yes	Conserved	One 8 mer poorly, one 7 mer moderately conserved
201	*Pdk1*	pyruvate dehydrogenase kinase	1.9	2.2	yes	yes	Mouse only	One 7 mer poorly conserved
202	*Atp8B4*	ATPase, class I, type 8B, member 4	1.2	2.2	no	yes	Conserved	One 8 mer highly conserved
203	*Mthfd2*	bifunctional methylenetetrahydrofolate	1.4	2.2	no	yes	Conserved	One 8 mer highly conserved
204	*Deb1*	SS18-like protein 2	-1.1	2.2	no	yes	Conserved	One 8 mer moderately conserved
205	*Tab3*	TGF-beta-activated kinase 1 and MAP3K7-binding	1.0	2.2	no	yes	Conserved	One 8 mer moderately conserved

Supplemental Table 3 (continued)

206	*Pla2G12A*	group XIIA secretory phospholipase A2	1.0	2.2	no	yes	Conserved	One 9 mer moderately conserved
207	*Katnal1*	katanin p60 ATPase-containing subunit A-like 1	1.0	2.2	no	yes	Conserved	One 9 mer poorly, one 8 mer highly, one 8 mer moderately
208	*Ugt1A7C*	UDP-glucuronosyltransferase 1-7C precursor	-1.0	2.2	no	yes	Conserved	One 8 mer moderately conserved
209	*Psme3*	proteasome activator complex subunit 3	1.3	2.2	no	yes	Conserved	One 7 mer highly conserved
210	*Socs3*	suppressor of cytokine signaling 3	1.1	2.2	no	yes	Conserved	One 7 mer highly, one 7 mer poorly conserved
211	*Itsn1*	intersectin-1 isoform 1	1.1	2.2	no	yes	Conserved	One 9 mer highly, one 9 mer poorly conserved
212	*Stat1*	signal transducer and activator of transcription	1.2	2.2	no	yes	Mouse only	One 8 mer poorly conserved
213	*Ppp2R5B*	serine/threonine-protein phosphatase 2A 56 kDa	1.1	2.2	no	yes	Conserved	One 8 mer, one 9 mer both highly conserved
214	*Nudt12*	peroxisomal NADH pyrophosphatase NUDT12	1.0	2.2	no	yes	Mouse only	One 7 mer poorly conserved
215	*Cycs*	cytochrome c, somatic	1.0	2.1	no	yes	Conserved	One 9 mer highly, one 7 mer moderately conserved
216	*Adpgk*	ADP-dependent glucokinase precursor	1.1	2.1	no	yes	Conserved	One 8 mer highly conserved
217	*Pfdn4*	prefoldin 4 isoform 3	1.0	2.1	no	yes	Conserved	One 9 mer highly conserved
218	*Nlrc5*	protein NLRC5	-1.0	2.1	no	yes	Mouse only	One 7 mer poorly conserved
219	*Pilra*	Paired immunoglobulin-like type 2 receptor alpha	1.0	2.1	no	yes	Mouse only	One 9 mer poorly conserved
220	*Ehbp1L1*	EH domain-binding protein 1-like protein 1	1.4	2.1	no	yes	Conserved	One 8 mer moderately conserved
221	*Plscr1*	phospholipid scramblase 1	1.0	2.1	no	yes	Mouse, Rat	One 7 mer poorly conserved
222	*Atg4D*	cysteine protease ATG4D	1.2	2.1	no	yes	Conserved	One 8 mer moderately conserved
223	*Setd8*	histone-lysine N-methyltransferase SETD8	1.1	2.1	no	yes	Conserved	One 8 mer highly conserved
224	*C1Galt1C1*	C1GALT1-specific chaperone 1	-1.0	2.1	no	yes	Conserved	One 7 mer highly, one 8 mer moderately conserved
225	*Spon1*	spondin-1 precursor	1.3	2.1	no	yes	Conserved	One 7 mer moderately conserved
226	*Rasgrp4*	RAS guanyl-releasing protein 4 isoform 1	1.2	2.1	no	yes	Conserved	One 7 mer moderately conserved

Supplemental Table 3 (continued)

227	*Hs6St1*	heparan-sulfate 6-O-sulfotransferase 1	1.3	2.1	no	yes	Conserved	One 9 mer-8 mer overlap highly conserved
228	*2700097O09Rik*	hypothetical protein LOC72658	-1.1	2.1	no	yes	Mouse, Rat	One 8 mer, one 9 mer both poorly conserved
229	*Fosl2*	fos-related antigen 2	1.4	2.1	no	yes	Conserved	One 7 mer poorly, one 8 mer, one 9 mer both highly conserved
230	*Gpr88*	probable G-protein coupled receptor 88	2.0	2.0	no	yes	Mouse only	One 7 mer poorly conserved
231	*Kcnj2*	inward rectifier potassium channel 2	1.0	2.0	no	yes	Conserved	One 9 mer highly conserved
232	*Kctd7*	BTB/POZ domain-containing protein KCTD7	1.2	2.0	no	yes	Mouse, Rat	One 7 mer poorly conserved
233	*Galnt3*	polypeptide N-acetylgalactosaminyltransferase 3	1.2	2.0	no	yes	Conserved	One 8 mer highly, one 7 mer moderately conserved
234	*Mafg*	transcription factor MafG	1.0	2.0	no	yes	Conserved	Oner 7 mer highly conserved
235	*Cbx5*	chromobox protein homolog 5	-1.0	2.0	no	yes	Conserved	One 7 mer highly conserved
236	*Mrpl20*	39S ribosomal protein L20, mitochondrial	-1.2	2.0	no	yes	Conserved	One 8 mer moderately conserved
237	*Mrpl33*	39S ribosomal protein L33, mitochondrial	1.0	2.0	no	yes	Conserved	One 7 mer highly conserved
238	*Znhit3*	Znhit3 protein	-1.2	2.0	no	yes	Mouse, Rat	One 7 mer poorly conserved
239	*Olfr1033*	olfactory receptor 1033	1.0	2.0	yes	yes	Mouse only	One 8 mer poorly conserved
240	*Map4K5*	mitogen-activated protein kinase kinase kinase	1.0	2.0	no	yes	Conserved	One 9 mer highly conserved
241	*Rnf11*	RING finger protein 11	1.2	2.0	no	yes	Conserved	One 8 mer highly conserved
242	*Yod1*	ubiquitin thioesterase OTU1	-1.2	2.0	no	yes	Conserved	One 7 mer, two 8 mers moderately, one 8 mer highly conserved
243	*Mospd1*	motile sperm domain-containing protein 1	1.0	2.0	no	yes	Conserved	One 9 mer moderately conserved
244	*Mri1*	methylthioribose-1-phosphate isomerase	2.1	2.0	no	yes	Mouse, Rat	One 8 mer poorly conserved
245	*Ndufs4*	NADH dehydrogenase [ubiquinone] iron-sulfur	-1.1	1.9	no	yes	Conserved	One 7 mer highly conserved
246	*Tmem106A*	transmembrane protein 106A	1.3	1.9	no	yes	Conserved	One 8 mer moderately conserved

Supplemental Table 3 (continued)

247	*Ier3*	radiation-inducible immediate-early gene IEX-1	1.0	1.9	no	yes	Conserved	One 7 mer, one 8 mer highly, one 7 mer poorly conserved
248	*Acer3*	alkaline ceramidase 3	-1.2	1.9	no	yes	Conserved	Two 7 mers both moderately conserved
249	*Tmem194*	transmembrane protein 194A isoform 1	1.2	1.9	no	yes	Mouse only	One 7 mer, one 9 mer both poorly conserved
250	*Rpgrip1L*	RPGR-interacting protein 1-like protein	1.0	1.9	no	yes	Conserved	One 7 mer moderately conserved
251	*1600002H07Rik*	hypothetical protein LOC72016	1.1	1.9	no	yes	Mouse only	One 7 mer poorly conserved
252	*Tbc1D24*	TBC1 domain family member 24	-1.2	1.9	no	yes	Conserved	One 8 mer, one 9 mer both moderately conserved
253	*Bcorl1*	BCL-6 corepressor-like protein 1	1.5	1.9	no	yes	Conserved	One 8 mer highly conserved
254	*Prdx3*	thioredoxin-dependent peroxide reductase	1.2	1.9	no	yes	Conserved	One 8 mer moderately conserved
255	*Pot1B*	hypothetical protein	1.1	1.9	no	yes	Mouse, Rat	One 8 mer poorly conserved
256	*Rnf149*	E3 ubiquitin-protein ligase RNF149 precursor	1.1	1.9	no	yes	Conserved	One 7 mer highly conserved
257	*Ahi1*	jouberin	1.1	1.9	no	yes	Conserved	One 8 mer poorly, one 8 mer moderately conserved
258	*Nhsl2*	NHS-like protein 2	1.0	1.9	no	yes	Conserved	One 8 mer highly, one 7 mer moderately conserved
259	*Relt*	tumor necrosis factor receptor superfamily, member 19-like, full	1.2	1.9	no	yes	Conserved	Two 8 mers, both highly conserved
260	*Wdr67*	WD repeat-containing protein 67 isoform 1	1.0	1.9	no	yes	Conserved	One 8 mer highly conserved
261	*Nlrp3*	NACHT, LRR and PYD domains-containing protein 3	1.2	1.9	no	yes	Conserved	One 8 mer poorly, one 8 mer moderately conserved
262	*Stx11*	syntaxin-11	1.2	1.9	no	yes	Mouse, Rat	One 7 mer poorly conserved
263	*Magohb*	protein mago nashi homolog 1-related	1.2	1.9	no	yes	Conserved	One 7 mer moderately conserved
264	*Zcchc3*	zinc finger, CCHC domain containing 3	1.3	1.9	no	yes	Conserved	One 7 mer highly conserved
265	*Ncr1*	Putative uncharacterized protein	1.2	1.9	no	yes	Mouse, Rat	One 9 mer poorly conserved
266	*Mier3*	mesoderm induction early response protein 3	1.1	1.8	no	yes	Conserved	Two 8 mers, both highly conserved

267	*Cish*	cytokine-inducible SH2-containing protein	1.3	1.8	no	yes	Conserved	Three overlapping (7 mer, 9 mer, 9 mer) all highly conserved
268	*Yipf4*	protein YIPF4	1.2	1.8	no	yes	Conserved	Two overlapping 7 mers highly, two more 7 mers both highly conserved
269	*Slc25A17*	peroxisomal membrane protein PMP34	1.5	1.8	no	yes	Conserved	Two 8 mers highly conserved
270	*Ulk1*	serine/threonine-protein kinase ULK1	1.1	1.8	no	yes	Conserved	One 8 mer highly conserved
271	*Picalm*	phosphatidylinositol-binding clathrin assembly	1.0	1.8	no	yes	Conserved	Two 7 mers overlap both highly conserved
272	*Eif4A1*	eukaryotic initiation factor 4A-I isoform 1	1.1	1.8	no	yes	Conserved	One 8 mer highly conserved
273	*Hnrpll*	heterogeneous nuclear ribonucleoprotein L-like	-1.1	1.8	no	yes	Conserved	One 8 mer highly conserved
274	*Nudt5*	ADP-sugar pyrophosphatase	1.0	1.8	no	yes	Conserved	One 8 mer moderately conserved
275	*Cops2*	COP9 signalosome complex subunit 2	-1.1	1.8	no	yes	Conserved	One 7 mer highly conserved
276	*Sept3*	neuronal-specific septin-3	1.0	1.8	no	yes	Conserved	One 8 mer highly conserved
277	*Celsr1*	cadherin EGF LAG seven-pass G-type receptor 1	1.0	1.8	no	yes	Conserved	One 8 mer highly, one 8 mer poorly conserved
278	*Eef1E1*	eukaryotic translation elongation factor 1	1.1	1.8	no	yes	Conserved	One 8 mer moderately, one 7 mer highly conserved
279	*Gm8369*	membrane-spanning 4-domains, subfamily A, member	1.7	1.8	no	yes	Mouse, Rat	One 7 mer poorly conserved
280	*Agap1*	arf-GAP with GTPase, ANK repeat and PH	1.1	1.8	no	yes	Conserved	One 8 mer highly conserved
281	*Asap3*	Hypothetical ankyrin repeat profile/serine-rich region/ankyrin-	1.1	1.8	no	yes	Mouse only	One 8 mer poorly conserved
282	*Neto2*	Neto2 protein	1.0	1.8	no	yes	Conserved	Two 8 mers, both moderately conserved
283	*Arl6Ip6*	ADP-ribosylation factor-like protein	1.1	1.8	no	yes	Conserved	Two 7 mers, both moderately conserved
284	*Plod2*	procollagen-lysine,2-oxoglutarate 5-dioxygenase	1.1	1.8	no	yes	Conserved	Two 8 mers, both highly conserved
285	*Slfn5*	schlafen family member 5	1.1	1.8	no	yes	Conserved	One 8 mer, one 7 mer, both moderately conserved
286	*Usp1*	ubiquitin carboxyl-terminal hydrolase 1	1.0	1.8	no	yes	Conserved	One 7 mer highly conserved

287	*Med30*	mediator of RNA polymerase II transcription	1.2	1.8	no	yes	Conserved	One 8 mer moderately conserved
288	*Klf11*	Krueppel-like factor 11	1.2	1.8	no	yes	Conserved	One 8 mer highly conserved
289	*Il1A*	interleukin-1 alpha precursor	-1.1	1.8	no	yes	Conserved	Three 7 mers, all highly conserved
290	*Mesdc1*	mesoderm development candidate 1	1.4	1.8	no	yes	Conserved	One 8 mer highly conserved
291	*Fundc2*	FUN14 domain-containing protein 2	-1.0	1.8	no	yes	Conserved	One 7 mer moderately, one 8 mer moderately to poorly conserved
292	*B230120H23Rik*	mitogen-activated protein kinase kinase kinase	-1.1	1.8	no	yes	Conserved	One 7 mer highly conserved
293	*Cbwd1*	Cobalamin synthase W domain-containing protein 1	1.1	1.8	no	yes	Conserved	One 8 mer highly conserved
294	*Rbm47*	RNA-binding protein 47	1.2	1.7	no	yes	Conserved	One 7 mer, one 8 mer both highly conserved
295	*Tmx4*	thioredoxin-related transmembrane protein 4	1.0	1.7	no	yes	Mouse, Rat	Two 8 mers poorly conserved
296	*Palb2*	partner and localizer of BRCA2	1.1	1.7	no	yes	Conserved	One 8 mer highly conserved
297	*Tmtc4*	transmembrane and TPR repeat-containing protein	1.5	1.7	no	yes	Conserved	One 8 mer, one 7 mer both moderately conserved
298	*Mrpl41*	39S ribosomal protein L41, mitochondrial	-1.0	1.7	no	yes	Mouse, Rat	One 8 mer poorly conserved
299	*Gdpd1*	glycerophosphodiester phosphodiesterase	1.2	1.7	no	yes	Conserved	One 8 mer highly conserved
300	*Tbx21*	T-box transcription factor TBX21	1.9	1.7	no	yes	Conserved	One 8 mer highly conserved
301	*Glipr2*	Golgi-associated plant pathogenesis-related	1.1	1.7	no	yes	Conserved	One 7 mer moderately conserved
302	*Uchl5*	ubiquitin carboxyl-terminal hydrolase isozyme L5	1.2	1.7	no	yes	Mouse, Rat	One 9 mer poorly conserved
303	*Ghitm*	growth hormone-inducible transmembrane protein	1.2	1.7	no	yes	Conserved	One 8 mer highly conserved
304	*Ell2*	RNA polymerase II elongation factor ELL2	1.2	1.7	no	yes	Conserved	One 9 mer, one 7 mer both highly conserved
305	*Slc30A9*	zinc transporter 9	-1.0	1.7	no	yes	Conserved	One 7 mer highly conserved
306	*H2-T24*	histocompatibility 2, T region locus 24	1.1	1.7	no	yes	Mouse only	One 9 mer poorly conserved

Supplemental Table 3 (continued)

307	*Ctsb*	cathepsin B preproprotein	1.4	1.7	no	yes	Mouse, Rat	One 8 mer poorly conserved
308	*Dgkg*	diacylglycerol kinase gamma	1.0	1.7	no	yes	Conserved	Two 8 mers highly conserved
309	*Tmem215*	transmembrane protein 215	1.9	1.7	no	yes	Conserved	One 8 mer moderately conserved
310	*Tinagl1*	tubulointerstitial nephritis antigen-like	1.5	1.7	no	yes	Conserved	One 8 mer highly conserved
311	*Dnajc6*	putative tyrosine-protein phosphatase auxilin	1.0	1.7	no	yes	Conserved	One 7 mer poorly, three 8 mers highly conserved
312	*Dgat2*	diacylglycerol O-acyltransferase 2	-1.4	1.7	no	yes	Mouse, Rat	One 7 mer poorly conserved
313	*Cpd*	carboxypeptidase D precursor	-1.0	1.7	no	yes	Conserved	One 7 mer poorly conserved
314	*Ran*	GTP-binding nuclear protein Ran	1.3	1.7	no	yes	Conserved	One 7 mer highly conserved
315	*Tcf7L2*	transcription factor 7-like 2	1.1	1.7	no	yes	Conserved	One 8 mer highly conserved
316	*Xkr5*	XK-related protein 5	1.0	1.7	no	yes	Mouse only	One 8 mer poorly conserved
317	*Daam1*	disheveled-associated activator of morphogenesis	-1.0	1.7	no	yes	Conserved	One 7 mer, one 9 mer and one 8 mer all highly conserved
318	*Cd300A*	CMRF35-like molecule 8	1.2	1.7	no	yes	Mouse only	Two 9 mers poorly conserved
319	*Snrpb2*	U2 small nuclear ribonucleoprotein B	1.0	1.7	no	yes	Conserved	One 8 mer highly conserved
320	*Dmxl2*	dmX-like protein 2	-1.2	1.7	no	yes	Conserved	One 9 mer highly conserved
321	*Stk3*	serine/threonine-protein kinase 3	-1.1	1.7	no	yes	Conserved	One 8 mer highly, one 9 mer-8 mer overlap both highly conserved
322	*Slc22A15*	hypothetical protein	1.0	1.7	no	yes	Mouse, Rat	One 7 mer poorly conserved
323	*Zfand6*	AN1-type zinc finger protein 6	1.1	1.7	no	yes	Conserved	Two 7 mers highly conserved
324	*Timm17A*	mitochondrial import inner membrane translocase	1.2	1.7	no	yes	Conserved	One 9 mer highly conserved
325	*Cox11*	cytochrome c oxidase assembly protein COX11,	-1.0	1.7	no	yes	Conserved	One 8 mer moderately conserved
326	*Usp14*	ubiquitin carboxyl-terminal hydrolase	1.1	1.7	no	yes	Conserved	One 7 mer highly conserved

Supplemental Table 3 (continued)

327	*Myo19*	Myosin head domain-containing protein 1	-1.0	1.7	no	yes	Conserved	One 7 mer moderately conserved
328	*Immp1L*	mitochondrial inner membrane protease subunit 1	-1.0	1.7	no	yes	Mouse only	One 7 mer poorly conserved
329	*Usp25*	ubiquitin carboxyl-terminal hydrolase 25	1.2	1.7	no	yes	Conserved	One 8 mer highly conserved
330	*Mpl*	thrombopoietin receptor	1.1	1.7	no	yes	Mouse, Rat	One 8 mer poorly conserved
331	*Arhgef12*	rho guanine nucleotide exchange factor 12	1.1	1.7	no	yes	Conserved	One 8 mer highly, one 8 mer moderately conserved
332	*Il12B*	interleukin-12 subunit beta precursor	1.0	1.7	no	yes	Conserved	One 8 mer highly conserved
333	*Kif1A*	kinesin-like protein KIF1A isoform a	1.0	1.7	no	yes	Conserved	One 8 mer moderately conserved
334	*Mrpl51*	39S ribosomal protein L51, mitochondrial	1.2	1.7	no	yes	Mouse, Rat	One 8 mer poorly conserved
335	*Tmtc3*	transmembrane and TPR repeat-containing protein	-1.2	1.7	no	yes	Conserved	Two 8 mers both highly conserved
336	*Vbp1*	prefoldin subunit 3	1.1	1.7	no	yes	Conserved	One 9 mer-8 mer overlap moderately conserved
337	*Chac1*	cation transport regulator-like protein 1	1.0	1.7	no	yes	Conserved	One 8 mer highly conserved
338	*Mybl1*	myb-related protein A	1.0	1.7	no	yes	Conserved	One 7 mer moderately, one 8 mer, one 7 mer both highly conserved
339	*Itga5*	integrin alpha-5 preproprotein	1.1	1.7	no	yes	Conserved	One 7 mer moderately conserved
340	*Trim37*	E3 ubiquitin-protein ligase TRIM37	1.1	1.7	no	yes	Mouse, Rat	Two seven mers poorly conserved
341	*Ubiad1*	ubiA prenyltransferase domain-containing protein	2.0	1.7	no; yes	yes	Conserved	One 8 mer highly conserved
342	*Srm*	spermidine synthase	1.4	1.7	no	yes	Conserved	One 8 mer moderately conserved
343	*Aa986860*	specifically androgen-regulated gene protein	1.0	1.6	no	yes	Conserved	One 7 mer moderately conserved
344	*Ccdc62*	coiled-coil domain containing 62	1.0	1.6	no	yes	Mouse only	One 8 mer poorly conserved
345	*Gm13154*	hypothetical protein LOC433804	1.0	1.6	yes	yes	Mouse, Rat	Two 7 mers poorly conserved
346	*Tuft1*	tuftelin	1.1	1.6	no	yes	Conserved	One 8 mer highly conserved

Supplemental Table 3 (continued)

347	*Eif5*	eukaryotic translation initiation factor 5	1.1	1.6	no	yes	Conserved	One 8 mer highly conserved
348	*Ppp1R3B*	protein phosphatase 1 regulatory subunit 3B	1.2	1.6	no	yes	Conserved	Two 8 mers highly conserved
349	*Ncoa7*	Nuclear receptor coactivator 7	-1.2	1.6	no	yes	Conserved	One 7 mer, one 9 mer both highly, one 9 mer poorly conserved
350	*Gas2*	growth arrest-specific protein 2	1.0	1.6	no	yes	Conserved	One 8 mer highly conserved
351	*Eif2S1*	eukaryotic translation initiation factor 2	-1.0	1.6	no	yes	Mouse, Rat	One 8 mer poorly conserved
352	*Dcaf12*	DDB1- and CUL4-associated factor 12	1.4	1.6	no	yes	Conserved	One 7 mer highly conserved
353	*Fgl2*	fibroleukin precursor	-1.1	1.6	no	yes	Conserved	One 8 mer poorly, one 8 mer moderately conserved
354	*Sort1*	sortilin precursor	1.1	1.6	no	yes	Mouse only	One 9 mer poorly conserved
355	*Neurl1A*	neuralized-like protein 1A	1.0	1.6	no	yes	Conserved	One 9 mer highly conserved
356	*Stxbp4*	syntaxin-binding protein 4	1.2	1.6	no	yes	Conserved	One 8 mer moderately conserved
357	*Pkn2*	serine/threonine-protein kinase N2	-1.0	1.6	no	yes	Conserved	One 7 mer highly conserved
358	*Armc9*	lisH domain-containing protein ARMC9	1.2	1.6	no	yes	Mouse, Rat	One 7 mer poorly conserved
359	*Vcam1*	vascular cell adhesion protein 1 precursor	-1.1	1.6	no	yes	Conserved	One 7 mer highly conserved
360	*Rnf139*	E3 ubiquitin-protein ligase RNF139	1.0	1.6	no	yes	Mouse, Rat	Two 7 mers both poorly conserved
361	*Nup35*	nucleoporin NUP53 isoform 2	-1.2	1.6	no	yes	Mouse, Rat	One 7 mer poorly conserved
362	*Fbxo42*	F-box only protein 42	1.2	1.6	no	yes	Conserved	One 7 mer highly conserved
363	*Gtf2A2*	general transcription factor II A	1.1	1.6	no	yes	Conserved	One 9 mer highly conserved
364	*Tubb3*	tubulin beta-3 chain	1.0	1.6	no	yes	Conserved	One 7 mer highly, one 7 mer poorly conserved
365	*Coro2B*	coronin-2B	1.0	1.6	no	yes	Conserved	One 8 mer highly conserved
366	*Gatm*	glycine amidinotransferase, mitochondrial	1.0	1.6	no	yes	Mouse only	Two 7 mers poorly conserved
367	*Cox17*	cytochrome c oxidase copper chaperone	1.3	1.6	no	yes	Conserved	One 7 mer highly conserved

Supplemental Table 3 (continued)

368	*Snrnp27*	U4/U6.U5 small nuclear ribonucleoprotein 27 kDa	1.0	1.6	no	yes	Conserved	One 8 mer highly, one 8 mer poorly conserved
369	*Rad21*	double-strand-break repair protein rad21	1.3	1.6	no	yes	Conserved	One 8 mer highly conserved
370	*Synj1*	synaptojanin-1	1.1	1.6	no	yes	Mouse, Rat	Two 7 mers both poorly conserved
371	*Nudcd1*	nudC domain-containing protein 1	1.0	1.6	no	yes	Conserved	One 7 mer highly, one 7 mer moderately conserved
372	*Cbx3*	chromobox protein homolog 3	1.1	1.6	no	yes	Conserved	One 7 mer moderately conserved
373	*Cdca4*	cell division cycle-associated protein 4	1.1	1.6	no	yes	Conserved	One 8 mer, one 7 mer both highly conserved
374	*Il15Ra*	interleukin 15 receptor, alpha chain	-1.1	1.6	no	yes	Conserved	One 7 mer highly conserved
375	*Mfap3L*	microfibrillar-associated protein 3-like	1.0	1.6	no	yes	Conserved	One 8 mer highly, one 7 mer moderately conserved
376	*Zmynd19*	zinc finger MYND domain-containing protein 19	1.1	1.6	no	yes	Conserved	One 8 mer highly conserved
377	*Samd3*	sterile alpha motif domain-containing protein 3	1.2	1.6	no	yes	Mouse, Rat	Two 7 mers both poorly conserved
378	*Myef2*	myelin expression factor 2 isoform 2	1.0	1.6	no	yes	Conserved	One 8 mer highly conserved
379	*Trpc6*	short transient receptor potential channel 6	1.0	1.6	no	yes	Conserved	One 8 mer highly conserved
380	*S1Pr5*	sphingosine 1-phosphate receptor 5	1.0	1.6	no	yes	Mouse only	One 9 mer poorly conserved
381	*Cdk2*	cell division protein kinase 2	1.3	1.6	no	yes	Conserved	One 7 mer highly conserved
382	*Wdr26*	WD repeat-containing protein 26	-1.0	1.6	no	yes	Conserved	One 7 mer highly conserved
383	*Atp6V0E*	V-type proton ATPase subunit e 1	1.1	1.6	no	yes	Mouse only	One 8 mer, one 9 mer, two 8 mers all poorly conserved
384	*Mrps14*	28S ribosomal protein S14, mitochondrial	1.1	1.6	no	yes	Mouse only	One 7 mer poorly conserved
385	*Riok3*	serine/threonine-protein kinase RIO3	1.2	1.6	no	yes	Conserved	One 7 mer highly conserved
386	*Cttnbp2*	cortactin-binding protein 2	1.0	1.6	no	yes	Conserved	One 7 mer highly, one 7 mer moderately conserved
387	*Sh3Glb1*	endophilin-B1	1.1	1.6	no	yes	Mouse, Rat	One 8 mer poorly conserved
388	*6030458C11Rik*	PF0489 protein C5orf22 homolog	-1.1	1.6	no	yes	Conserved	One 9 mer moderately conserved

Supplemental Table 3 (continued)

389	*Dmwd*	dystrophia myotonica WD repeat-containing	1.2	1.6	no	yes	Conserved	One 8 mer highly conserved
390	*Rnd1*	rho-related GTP-binding protein Rho6 precursor	1.0	1.6	no	yes	Conserved	One 8 mer highly conserved
391	*Arl5A*	ADP-ribosylation factor-like protein 5A	1.5	1.6	no	yes	Conserved	One 7 mer highly conserved
392	*Fgr*	tyrosine-protein kinase Fgr	1.3	1.6	no	yes	Conserved	One 8 mer highly conserved
393	*Ap1S2*	AP-1 complex subunit sigma-2	-1.1	1.5	no	yes	Mouse, Rat	One 7 mer, one 8 mer, another 7 mer all poorly conserved
394	*Plau*	Plasminogen activator, urokinase	1.3	1.5	no	yes	Conserved	One 8 mer moderately conserved,
395	*Hspbap1*	HSPB1-associated protein 1	1.1	1.5	no	yes	Mouse, Rat	One 9 mer, one 8 mer both poorly conserved

Supplemental Table 4: Analysis of exonic vs. intronic RNA-Seq reads

Shown are the ratios of the average double KO and triple KO exon and intron reads to the average WT exon and intron reads for each group of samples for the 385 transcripts that were up-regulated in the triple KO RNA-Seq dataset but not in the double KO dataset. We excluded 10 of the 395 transcripts from this analysis because of low read counts in some of the samples, leaving 395 evaluable transcripts. Shown also are the "ratios of ratios" for exon and intron reads. Fifty-two transcripts were found to have "ratios of ratios" greater than 1.5 (indicated in green). All the transcripts contained at least one potential TTP binding site 7-mer. Five additional transcripts were identified by subjective evaluation of expression patterns alone (indicated in red).

Gene Symbol	DKO/WT exon	TKO/WT exon	DKO/WT intron	TKO/WT intron	Ratio DKO exon ratio/DKO intron ratio	Ratio TKO exon ratio/TKO intron ratio
Apol11b	10.13	748.30	2.05	1003.13	4.94	0.75
Ltf	4.11	68.11	2.52	78.09	1.63	0.87
Gypa	1.62	43.20	1.14	103.69	1.42	0.42
Slfn4	1.34	33.46	1.30	47.53	1.03	0.70
Tmcc2	1.32	19.73	0.94	17.84	1.40	1.11
Tfrc*	0.94	15.24	0.65	3.75	1.45	**4.06**
Abcg4	1.17	34.26	0.81	47.30	1.44	0.72
Oas3	1.81	13.40	1.28	14.30	1.41	0.94
E2f8	1.14	10.74	0.71	13.77	1.61	0.78
Birc5	1.11	11.28	0.66	13.56	1.68	0.83
Cenpf	0.94	10.25	0.78	16.71	1.21	0.61
Sox6	1.39	33.96	1.09	47.97	1.28	0.71
Sgol1	0.86	10.76	0.80	11.74	1.08	0.92
Kif18b	1.25	9.85	0.61	9.96	2.05	0.99
Cdc6	1.20	9.39	0.61	8.22	1.97	1.14
Lmo2	1.25	1.63	0.92	1.46	1.35	1.12
Gpr146	0.92	1.26	0.73	1.25	1.26	1.01
Ccna2	1.11	9.12	0.67	13.96	1.66	0.65
Tmem56	1.03	23.40	1.93	21.75	0.53	1.08
Depdc1a	0.73	13.91	0.66	9.00	1.11	**1.55**
Clcn3	0.96	2.13	0.63	2.38	1.52	0.90
Anln	0.92	1.29	0.78	0.97	1.18	1.33
Kntc1	1.11	8.07	0.63	5.24	1.76	**1.54**
Ifi44	1.44	8.64	1.26	7.57	1.14	1.14
Ccne2	0.80	13.24	0.68	4.66	1.18	**2.84**
Ccnb1	0.99	8.02	0.86	10.19	1.15	0.79
Slc25a21	0.76	9.49	0.74	29.56	1.03	0.32
*Ncapg**	0.87	7.20	0.73	3.42	1.19	**2.11**
Prc1	0.95	7.48	0.79	3.75	1.20	**1.99**
Clspn	1.04	7.69	0.93	9.71	1.12	0.79
Ache	1.19	7.44	0.95	10.08	1.25	0.74
Chac2	1.01	7.32	0.66	4.43	1.53	**1.65**
Fam109b	0.72	7.90	0.50	7.72	1.44	1.02
Kif18a	0.69	7.15	0.64	5.39	1.08	1.33
C530008M17Rik	1.20	7.00	0.61	6.05	1.97	1.16
Nt5c3	1.11	5.42	0.77	4.19	1.44	1.29
Nuf2	1.13	7.14	0.93	9.56	1.22	0.75
Pif1	1.07	7.39	0.89	8.78	1.20	0.84
Odf2	1.14	1.31	0.82	1.34	1.39	0.98
Cenpe	0.86	6.81	0.76	6.98	1.13	0.98
Gda	1.10	6.82	0.74	19.27	1.49	0.35
Kif14	0.98	9.47	0.62	12.29	1.58	0.77
Cenpi	0.82	6.19	0.83	5.56	0.99	1.11
C5ar1	1.13	6.64	0.84	14.24	1.35	0.47
Bub1	0.77	6.82	0.73	6.76	1.05	1.01
Lilra5	2.74	5.74	2.05	4.67	1.34	1.23
Kifc1	1.19	6.12	0.65	6.12	1.83	1.00
Slc14A1	0.90	1.45	0.67	0.62	1.35	**2.34**
Nek2	1.18	5.80	0.77	10.95	1.53	0.53
Mmp9	1.25	5.68	1.19	9.56	1.05	0.59
Kif2c	1.08	5.60	0.65	7.39	1.66	0.76
Ppp1r15a	1.09	5.43	1.45	3.97	0.75	1.37
Hmgb2*	0.95	5.38	0.90	4.14	1.06	1.30
Pip5K1B	1.17	3.39	0.74	5.55	1.58	0.61
Mfsd2b	1.08	5.22	0.63	6.09	1.71	0.86
Usp18	1.40	4.04	0.94	1.63	1.49	**2.48**
Tfdp2	1.03	4.48	0.61	5.04	1.69	0.89
March8	0.84	5.01	0.69	13.35	1.22	0.38
Slc25a37	1.13	4.96	0.87	3.61	1.30	1.37
C330027C09Rik	0.82	4.93	0.73	3.58	1.12	1.38
Tjap1	1.12	0.96	0.97	1.36	1.16	0.71
Xpo7	1.02	4.89	0.64	7.48	2.48	0.65
Mpp2	1.06	4.74	0.76	7.15	1.39	0.66
Slc16a10	1.02	4.75	0.58	5.40	1.76	0.88
4930430F08Rik	0.93	4.58	0.89	2.84	1.05	**1.61**
Ncapg2	0.72	4.71	0.40	2.81	1.80	**1.68**
Slc2a4	0.88	22.02	0.46	66.55	1.91	0.33
Ube2t	0.88	4.64	0.92	4.06	0.96	1.14
Iqgap3	0.87	4.55	0.58	5.33	1.50	0.85
Pask	0.95	4.54	0.73	5.07	1.30	0.90
Ifit1	1.13	4.99	0.14	12.42	7.94	0.40
Sgol2	0.84	5.54	0.62	6.23	1.35	0.89
Cep76*	0.99	4.50	0.79	2.63	1.25	**1.71**
Troap	0.95	6.39	0.62	7.61	1.53	0.84
Cep290	0.98	4.64	0.95	5.39	1.03	0.86
Ssx2ip	0.98	4.37	0.59	4.47	1.66	0.98
E2f2	1.21	4.26	0.89	3.97	1.36	1.07
Emilin2	0.98	4.86	0.58	13.11	1.69	0.37
Whrn	7.43	4.51	7.61	7.25	0.98	0.62
Sgk3	0.98	1.50	0.77	1.57	1.28	0.96
E2f7	1.22	7.97	0.87	8.13	1.40	0.98
2810417H13Rik	1.18	4.10	0.88	3.38	1.35	1.21
Bard1	0.94	4.09	0.49	4.67	1.92	0.88
Mastl	0.68	5.03	0.65	4.02	1.05	1.25
St3gal5	1.20	4.55	0.60	4.73	2.00	0.96
Bcl2l1	1.42	4.13	0.68	5.30	2.09	0.78
Metap2	0.95	3.91	0.89	2.91	1.07	1.34
Ccrn4l	0.88	3.94	0.38	2.44	2.32	**1.61**
Cpeb3	1.08	4.16	0.70	8.74	1.54	0.48
Cd24a	1.10	4.05	0.89	3.14	1.24	1.29
Acp1	0.94	3.67	0.81	3.31	1.16	1.11
Dusp8	0.88	7.10	1.00	9.11	0.88	0.78
Il1rl1	0.81	4.20	0.69	4.11	1.17	1.02
*Tmem120b**	0.95	3.24	0.72	1.90	1.32	**1.71**
Svip	0.81	3.81	0.82	4.42	0.99	0.86
Nlrp12	0.81	6.53	0.58	10.45	1.39	0.62
Zwilch	0.84	3.65	0.58	3.65	1.45	1.00
*Pi4k2b**	0.82	3.44	0.68	1.80	1.21	**1.91**
Brip1	0.86	3.54	0.64	5.37	1.34	0.66

Ranbp10	0.96	3.57	0.69	3.49	1.39	1.02
Cenpl	0.94	3.78	0.66	3.56	1.42	1.06
Hagh	1.05	3.36	0.87	2.31	1.21	1.45
Mad2l1	0.92	3.56	0.70	2.33	1.31	**1.53**
Ccdc34	1.06	3.37	0.70	2.77	1.51	1.22
5730508B09Rik	0.89	3.47	0.55	2.72	1.62	1.28
Klra2	0.95	3.85	0.63	4.56	1.51	0.84
*Dek**	0.89	3.41	0.65	1.79	1.37	**1.91**
Mxd1	1.00	3.49	0.72	2.99	1.39	1.17
Eif2Ak2	0.96	3.49	0.76	5.28	1.27	0.66
Plk4	0.86	3.27	0.67	1.95	1.28	**1.68**
Gbp10	0.83	5.53	0.62	6.43	1.35	0.86
Gadd45a	1.15	3.14	0.97	2.56	1.19	1.23
Gcnt2	0.93	2.49	0.75	2.36	1.24	1.06
Slc22a23	0.93	3.11	0.57	6.69	1.63	0.46
Chtf18	1.13	3.04	0.79	2.80	1.43	1.09
Cks1b	1.07	3.05	0.99	3.35	1.08	0.91
Otub2	0.97	2.57	0.81	1.66	1.20	**1.55**
Igj	1.05	3.07	0.92	2.97	1.14	1.03
E2f1	1.03	2.86	0.93	3.47	1.11	0.82
Mcm2	1.21	2.94	0.87	3.75	1.39	0.78
Ccrl2	1.30	2.86	0.64	3.33	2.03	0.86
Xk	1.13	2.95	0.64	2.03	1.75	1.46
Clec4a2	0.95	2.84	0.73	2.33	1.30	1.22
Mtfr1	1.05	2.82	0.79	1.20	1.33	**2.35**
Fam132B	1.25	20.22	1.18	10.21	1.06	**1.98**
Asb1	0.92	2.93	0.80	3.27	1.15	0.90
Cmas*	1.21	2.63	0.80	1.38	1.51	**1.91**
Vcan	0.72	5.57	0.48	4.51	1.50	1.23
Arhgap19	1.11	3.00	0.80	3.17	1.39	0.95
Oaf	0.96	2.87	0.59	3.09	1.63	0.93
Gch1	0.97	3.05	0.97	2.94	0.99	1.04
Lbp	1.09	4.24	0.80	4.49	1.37	0.94
Il1b	1.09	2.91	0.95	3.31	1.15	0.88
Trak2	0.90	2.65	0.64	2.74	1.41	0.97
Sgms2	0.94	2.64	0.47	4.04	2.00	0.65
P2ry1	1.18	2.69	0.91	3.12	1.30	0.86
Psmc3ip	1.00	2.40	0.87	1.80	1.15	1.33
Net1	0.98	1.27	0.75	1.96	1.31	0.65
Mcm5	1.28	2.50	0.78	2.43	1.64	1.03
Gas2l3	0.74	2.41	0.37	3.27	2.00	0.74
Scoc	0.93	2.46	1.13	2.64	0.82	0.93
Arl4A	0.87	2.60	0.64	3.18	1.36	0.82
Cd300lf	1.05	2.47	0.94	2.50	1.12	0.99
Minpp1	1.05	2.49	0.62	2.51	1.69	0.99
Fut1	1.26	9.64	1.00	8.91	1.26	1.08
March5	0.98	2.08	0.72	1.55	1.36	1.34
Fbxo48	0.83	2.37	0.96	2.14	0.87	1.11
Piga	0.93	2.40	0.79	1.82	1.18	1.32
Usp46	0.90	2.45	0.50	4.34	1.80	0.56
Reep4	1.77	2.27	1.63	2.08	1.09	1.09
Dck	1.07	2.32	0.65	1.65	1.64	1.41
Usp32	0.88	2.27	0.56	2.76	1.58	0.82
Hace1	0.85	2.30	0.70	2.06	1.21	1.12
Sh2D1B1	1.27	2.41	0.91	2.61	1.40	0.93
Gsr	0.83	2.21	0.49	3.12	1.69	0.71
Ifih1	1.03	2.27	0.60	2.60	1.70	0.87
Casp4	0.93	2.23	0.90	1.80	1.03	1.24
Vopp1	1.11	2.32	0.95	5.96	1.17	0.39
Ccr2	0.94	2.29	0.76	2.05	1.24	1.12
Gca	0.89	2.22	0.67	2.32	1.33	0.96
Klhl12	1.15	2.17	0.82	2.49	1.40	0.87
Rbbp8	0.86	2.27	0.75	1.45	1.14	**1.57**
Parvb	1.21	2.08	0.87	3.40	1.39	0.61
Suv39H2	0.71	1.65	0.78	1.07	0.91	**1.55**
Atad2	0.94	2.13	0.63	2.04	1.48	1.04
Apoo	0.88	1.82	0.68	1.18	1.29	**1.55**
Tarsl2*	0.84	2.06	0.59	1.56	1.42	1.32
Mfsd9	0.96	2.14	0.81	7.61	1.19	0.28
Tnfsf14	1.28	2.17	1.07	2.21	1.20	0.98
B4galt6	1.11	2.12	0.78	3.06	1.42	0.69
Ncapd3	0.82	2.07	0.71	2.12	1.15	0.98
Brpf3	0.95	2.15	0.74	2.84	1.28	0.76
Sass6	0.90	2.00	0.71	1.21	1.26	**1.65**
Cdkn2d*	1.13	2.06	0.92	1.57	1.23	1.31
Mx1	0.87	2.06	0.76	2.09	1.15	0.99
Neu3	0.95	2.08	0.65	1.96	1.46	1.06
Rhou	1.31	5.16	0.66	4.22	1.99	1.22
Creg1	0.97	2.09	0.80	3.09	1.21	0.68
Agfg2	1.16	1.97	0.70	2.13	1.65	0.93
Xcl1	1.02	1.85	0.74	2.02	1.38	0.92
Zfp367	0.82	2.04	0.60	1.58	1.35	1.29
Evi5	0.77	2.08	0.58	3.78	1.33	0.55
Timm8B	0.84	1.95	1.64	0.97	0.51	**2.02**
Lrrc39	0.91	1.62	0.73	1.15	1.24	1.42
Arhgap11A	1.00	1.99	0.82	1.92	1.22	1.04
Apold1	1.11	2.07	2.00	1.87	0.55	1.11
Rgs18	0.89	2.02	0.68	1.25	1.30	**1.62**
Pdgfc	0.92	2.07	0.72	3.03	1.28	0.68
Endod1	0.93	2.02	0.65	2.13	1.43	0.95
Cox7A2	0.84	1.89	0.83	0.92	1.01	**2.04**
Slc11A2	1.19	2.07	0.84	2.07	1.41	1.00
Pls1	1.32	1.86	0.71	1.83	1.86	1.02
Thbs1	1.51	1.88	0.41	2.44	3.68	0.77
Slc16a3	1.14	2.20	0.87	2.48	1.31	0.89
Cln8	0.91	1.95	0.75	2.11	1.20	0.93
Pdk1	1.83	2.10	1.68	2.11	1.09	1.00
Atp8b4	1.02	1.93	0.65	2.01	1.57	0.96
Mthfd2	1.22	1.91	1.03	1.56	1.18	1.22
Deb1*	0.78	1.65	1.08	1.11	0.72	1.49
Tab3	0.92	1.92	0.61	2.14	1.52	0.90
Pla2g12a	0.85	1.82	0.49	1.01	1.73	**1.80**
Katnal1	0.92	1.89	0.74	2.00	1.24	0.94
Ugt1A7C	0.92	2.37	0.60	4.42	1.54	0.54
Psme3	1.17	1.89	0.87	1.93	1.34	0.98
Socs3	0.99	1.92	0.64	1.47	1.55	1.31
Itsn1	0.96	1.68	0.58	2.50	1.66	0.67

Stat1	1.12	1.76	0.88	2.30	1.28	0.77
Ppp2R5B	0.97	1.82	0.92	1.71	1.06	1.06
Nudt12	0.79	1.92	0.62	2.21	1.27	0.87
Cycs	0.90	1.86	1.04	1.02	0.86	**1.83**
Adpgk	0.98	1.89	0.79	2.16	1.24	0.88
Pfdn4	0.92	1.79	0.95	0.86	0.96	**2.07**
Nlrc5	0.88	1.94	0.77	2.32	1.15	0.84
Pilra	0.94	1.88	0.73	2.40	1.29	0.78
Ehbp1L1	1.09	1.80	0.81	2.18	1.35	0.83
Plscr1	0.90	1.83	0.66	1.79	1.36	1.02
Atg4D	1.04	1.44	0.81	1.32	1.29	1.09
Setd8	0.99	1.83	0.68	2.19	1.46	0.84
C1Galt1C1	0.86	1.86	0.91	0.90	0.94	**2.06**
Spon1	1.23	1.85	0.93	3.31	1.32	0.56
Rasgrp4	1.11	1.63	0.91	1.98	1.22	0.82
Hs6St1	1.20	1.82	0.65	1.95	1.83	0.93
2700097O09Rik	0.91	1.84	0.76	1.16	1.20	**1.59**
Fosl2	1.23	1.90	0.85	1.96	1.45	0.97
Gpr88	2.01	1.76	1.00	1.41	2.01	1.25
Kcnj2*	0.93	1.82	0.55	1.08	1.69	**1.69**
Kctd7	1.08	1.75	0.50	1.74	2.16	1.01
Galnt3	1.02	1.75	0.65	2.22	1.57	0.79
Mafg	0.92	1.76	0.82	1.66	1.13	1.07
Cbx5	0.91	1.94	0.51	1.83	1.80	1.06
Mrpl20	0.78	1.68	0.89	1.02	0.88	**1.65**
Mrpl33	0.92	1.85	0.85	1.19	1.09	**1.56**
Znhit3	0.70	1.57	0.93	0.93	0.75	**1.69**
Olfr1033	2.70	10.34	7.01	19.65	0.38	0.53
Map4K5	0.88	1.63	0.58	1.44	1.52	1.14
Rnf11	1.04	1.73	0.55	1.99	1.88	0.87
Yod1	0.76	1.73	0.55	1.29	1.38	1.34
Mospd1	0.88	1.65	0.67	1.52	1.31	1.09
Mri1	1.84	1.77	3.06	5.27	0.60	0.34
Ndufs4	0.88	1.83	0.71	0.86	1.24	**2.12**
Tmem106A	1.11	1.72	0.87	2.14	1.27	0.80
Ier3*	1.03	1.59	1.50	2.00	0.69	0.80
Acer3	0.77	1.71	0.54	1.85	1.43	0.93
Tmem194	1.05	1.73	0.50	1.39	2.11	1.25
Rpgrip1L	1.10	1.70	0.93	1.98	1.18	0.86
1600002H07Rik	0.97	1.65	0.77	1.79	1.26	0.92
Tbc1D24	0.68	1.63	0.65	1.70	1.05	0.96
Bcorl1	1.29	1.66	0.56	1.77	2.33	0.94
Prdx3	1.03	1.65	0.79	1.14	1.29	1.45
Pot1B	1.00	1.97	1.03	3.25	0.98	0.61
Rnf149	0.95	1.64	0.66	1.62	1.44	1.01
Ahi1	1.06	1.56	0.73	1.50	1.46	1.04
Nhsl2*	0.97	1.69	1.06	0.95	0.92	**1.78**
Relt	1.01	1.65	0.85	1.78	1.18	0.93
Nlrp3	1.12	1.65	0.73	1.76	1.53	0.94
Stx11	1.06	1.72	0.66	1.79	1.60	0.96
Magohb	1.03	1.44	0.73	1.16	1.41	1.24
Ncr1	1.04	1.67	1.29	2.62	0.80	0.64
Mier3	0.97	1.62	0.62	1.36	1.57	1.20
Cish	1.18	1.61	0.82	1.42	1.44	1.13
Yipf4	1.10	1.59	0.78	1.32	1.41	1.20
Slc25A17	1.22	1.46	1.20	1.53	1.01	0.95
Ulk1	0.96	1.54	0.76	1.78	1.27	0.87
Picalm	0.92	1.67	0.66	1.73	1.39	0.97
Eif4A1	0.92	1.27	0.89	0.99	1.03	1.28
Nudt5	0.89	1.48	0.80	1.12	1.11	1.31
Cops2	0.83	1.56	0.75	1.00	1.12	**1.56**
Sept3	0.63	1.66	0.57	2.24	1.10	0.74
Celsr1	1.19	1.65	1.16	3.01	1.03	0.55
Eef1E1	1.03	1.55	0.73	1.07	1.41	1.46
Gm8369	1.40	1.52	1.10	1.74	1.28	0.88
Agap1	0.96	1.60	0.74	2.41	1.29	0.66
Asap3	1.56	1.47	0.69	1.35	2.26	1.09
Neto2	0.67	1.57	0.76	2.11	0.88	0.74
Arl6Ip6	0.99	1.58	0.92	1.83	1.08	0.86
Plod2	0.98	1.49	0.72	1.25	1.37	1.19
Slfn5	1.03	1.56	0.73	2.47	1.41	0.63
Usp1	0.92	1.56	0.75	1.21	1.22	1.29
Med30	1.01	1.43	0.65	0.68	1.56	**2.10**
Klf11	1.11	1.58	0.69	2.48	1.60	0.64
Il1A	0.84	1.51	0.81	1.37	1.05	1.10
Fundc2	0.91	1.61	0.77	1.33	1.18	1.21
Cbwd1	0.99	1.63	0.85	1.42	1.17	1.15
Rbm47	1.11	1.55	0.73	1.92	1.51	0.81
Tmx4	0.90	1.53	0.65	2.22	1.38	0.69
Palb2	0.93	1.62	0.73	1.69	1.27	0.96
Tmtc4	1.40	1.53	0.91	1.49	1.55	1.03
Mrpl41	0.91	1.52	0.98	0.92	0.92	**1.66**
Gdpd1	1.06	1.49	0.80	2.16	1.33	0.69
Tbx21	1.70	1.60	0.81	2.16	2.10	0.74
Glipr2	0.99	1.56	0.88	1.57	1.13	0.99
Uchl5	1.05	1.46	0.78	1.11	1.35	1.31
Ghitm	1.06	1.82	0.58	0.93	1.82	**1.96**
Ell2	1.03	1.51	0.69	1.82	1.50	0.83
Slc30A9	0.86	1.53	0.77	1.78	1.11	0.86
H2-T24	0.93	1.53	0.75	1.38	1.24	1.11
Ctsb	1.25	1.49	0.81	2.01	1.55	0.74
Dgkg	1.00	2.53	0.61	2.81	1.63	0.90
Tmem215	1.61	1.56	1.08	3.50	1.48	0.44
Tinagl1	1.30	1.45	0.92	2.15	1.41	0.67
Dnajc6	0.64	1.12	0.45	1.42	1.43	0.79
Dgat2	0.64	1.49	0.57	1.77	1.12	0.84
Cpd	0.85	1.48	0.55	2.27	1.55	0.65
Ran	1.18	1.46	1.02	1.39	1.16	1.05
Tcf7L2	1.02	1.43	0.58	1.90	1.75	0.75
Xkr5	0.76	3.31	0.38	3.66	1.98	0.90
Daam1	0.89	1.48	0.56	1.62	1.59	0.91
Cd300A	1.07	1.47	0.78	1.72	1.38	0.85
Snrpb2	0.89	1.44	0.84	0.84	1.06	**1.71**
Dmxl2	0.73	1.47	0.61	1.87	1.20	0.79
Stk3	0.88	1.53	0.70	1.89	1.26	0.81
Slc22A15	0.79	1.42	0.65	2.20	1.22	0.65
Zfand6	0.97	1.41	0.77	1.05	1.25	1.35

Timm17A	1.08	1.62	0.77	1.10	1.40	1.48
Cox11	0.88	1.48	0.68	1.36	1.29	1.09
Usp14	0.98	1.44	0.74	1.29	1.32	1.12
Myo19	0.90	1.43	0.78	1.36	1.15	1.05
Immp1L	0.88	1.39	0.72	0.92	1.23	**1.51**
Usp25	1.08	1.45	0.73	1.95	1.48	0.74
Mpl	1.83	1.62	0.90	2.51	2.03	0.64
Arhgef12	0.92	1.44	0.60	2.15	1.54	0.67
Il12B	0.58	1.43	0.41	0.84	1.42	**1.72**
Kif1A	1.66	2.03	0.84	3.24	1.97	0.63
Mrpl51	1.10	1.51	1.05	1.47	1.04	1.03
Tmtc3	0.74	1.43	0.50	0.96	1.50	1.48
Vbp1	0.97	1.43	0.64	0.91	1.50	**1.57**
Chac1	1.30	8.79	1.00	7.75	1.30	1.13
Mybl1	0.67	1.55	0.57	1.46	1.17	1.06
Itga5	0.94	1.42	0.50	2.01	1.90	0.71
Trim37	0.98	1.51	0.83	0.71	1.18	**2.13**
Ubiad1	1.82	1.45	0.93	1.47	1.96	0.99
Srm	1.24	1.40	0.71	1.14	1.74	1.23
Aa986860	1.02	3.08	0.67	3.66	1.52	0.84
Ccdc62	1.11	1.57	0.90	1.38	1.23	1.14
Gm13154	5.24	8.74	5.71	7.63	0.92	1.15
Tuft1	1.02	1.39	0.72	1.50	1.42	0.93
Eif5	0.92	1.47	0.79	1.29	1.16	1.14
Ppp1r3b	1.11	1.45	1.05	1.75	1.06	0.83
Ncoa7	0.83	1.57	0.69	1.63	1.19	0.96
Gas2	0.91	1.35	0.52	1.05	1.75	1.29
Eif2S1	0.87	1.42	0.73	0.92	1.20	**1.55**
Dcaf12	1.22	1.40	0.77	1.21	1.58	1.16
Fgl2	0.83	1.44	0.70	2.85	1.17	0.50
Sort1	0.97	1.38	0.74	1.35	1.31	1.02
Neurl1A	1.99	2.85	1.56	4.94	1.27	0.58
Stxbp4	1.13	1.41	0.71	1.63	1.60	0.87
Pkn2	0.88	1.37	0.63	1.42	1.40	0.96
Armc9	1.09	1.31	0.97	0.73	1.13	**1.79**
Vcam1	0.79	1.40	0.61	1.59	1.30	0.88
Rnf139	0.91	1.43	0.60	1.42	1.51	1.01
Nup35	0.74	1.36	0.69	1.41	1.08	0.97
Fbxo42	1.08	1.37	0.57	1.42	1.88	0.97
Gtf2A2	0.98	1.21	0.81	0.98	1.22	1.23
Tubb3	0.45	5.01	1.09	5.17	0.42	0.97
Coro2B	1.34	1.44	3.25	18.87	0.41	0.08
Gatm	0.92	1.36	0.60	1.48	1.53	0.92
Cox17	1.12	1.27	0.94	0.86	1.19	1.48
Snrnp27	0.89	1.39	0.84	1.02	1.07	1.37
Rad21	1.15	1.36	0.75	1.49	1.52	0.91
Synj1	0.90	1.32	0.57	1.62	1.57	0.82
Nudcd1	0.88	1.42	0.66	1.10	1.33	1.30
Cbx3	1.00	1.37	0.74	1.12	1.36	1.22
Cdca4	1.02	1.43	0.76	1.19	1.34	1.20
Il15ra	0.74	1.39	0.65	1.48	1.14	0.94
Mfap3L	0.82	1.38	0.92	1.19	0.89	1.16
Zmynd19	1.01	1.39	0.72	1.30	1.40	1.08
Samd3	1.08	1.49	0.78	1.70	1.38	0.88
Myef2	0.88	1.32	0.70	1.13	1.25	1.16
Trpc6	0.90	1.66	1.03	1.54	0.87	1.08
S1Pr5	1.05	1.54	0.67	1.82	1.56	0.85
Cdk2	1.10	1.31	0.89	1.18	1.23	1.11
Wdr26	0.89	1.37	0.71	1.43	1.26	0.95
Atp6V0E	0.98	1.38	0.76	0.94	1.30	1.47
Mrps14	1.01	1.32	0.46	0.15	2.18	**8.93**
Riok3	1.02	1.39	0.75	1.26	1.36	1.11
Cttnbp2	1.07	1.41	0.89	2.38	1.21	0.59
Sh3Glb1	1.04	1.37	0.70	1.05	1.50	1.30
6030458C11Rik	0.88	1.28	0.73	1.47	1.21	0.87
Dmwd	1.06	1.34	0.83	1.28	1.28	1.05
Rnd1	0.81	1.75	0.85	2.20	0.95	0.80
Arl5A	1.42	1.41	1.21	1.76	1.18	0.80
Fgr	1.11	1.35	0.60	1.47	1.87	0.92
Ap1S2	0.88	1.33	0.58	1.23	1.50	1.08
Plau	1.11	1.37	0.69	2.10	1.60	0.65
Hspbap1	0.96	1.27	0.72	1.88	1.33	0.68

Supplemental Table 5: Cell subtype enrichment in DKO and TKO spleens by the DCQ method.

Shown are the cell subtypes that were significantly enriched or depleted in the TKO or DKO spleens relative to their WT counterparts, as determined by the DCQ method (1). Cell type abbreviations are as in (1). The p values of the comparisons are shown, along with the average enrichment, cell type specified, and original tissue source of the specified cell type, along with the antibodies that identify that cell type. See the text for further details.

Subtypes in TKO	P value	Direction	Average enrichment score	Cell types	Tissue source	Ab reactivity
GN.URAC.PC	0	up	0.05	Granulocyte	Peritoneal Cavity (PC)	CD11b+ Ly6-G+
MF.II+480LO.PC	0	up	0.05	Macrophage	Peritoneal Cavity (PC)	B220- F4/80lo CD115hi MHCII+
GN.BL	0	up	0.04	Granulocyte	Blood (BL)	CD11b+ Ly6-G+
GN.THIO.PC	0.02	up	0.03	Granulocyte	Peritoneal Cavity (PC)	CD11b+ Ly6-G+
GN.BM	0.02	up	0.03	Granulocyte	Bone marrow (BM)	CD11b+ Ly6-G+ 7/4hi
GN.ARTH.SYNF	0.03	up	0.03	Granulocyte	Bone marrow (BM)	CD11b+ Ly6-G+
DC.103+11B+.SI	0.03	up	0.03	Dendritic cell	Small intestine (SI)	PI- CD45+ MHCII+ CD11chi CD103+ CD11b+
GN.ARTH.BM	0.04	up	0.03	Granulocyte	Bone marrow (BM)	CD11b+ Ly6-G+
SC.MEP.BM	0.01	up	0.02	Stem cell	Bone marrow (BM)	Lin- IL7R- Sca1- ckit+ FcgRloCD34-
NK.H+.MCMV7.SP	0.04	up	0.02	NK cell	Spleen (Sp)	CD3- NK1.1+ Ly49H+
MO.6C+II-.BM	0.04	up	0.02	Monocyte	Bone marrow (BM)	B220- CD3- CD115+ Ly-6C+ MHCII-
T.4SP24-.TH	0.03	down	-0.01	αβ T cell	Thymus (Th)	CD4+ CD8- TCRhi CD24-/lo
T.4MEM.LN	0.03	down	-0.01	αβ T cell	Subcutaneous LN (SLN)	CD4+ CD8- TCR+ CD25- CD44hi CD122lo
T.DPSM.TH	0	down	-0.02	αβ T cell	Thymus (Th)	CD4+ CD8+ TCR-/lo FSClo
T.4SP69+.TH	0	down	-0.02	αβ T cell	Thymus (Th)	CD4+ CD8- TCRhi CD69+
T.4SP24INT.TH	0	down	-0.02	αβ T cell	Thymus (Th)	CD4- CD8+ TCRhi CD24int
T.4NVE.MLN	0.01	down	-0.02	αβ T cell	Mesenteric LN (MLN)	CD4+ CD8- TCR+ CD25- CD62Lhi CD44lo
B.FRE.BM	0.02	down	-0.02	B cell	Bone marrow (BM)	AA4+ IgM+ CD19+ HSA+
T.DP.TH	0.02	down	-0.02	αβ T cell	Thymus (Th)	CD4+ CD8+ TCR-/lo CD69-
T.DP69+.TH	0	down	-0.03	αβ T cell	Thymus (Th)	CD4+ CD8+ TCRlo/int CD69+
DC.IIHILANG-103-11BLO.SLN	0	down	-0.03	Dendritic cell	Skin draining lymph nodes (SDLN)	CD11c+ MHCIIhi langerin- CD103- CD11b
T.4NVE.PP	0.02	down	-0.03	αβ T cell	Peyer's patches (PP)	CD4+ CD8- TCR+ CD25- CD62Lhi CD44lo
T.4+8INT.TH	0	down	-0.04	αβ T cell	Thymus (Th)	CD4+ CD8int TCRhi CD69
T.8NVE.PP	0	down	-0.04	αβ T cell	Peyer's patches (PP)	CD4- CD8+ TCR+ CD25- CD62Lhi CD44lo
Subtypes in DKO	**P value**	**Direction**	**Average enrichment score**	**Cell types**	**Tissue source**	**Ab reactivity**
MO.6C-II-.BM	0	up	0.05	Monocyte	Bone marrow (BM)	B220- CD3- CD115+ Ly-6C- MHCII- CD43+
EP.MECHI.TH	0	up	0.04	Stromal	Thymus (Th)	CD45- EpCAM+ Ly51- MHCIIhi
TGD.SP	0.02	down	-0.02	γδ T cell	Spleen (Sp)	TCRd+ CD3E+ CD4- CD8-
MF.MEDL.SLN	0.03	down	-0.02	Macrophage	Skin draining lymph nodes (SDLN)	CD11b+ B220- CD90- SiglecF- CD103- Ly6G- CD169+ CD11c+ F4/80+
DC.8+.TH	0.03	down	-0.02	Dendritic cell	Thymus (Th)	MHCII+ CD11c+ CD8a+ CD4- CD11b-

1. Altboum Z*, et al.* (2014) Digital cell quantification identifies global immune cell dynamics during influenza infection. *Molecular systems biology* 10:720.